

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: April 6, 2006, 08:54:46 ; Search time 37.1186 Seconds  
(without alignments)  
59.186 Million cell updates/sec

Title: US-10-089-500-3

Perfect score: 28

Sequence: 1 HYAMS 5

Scoring table: BLOSUM62  
Gapol 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database : A\_Geneseq 21.\*  
1: Genesep1980s.\*  
2: Genesep1990s.\*  
3: Genesep2000s.\*  
4: Genesep2001s.\*  
5: Genesep2002s.\*  
6: Genesep2003as.\*  
7: Genesep2003bs.\*  
8: Genesep2004s.\*  
9: Genesep2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	28	100.0	5	4 AAB81979	AAB81979 Gangliosid
2	28	100.0	5	6 ABU11004	ABU11004 Modified
3	28	100.0	5	9 ADZ57810	ADZ57810 Gangliosid
4	28	100.0	119	3 AAB14979	AAB14979 Staphyloc
5	28	100.0	119	4 AAB81985	AAB81985 Gangliosid
6	28	100.0	119	4 AAB81989	AAB81989 Gangliosid
7	28	100.0	119	6 ABU11012	ABU11012 Modified
8	28	100.0	119	6 ABU11010	ABU11010 Modified
9	28	100.0	119	6 ABR83239	ABR83239 S. aureus
10	28	100.0	119	6 ABR83238	ABR83238 S. aureus
11	28	100.0	119	6 ABU16272	ABU16272 Protein e
12	28	100.0	119	6 ABU43645	ABU43645 Protein e
13	28	100.0	119	6 ABW71799	ABW71799 Staphyloc
14	28	100.0	119	9 ADW94782	ADW94782 Profilifera
15	28	100.0	119	9 ADZ57816	ADZ57816 Gangliosid
16	28	100.0	119	9 ADZ57818	ADZ57818 Gangliosid
17	28	100.0	119	9 ADZ57821	ADZ57821 Gangliosid
18	28	100.0	130	2 AAR33256	AAR33256 Rat immun
19	28	100.0	130	2 AAR53341	AAR53341 L c
20	28	100.0	130	2 AAY28369	AAY28369 PKM641 HA
21	28	100.0	130	3 AAB01627	AAB01627 Murine im
22	28	100.0	138	4 AAB81977	AAB81977 Gangliosid
23	28	100.0	138	6 ABU11002	ABU11002 Modified
24	28	100.0	156	4 ABG28979	ABG28979 Novel hum

25	28	100.0	280	4 AAB96839	AAB96839 Putative
26	28	100.0	280	8 ADN46873	ADN46873 Thermococ
27	28	100.0	412	8 ADS21217	ADS21217 Bacteri
28	28	100.0	424	8 ADS64477	ADS64477 Pseudomon
29	28	100.0	496	9 ABM91663	ABM91663 M. xanthu
30	28	100.0	514	7 ABO71592	ABO71592 Pseudomon
31	28	100.0	582	4 AAB81987	AAB81987 Gangliosid
32	28	100.0	582	4 AAB81991	AAB81991 Gangliosid
33	28	100.0	1268	4 AAM79111	AAM79111 Human pro
34	28	100.0	1268	9 ADX06569	ADX06569 Cyclin-de
35	28	100.0	1270	4 AAM80095	AAM80095 Human pro
36	28	100.0	1669	4 ABB63980	ABB63980 Drosophi
37	25	89.3	14	4 AAM97232	AAM97232 Human pap
38	25	89.3	50	3 AAB34620	AAB34620 Human sec
39	25	89.3	76	4 AAO03185	AAO03185 Human pol
40	25	89.3	108	4 AAO03855	AAO03855 Human pol
41	25	89.3	113	6 ADB07666	ADB07666 Alloiococ
42	25	89.3	116	4 AAG81907	AAG81907 S. epider
43	25	89.3	126	6 ABU49557	ABU49557 Protein e
44	25	89.3	133	6 ADB07674	ADB07674 Alloiococ
45	25	89.3	134	6 ADB07668	ADB07668 Alloiococ
46	25	89.3	146	4 AAO02622	AAO02622 Human pol
47	25	89.3	150	4 AAU17373	AAU17373 Novel sig
48	25	89.3	150	7 ADB94081	ADB94081 Human nov
49	25	89.3	164	4 ABG21786	ABG21786 Novel hum
50	25	89.3	180	5 AAG66027	AAG66027 Ryk prote
51	25	89.3	181	5 AAG66026	AAG66026 Ryk prote
52	25	89.3	191	5 AAG66025	AAG66025 Ryk prote
53	25	89.3	204	5 AAG66034	AAG66034 Human Ryk
54	25	89.3	214	6 ADB10122	ADB10122 Alloiococ
55	25	89.3	215	6 ADB10120	ADB10120 Alloiococ
56	25	89.3	218	5 AAG66032	AAG66032 Human Ryk
57	25	89.3	221	5 ABG93086	ABG93086 S. cerevi
58	25	89.3	236	4 ABB52808	ABB52808 Escherich
59	25	89.3	247	7 ADM26780	ADM26780 Hyperther
60	25	89.3	259	4 AAU27699	AAU27699 Fruit fly
61	25	89.3	291	7 ABM87524	ABM87524 Rice abio
62	25	89.3	308	4 AAG81989	AAG81989 S. epider
63	25	89.3	308	4 AAG82806	AAG82806 S. epider
64	25	89.3	317	5 ABB57333	ABB57333 Mouse isc
65	25	89.3	318	5 ABP39007	ABP39007 Staphyloc
66	25	89.3	318	6 ABW71334	ABW71334 Staphyloc
67	25	89.3	318	8 ADS06263	ADS06263 Staphyloc
68	25	89.3	322	4 AAU18370	AAU18370 Human end
69	25	89.3	332	6 ABM69527	ABM69527 Photorhab
70	25	89.3	334	8 ADT66645	ADT66645 Murine ch
71	25	89.3	334	9 ABB38323	ABB38323 L. pneumo
72	25	89.3	352	4 AAG98978	AAG98978 E. coli g
73	25	89.3	352	6 ABU47907	ABU47907 Protein e
74	25	89.3	352	6 ABU45103	ABU45103 Protein e
75	25	89.3	352	6 ABU47160	ABU47160 Protein e
76	25	89.3	352	6 ABU28161	ABU28161 Protein e
77	25	89.3	352	6 ABU14794	ABU14794 Protein e
78	25	89.3	353	6 ABU44762	ABU44762 Protein e
79	25	89.3	354	6 ABU41202	ABU41202 Protein e
80	25	89.3	356	6 ABU31599	ABU31599 Protein e
81	25	89.3	357	9 ABB37414	ABB37414 L. pneumo
82	25	89.3	358	6 ABU27760	ABU27760 Protein e
83	25	89.3	359	6 ABU48025	ABU48025 Protein e
84	25	89.3	359	7 ADF05146	ADF05146 Bacteri
85	25	89.3	361	6 ABU14927	ABU14927 Protein e
86	25	89.3	367	6 ABR42680	ABR42680 Pseudomon
87	25	89.3	367	6 ABU38740	ABU38740 Protein e
88	25	89.3	371	5 AAB16516	AAB16516 Rice caff
89	25	89.3	371	7 ADI29686	ADI29686 Rice caff
90	25	89.3	371	8 ADJ96496	ADJ96496 Rice caff
91	25	89.3	406	5 AAY33266	AAY33266 E. coli b
92	25	89.3	408	5 AAG66033	AAG66033 Human Ryk
93	25	89.3	410	7 ABO63561	ABO63561 Klebsiell
94	25	89.3	414	5 AAG66031	AAG66031 Human Ryk
95	25	89.3	439	7 ADB74299	ADB74299 Mycobacte
96	25	89.3	440	7 ADF07894	ADF07894 Bacteri
97	25	89.3	442	6 ABU26286	ABU26286 Protein e



98	25	89.3	464	8	ADN19563	Adn19563 Bacterial	171	24	85.7	87	8	ADX89697	Adx89697 Plant ful
99	25	89.3	473	6	ADA33425	Ada33425 Acinetoba	172	24	85.7	88	2	AAW38707	Aaw38707 S. pneumo
100	25	89.3	475	5	ADY59621	Ady59621 Candida u	173	24	85.7	88	2	ADS91361	Ads91361 Protein k
101	25	89.3	488	5	AB90882	Ab90882 Herpicida	174	24	85.7	102	4	AAE01038	Aae01038 Human DDC
102	25	89.3	492	9	AE841602	Aeb41602 L. pneumo	175	24	85.7	102	5	ABU05650	Abu05650 M. tuberc
103	25	89.3	494	2	AA228447	Aay28447 Bacillus	176	24	85.7	103	3	ASU05650	Asu05650 Arabidops
104	25	89.3	496	4	ABB59339	Abb59339 Drosophil	177	24	85.7	103	3	AAE52614	Aae52614 Arabidops
105	25	89.3	509	8	AD317024	Adsl7024 Pseudonoc	178	24	85.7	108	7	ADB64917	Adb64917 Human pro
106	25	89.3	543	9	AE847172	Aeb47172 Chimpanze	179	24	85.7	116	4	AAU02532	Aau02532 Anti-adip
107	25	89.3	543	9	AE847152	Aeb47152 Chimpanze	180	24	85.7	116	4	AAU02532	Aau02532 Anti-adip
108	25	89.3	543	9	AE847145	Aeb47145 Chimpanze	181	24	85.7	117	6	ABR83646	AbR83646 m734VH am
109	25	89.3	543	9	AE847146	Aeb47146 Chimpanze	182	24	85.7	118	8	ADX70728	Adx70728 Plant ful
110	25	89.3	593	2	AAE42479	Aar42479 Mouse RYK	183	24	85.7	118	9	AEA44947	Aea44947 Apolipoppr
111	25	89.3	594	9	AD280639	Ad280639 Amino aci	184	24	85.7	120	8	ADL93516	Adl93516 Human CD4
112	25	89.3	594	9	AD271195	Adz71195 Mouse RYK	185	24	85.7	122	5	AAU75745	Aau75745 AAV294 an
113	25	89.3	604	5	ABE89726	Abb89726 Human pol	186	24	85.7	122	9	ADY21965	Ady21965 Antibody
114	25	89.3	604	7	ADC06751	Adc06751 Human RYK	187	24	85.7	124	3	AAE38021	Aae38021 Fragment
115	25	89.3	604	7	AD5E9806	Ad5E9806 Human Pro	188	24	85.7	124	9	ADY21961	Ady21961 Antibody
116	25	89.3	604	8	ADQ89882	Adq89882 Antagonis	189	24	85.7	127	5	ABG70369	Abg70369 Novel hum
117	25	89.3	604	8	ADU04622	Adu04622 Human rec	190	24	85.7	128	4	AAE63584	Aae63584 Human gas
118	25	89.3	604	8	ADU86509	Adu86509 Human RYK	191	24	85.7	132	3	AAE06068	Aae06068 Arabidops
119	25	89.3	604	9	AD280637	Ad280637 Amino aci	192	24	85.7	132	3	AAE47191	Aae47191 Arabidops
120	25	89.3	604	9	AD271193	Adz71193 Human RYK	193	24	85.7	132	3	AAE52647	Aae52647 Arabidops
121	25	89.3	604	9	ABE69208	Aeb69208 Human mod	194	24	85.7	132	3	AAE47188	Aae47188 Arabidops
122	25	89.3	606	2	AAE42480	Aar42480 Human RYK	195	24	85.7	132	3	AAE52613	Aae52613 Arabidops
123	25	89.3	607	5	AAE66030	Aag66030 Amino aci	196	24	85.7	132	3	AAE07756	Aae07756 Arabidops
124	25	89.3	607	8	ADJ96659	Adj96659 Human tyr	197	24	85.7	132	3	AAE11031	Aae11031 Arabidops
125	25	89.3	610	6	ABE54215	AbE54215 Human NOV	198	24	85.7	132	3	AAE47185	Aae47185 Arabidops
126	25	89.3	628	7	ABO75995	AbO75995 Pseudomon	199	24	85.7	133	8	ADQ65770	Adq65770 Novel hum
127	25	89.3	631	8	ADJ32366	Adj32366 Rice phos	200	24	85.7	137	7	ADB65087	AdB65087 Human pro
128	25	89.3	635	4	ABE62805	AbE62805 Drosophil	201	24	85.7	140	5	AAE22538	Aae22538 Murine an
129	25	89.3	648	6	ADB11524	Abd11524 Alloloco	202	24	85.7	140	5	AAE20201	Aae20201 Murine 44
130	25	89.3	655	8	ADY09831	Ady09831 Plant ful	203	24	85.7	140	8	ADJ31875	Adj31875 Murine 44
131	25	89.3	716	6	ADB11522	Abd11522 Alloloco	204	24	85.7	144	8	ADR89758	AdR89758 Human PRK
132	25	89.3	735	2	AAW69761	Aaw69761 Acetobact	205	24	85.7	144	8	ADU65102	AdU65102 Human PKA
133	25	89.3	787	6	ABM67783	Abm67783 Photorhab	206	24	85.7	145	8	ABO62784	AbO62784 Klebsiell
134	25	89.3	840	5	ABE55565	AbE55565 Lactococc	207	24	85.7	145	8	ADY04239	AdY04239 Plant ful
135	25	89.3	840	5	ABE55565	AbE55565 Lactococc	208	24	85.7	149	8	AAE64737	Aae64737 Human 5'
136	25	89.3	861	4	ADB29488	AdB29488 Bacterial	209	24	85.7	149	8	ADU72301	AdU72301 Signal pe
137	25	89.3	866	3	AAE35864	Aag35864 Arabidops	210	24	85.7	149	9	ADZ73292	AdZ73292 Human inc
138	25	89.3	874	3	AAE35863	Aag35863 Arabidops	211	24	85.7	150	4	AAU14622	Aau14622 Novel bon
139	25	89.3	887	3	AAE35862	Aag35862 Arabidops	212	24	85.7	151	8	ADX95632	Adx95632 Plant ful
140	25	89.3	979	4	ABE61290	AbE61290 Drosophil	213	24	85.7	151	8	ADX90483	Adx90483 Plant ful
141	25	89.3	1012	8	ADZ29671	Adz29671 Bacterial	214	24	85.7	161	4	AAE73680	Aae73680 Human col
142	25	89.3	1020	6	ABW67204	Abm67204 Photorhab	215	24	85.7	165	2	AAW80683	Aaw80683 S. pneumo
143	25	89.3	1070	4	ABE62892	AbE62892 Drosophil	216	24	85.7	168	8	ADZ43899	AdZ43899 Bacterial
144	25	89.3	1072	9	ADZ26395	Adz26395 Novel cel	217	24	85.7	174	8	ADL06095	AdL06095 M. catarr
145	25	89.3	1103	8	ADQ89060	Adq89060 Human uro	218	24	85.7	174	8	ADT06049	AdT06049 Bacillus
146	25	89.3	1296	4	ABE66103	AbE66103 Drosophil	219	24	85.7	176	3	AAE11030	Aae11030 Arabidops
147	25	89.3	2640	4	ABG25725	Abg25725 Novel hum	220	24	85.7	176	3	AAE07755	Aae07755 Arabidops
148	25	89.3	3390	8	ADZ42671	Adz42671 Bacterial	221	24	85.7	176	3	AAE47184	Aae47184 Arabidops
149	24	85.7	5	8	ADJ93542	Adj93542 Human CD4	222	24	85.7	176	3	AAE06067	Aae06067 Arabidops
150	24	85.7	5	9	AEA44877	Aea44877 Apolipoppr	223	24	85.7	176	3	AAE47187	Aae47187 Arabidops
151	24	85.7	5	9	ADW52741	Adw52741 Hedgehog	224	24	85.7	176	3	AAE47190	Aae47190 Arabidops
152	24	85.7	11	9	ADW52746	Adw52746 Hedgehog	225	24	85.7	178	3	AAE47183	Aae47183 Arabidops
153	24	85.7	13	9	ADW52744	Adw52744 Hedgehog	226	24	85.7	178	3	AAE47189	Aae47189 Arabidops
154	24	85.7	22	8	ADZ33833	Adz33833 CMET-HGF	227	24	85.7	178	3	AAE06066	Aae06066 Arabidops
155	24	85.7	44	3	ADZ38023	Adz38023 Fragment	228	24	85.7	178	3	AAE11029	Aae11029 Arabidops
156	24	85.7	44	3	ADZ07024	Adz07024 Staphyloc	229	24	85.7	178	3	AAE47186	Aae47186 Arabidops
157	24	85.7	46	7	ADG18107	Adg18107 HumancAPK	230	24	85.7	178	3	AAE07754	Aae07754 Arabidops
158	24	85.7	49	4	AAO07751	Aao07751 Human pol	231	24	85.7	180	8	ADL06016	AdL06016 M. catarr
159	24	85.7	60	5	ABP01605	Abp01605 Human ORF	232	24	85.7	181	4	AAE06215	Aae06215 Human Cal
160	24	85.7	63	2	AAE76966	Aar76966 HSV-neutr	233	24	85.7	181	8	ADR89757	AdR89757 Human PRK
161	24	85.7	63	7	ABO67108	AbO67108 Klebsiell	234	24	85.7	181	8	ADU69101	AdU69101 Human PKA
162	24	85.7	68	5	ABP05573	AbP05573 Human ORF	235	24	85.7	183	4	ABG07736	AbG07736 Novel hum
163	24	85.7	79	4	AAU59454	Aau59454 Propionib	236	24	85.7	185	9	ABE40933	Abe40933 L. pneumo
164	24	85.7	79	6	ABM55973	Abm55973 Propionib	237	24	85.7	186	9	ABE37620	Abe37620 L. pneumo
165	24	85.7	83	4	ABE68701	AbE68701 Drosophil	238	24	85.7	187	8	ADL06015	AdL06015 M. catarr
166	24	85.7	84	4	AAU61002	Aau61002 Propionib	239	24	85.7	189	4	AAU42273	Aau42273 Propionib
167	24	85.7	84	6	ABM57521	Abm57521 Propionib	240	24	85.7	189	3	AAU52612	Aau52612 Arabidops
168	24	85.7	85	8	ABO57485	AbO57485 Human gen	241	24	85.7	189	6	ABM38792	Abm38792 Propionib
169	24	85.7	86	3	AAE56591	Aae56591 Arabidops	242	24	85.7	191	4	AAU31778	Aau31778 Novel hum
170	24	85.7	86	3	AAE59246	Aae59246 Arabidops	243	24	85.7	193	6	ABU29799	AbU29799 Protein e

244	24	85.7	205	6	ABR56292	Murine Tc	317	24	85.7	325	7	ADC94393	Adc94393 E. faeciu
245	24	85.7	205	9	ADx55700	Fine chem	318	24	85.7	328	8	ADY13506	Plant ful
246	24	85.7	207	8	ADJ36535	Human par	319	24	85.7	329	7	ADL34482	Adl34482 Protein k
247	24	85.7	207	8	ADx89756	Human PRK	320	24	85.7	333	4	AAB99942	Rabbit ch
248	24	85.7	207	8	ADu69100	Human PKA	321	24	85.7	333	9	ADZ88787	Adz88787 Breast sp
249	24	85.7	207	9	AEb15283	C Glutami	322	24	85.7	334	2	AAR65489	Aar65489 Human cho
250	24	85.7	207	9	AEb15281	C Glutami	323	24	85.7	334	2	AAR65490	Human cho
251	24	85.7	210	4	AAM25244	Human pro	324	24	85.7	334	2	AAR65487	Human cho
252	24	85.7	213	5	ABG93323	C. albica	325	24	85.7	334	2	AAR65486	Human cho
253	24	85.7	213	7	ADD47571	Human pro	326	24	85.7	334	2	AAW44784	Human cho
254	24	85.7	213	7	ADx59965	Human pro	327	24	85.7	334	4	AAB99816	AGC prote
255	24	85.7	213	7	ADD47575	Human pro	328	24	85.7	334	4	AAB99943	Rat chond
256	24	85.7	213	9	ADx59961	Human pro	329	24	85.7	334	4	AAB99940	Human cho
257	24	85.7	213	9	ADx55642	Fine chem	330	24	85.7	334	5	ABB99319	Amino aci
258	24	85.7	214	9	ADx55678	Fine chem	331	24	85.7	334	5	ABB99320	Amino aci
259	24	85.7	222	4	AAE00099	B. lichen	332	24	85.7	334	6	ABU56503	Lung can
260	24	85.7	230	8	ADr10281	Human pro	333	24	85.7	334	7	ADx55076	Human pro
261	24	85.7	230	9	ABM92463	M. xanthu	334	24	85.7	334	7	ADx55074	Rat Prote
262	24	85.7	232	8	ADY13601	Plant ful	335	24	85.7	334	7	ADN39394	Cancer/an
263	24	85.7	235	3	AAB43848	Human can	336	24	85.7	334	8	ADT66643	Rat chond
264	24	85.7	235	4	AAU23699	Novel hum	337	24	85.7	334	8	ADT66641	Human cho
265	24	85.7	235	4	AAU23699	Novel hum	338	24	85.7	335	4	AAB99941	Bovine ch
266	24	85.7	235	6	ABM49292	Propionib	339	24	85.7	337	6	ABM69545	PhotOrhab
267	24	85.7	241	7	ADx58850	Human pol	340	24	85.7	339	7	ADC32786	Human nov
268	24	85.7	248	6	ABM70172	PhotOrhab	341	24	85.7	339	7	ADx09390	Novel pro
269	24	85.7	250	7	ADx80009	Mycobacte	342	24	85.7	340	9	ADZ64608	Human pro
270	24	85.7	255	7	ADx04855	Bacterial	343	24	85.7	340	9	AAE04829	Human pro
271	24	85.7	255	9	ADV91665	Human can	344	24	85.7	343	6	ABU08483	Mouse Cs
272	24	85.7	260	2	AAW14398	Human DNA	345	24	85.7	343	6	ABU08481	Human Cs
273	24	85.7	260	2	AAV43303	Mouse pr	346	24	85.7	345	5	ADL05313	M. catar
274	24	85.7	260	2	AAV43302	Bovine pr	347	24	85.7	349	5	ABP41860	Human ova
275	24	85.7	264	7	ADJ71033	Human hea	348	24	85.7	351	4	AAW25540	Human pro
276	24	85.7	268	3	AAV44973	Recombina	349	24	85.7	351	4	AAE04829	Human pro
277	24	85.7	268	3	AAV44972	Recombina	350	24	85.7	351	6	ABU08469	Human cal
278	24	85.7	269	4	ABx61541	3DX sfv p	351	24	85.7	351	8	ADJ36521	Human CAM
279	24	85.7	270	9	ADY21963	Single ch	352	24	85.7	351	8	ADJ36540	Mouse pro
280	24	85.7	270	9	ADY21967	Antibody	353	24	85.7	351	8	ADx89760	Human PRK
281	24	85.7	277	5	ABE81189	Murine CA	354	24	85.7	351	8	ABM82053	Tumour-ag
282	24	85.7	284	7	ABO61145	Klebsiell	355	24	85.7	351	8	ADx92978	Protein k
283	24	85.7	284	7	ABO67387	Klebsiell	356	24	85.7	351	8	ADx92991	Protein k
284	24	85.7	284	8	ADJ38866	PKA amino	357	24	85.7	351	8	ADu69104	Human PKA
285	24	85.7	286	9	ADx71559	c-AMP dep	358	24	85.7	351	9	AEb16431	MAPK, 8/2
286	24	85.7	288	4	ABx59787	Drosophil	359	24	85.7	355	8	ADx69106	Plant ful
287	24	85.7	292	8	ADx21633	Bacterial	360	24	85.7	355	4	ABx80119	Corynebac
288	24	85.7	295	4	ABx99846	AGC prote	361	24	85.7	356	4	ABx80159	Corynebac
289	24	85.7	295	8	ADJ38894	PKA gamma	362	24	85.7	357	4	AAE04718	Human cat
290	24	85.7	295	9	ABM97008	M. xanthu	363	24	85.7	357	6	ABU33336	Protein e
291	24	85.7	296	2	AAR65488	Human cho	364	24	85.7	357	9	ABx40048	L. pneumo
292	24	85.7	296	2	AAR65491	Human cho	365	24	85.7	358	9	ABx36656	L. pneumo
293	24	85.7	296	5	ABx99321	Amino aci	366	24	85.7	360	4	AAE04719	Human cat
294	24	85.7	296	9	ADx88788	Breast sp	367	24	85.7	360	4	ADD14109	Human arc
295	24	85.7	298	9	ADx85482	Catalytic	368	24	85.7	360	8	ADJ36529	Human tes
296	24	85.7	305	4	ADY651328	Propionib	369	24	85.7	366	8	ADN21484	Bacterial
297	24	85.7	305	6	ABM57847	Propionib	370	24	85.7	367	6	ABU33116	Protein e
298	24	85.7	308	4	ABx89838	C glutami	371	24	85.7	367	9	ABx36606	L. pneumo
299	24	85.7	310	6	ABU44250	Protein e	372	24	85.7	367	9	ABx36606	L. pneumo
300	24	85.7	312	8	ADY05390	Plant ful	373	24	85.7	371	2	AAW98360	Human nov
301	24	85.7	313	7	ADG75687	Human pro	374	24	85.7	372	2	AAW98360	H. pylori
302	24	85.7	314	6	ABx57468	AGC famil	375	24	85.7	372	4	ABx60318	Helicobac
303	24	85.7	316	7	ADx99078	Human dia	376	24	85.7	372	5	ABP51950	Helicobac
304	24	85.7	316	7	ADx99078	Human RPP	377	24	85.7	375	5	AAU72876	Human asp
305	24	85.7	317	2	AAW21949	E6-bindin	378	24	85.7	379	5	ABG76498	DNA encod
306	24	85.7	317	5	ABG65817	Human ret	379	24	85.7	380	9	ADY66050	S. manso
307	24	85.7	317	7	ADx62228	Human pro	380	24	85.7	389	9	ABM92903	M. xanthu
308	24	85.7	317	8	ADx018167	Human sof	381	24	85.7	389	9	ADx88789	Breast sp
309	24	85.7	317	8	ADP23207	PRO polyp	382	24	85.7	400	4	AAE04715	Human cat
310	24	85.7	318	6	ADx20626	Protein e	383	24	85.7	409	7	ADH88283	Enterococ
311	24	85.7	318	7	ADD48786	Rat Prote	384	24	85.7	409	8	ADx08223	Bacterial
312	24	85.7	318	7	ADx62226	Human pro	385	24	85.7	409	8	ADx66137	Plant ful
313	24	85.7	320	9	AEA10611	Human pro	386	24	85.7	415	6	ABR83648	TS1 VH ch
314	24	85.7	321	8	ADJ76231	Marker ge	387	24	85.7	415	7	ADx08462	Novel pro
315	24	85.7	321	8	ADJ76200	Marker ge	388	24	85.7	416	3	ABx56817	Human pro
316	24	85.7	324	6	ABU29976	Protein e	389	24	85.7	422	8	ADx10744	Human the

330	24	85.7	426	6	ABU18614	Abu18614 Protein e	463	24	85.7	608	8	ADK47809	Adk47809 Streptoco
331	24	85.7	427	8	ADR50801	Adr50801 Human c-t	464	24	85.7	609	3	AAy81508	AAy81508 Streptoco
332	24	85.7	439	6	ABP78252	Abp78252 N. gonorr	465	24	85.7	609	3	ABP26836	ABP26836 Streptoco
333	24	85.7	442	4	ABB63619	Abb63619 Drosophil	466	24	85.7	609	8	ADV89237	Adv89237 Streptoco
334	24	85.7	442	4	ABB63620	Abb63620 Drosophil	467	24	85.7	609	8	ADV80490	Adv80490 Streptoco
335	24	85.7	447	9	ABU21178	Abu21178 Pantocoea c	468	24	85.7	609	8	ADV82544	Adv82544 Streptoco
336	24	85.7	451	8	ADN97505	Adn97505 Artificialia	469	24	85.7	611	4	ABP71064	Abp71064 Drosophil
337	24	85.7	466	8	ADS28439	Ads28439 Bacterial	470	24	85.7	612	5	ABP25476	Abp25476 Streptoco
338	24	85.7	471	7	ABM86647	Abm86647 Rice abio	471	24	85.7	615	8	ADS29584	Ads29584 Bacterial
339	24	85.7	472	4	AGS89856	Ag89856 C glutami	472	24	85.7	617	8	ADR96461	Adr96461 Novel S.
400	24	85.7	476	7	ADM06127	Adm06127 Human pro	473	24	85.7	617	9	AEA60331	Aea60331 Streptoco
401	24	85.7	477	4	AAB80118	Aab80118 Corynebac	474	24	85.7	630	5	ABM72785	Abm72785 Staphyloc
402	24	85.7	477	4	AAB80158	Aab80158 Corynebac	475	24	85.7	632	5	ABB47801	Abb47801 Listeria
403	24	85.7	484	4	ABG00076	Abg00076 Novel hum	476	24	85.7	646	3	AAy57307	AAy57307 P. aerugi
404	24	85.7	487	4	AUA46114	Aua46114 Propionib	477	24	85.7	648	8	ADY11085	Ady11085 Plant ful
405	24	85.7	487	6	ABM42633	Abm42633 Propionib	478	24	85.7	667	4	ABB64511	Abb64511 Drosophil
406	24	85.7	502	9	ADY21971	Ady21971 Antibody	479	24	85.7	670	3	AAy57314	AAy57314 P. aerugi
407	24	85.7	502	9	ADY21969	Ady21969 Antibody	480	24	85.7	686	7	ABO80650	Ab808650 Pseudomon
408	24	85.7	503	4	AAU14716	Aau14716 Novel bon	481	24	85.7	693	7	ADJ70423	Adj70423 Human hea
409	24	85.7	503	5	ABU65067	Abu65067 Human NOV	482	24	85.7	712	8	ADN97543	Adn97543 Artificialia
410	24	85.7	503	8	ADN61785	Adn61785 Human nov	483	24	85.7	713	8	ADN97491	Adn97491 Artificialia
411	24	85.7	505	5	ABH83055	Abh83055 Rat amino	484	24	85.7	715	4	ABB63050	Abb63050 Drosophil
412	24	85.7	505	5	ABB83054	Abb83054 Human kin	485	24	85.7	715	8	ADN97489	Adn97489 Artificialia
413	24	85.7	505	5	ABU65068	Abu65068 Human NOV	486	24	85.7	727	3	AAy76841	AAy76841 Neirin pr
414	24	85.7	505	5	AEA19161	Aea19161 Human kin	487	24	85.7	727	3	AAy76841	AAy76841 Neirin pr
415	24	85.7	505	7	ADP61937	Adp61937 Rat Prote	488	24	85.7	727	7	ADB81218	Adb81218 Vertebrat
416	24	85.7	505	7	ADP61941	Adp61941 Rat Prote	489	24	85.7	743	4	AAAB94084	AAb94084 Human pro
417	24	85.7	505	7	ADB61939	Adb61939 Human Pro	490	24	85.7	744	4	ABAB95345	Abb95345 Human pro
418	24	85.7	505	7	ADB61943	Adb61943 Human Pro	491	24	85.7	744	4	ABAB94361	Abb94361 Human pro
419	24	85.7	505	8	ADN61787	Adn61787 Human nov	492	24	85.7	744	5	ABB49954	Abb49954 Listeria
420	24	85.7	508	4	AAU23159	Aau23159 Novel hum	493	24	85.7	748	6	ADB12089	Adb12089 Alloiococ
421	24	85.7	512	8	ADN97497	Adn97497 Artificialia	494	24	85.7	750	3	ABAB26599	Abab26599 Synchocy
422	24	85.7	513	4	AAU03510	Aau03510 Human pro	495	24	85.7	752	8	ADR08902	Adr08902 Human pro
423	24	85.7	513	4	AAE04361	Aae04361 Human kin	496	24	85.7	752	4	AGS98956	Ag898956 E. coli g
424	24	85.7	513	6	ABU21734	Abu21734 Protein e	497	24	85.7	756	8	ADK45232	Adk45232 Bacterial
425	24	85.7	513	9	AEA15489	Aea15489 Human pol	498	24	85.7	757	8	ADK42692	Adk42692 Bacterial
426	24	85.7	517	8	ADN97495	Adn97495 Artificialia	499	24	85.7	757	8	ADN17587	Adn17587 Bacterial
427	24	85.7	518	8	ADN97493	Adn97493 Artificialia	500	24	85.7	761	6	ADB12087	Adb12087 Alloiococ
428	24	85.7	521	8	ADS44260	Ads44260 Bacterial	501	24	85.7	778	6	AAU35135	Aau35135 Enterococ
429	24	85.7	524	8	ADS21147	Ads21147 Bacterial	502	24	85.7	778	6	ABU29211	Abu29211 Protein e
430	24	85.7	527	7	ABO65585	Ab865585 Klebsiell	503	24	85.7	789	7	ADH87054	Adh87054 Enterococ
431	24	85.7	527	9	ABM96031	Abm96031 M. xanthu	504	24	85.7	793	4	ABB65110	Abb65110 Drosophil
432	24	85.7	540	4	ABBE1662	Abbe1662 Drosophil	505	24	85.7	804	9	ADX07630	Adx07630 Cyclin-de
433	24	85.7	543	5	ABU65069	Abu65069 Human NOV	506	24	85.7	831	8	ADO15511	Ado15511 Immunorea
434	24	85.7	543	8	ADN61789	Adn61789 Human nov	507	24	85.7	837	4	ABB68265	Abb68265 Drosophil
435	24	85.7	543	8	ADM66585	Adm66585 Human kin	508	24	85.7	845	8	ADS21821	Ads21821 Bacterial
436	24	85.7	548	8	ADN17887	Adn17887 Bacterial	509	24	85.7	852	4	AAm93785	Aam93785 Human pol
437	24	85.7	552	8	ADN97513	Adn97513 Artificialia	510	24	85.7	852	4	AAAB47562	AAab47562 Protease
438	24	85.7	554	7	ADP06601	Adp06601 Bacterial	511	24	85.7	852	5	ABP69443	Abp69443 Human pol
439	24	85.7	557	4	AAy97750	Aay97750 G. oxydan	512	24	85.7	852	5	ABG32363	Abg32363 Human ATP
440	24	85.7	559	6	ABM68539	Abm68539 Photorhab	513	24	85.7	852	7	ADC10040	Adc10040 Human NOV
441	24	85.7	559	6	ABU19336	Abu19336 Protein e	514	24	85.7	852	7	ADM56266	Adm56266 Human ATP
442	24	85.7	561	5	AAU79458	Aau79458 Human nov	515	24	85.7	852	8	ADL31771	Adl31771 Human pro
443	24	85.7	571	4	AAAB94288	Aab94288 Human pro	516	24	85.7	852	9	ADV85873	Adv85873 Human pro
444	24	85.7	572	6	ABU21144	Abu21144 Protein e	517	24	85.7	856	4	AAAB94310	AAab94310 Human pro
445	24	85.7	575	4	ABBE1825	Abbe1825 Drosophil	518	24	85.7	856	9	ADX07626	Adx07626 Cyclin-de
446	24	85.7	581	4	AAAB95332	Aab95332 Human pro	519	24	85.7	866	9	ADZ225526	Adz225526 Cytokine
447	24	85.7	581	4	ABAB99179	Abab99179 Human pro	520	24	85.7	866	4	AAm40262	Aam40262 Human pol
448	24	85.7	581	8	ADR08963	Adr08963 Human pro	521	24	85.7	866	7	ADB79761	Adb79761 Rat Janus
449	24	85.7	583	5	ABP69334	Abp69334 Human pol	522	24	85.7	866	7	ADE55520	Ad55520 Rat Prote
450	24	85.7	583	6	ABU49710	Abu49710 Protein e	523	24	85.7	882	7	ABR56262	AbR56262 Mouse Jun
451	24	85.7	590	8	ADN17896	Adn17896 Bacterial	524	24	85.7	883	4	ABG14730	Abg14730 Novel hum
452	24	85.7	590	8	ADN46811	Adn46811 Thermococ	525	24	85.7	908	8	ADQ67576	Adq67576 Novel hum
453	24	85.7	595	2	AAW85021	Aaw85021 mPKAc-gre	526	24	85.7	923	4	AAAM42048	AAam42048 Human pol
454	24	85.7	595	3	AAy70776	Aay70776 PKAc-F64L	527	24	85.7	928	2	AAW88417	Aaw88417 Chlamydia
455	24	85.7	596	4	ABAB93779	Abab93779 Human pro	528	24	85.7	928	3	AAy90236	Aay90236 Chlamydia
456	24	85.7	596	4	ABBE6026	Abbe6026 Drosophil	529	24	85.7	928	5	ABAB90583	Abab90583 Chlamydia
457	24	85.7	604	4	ABBS8752	Abbs8752 Drosophil	530	24	85.7	931	8	ADN26757	Adn26757 Protein e
458	24	85.7	604	4	ABBS8752	Abbs8752 Drosophil	531	24	85.7	931	8	ADN22445	Adn22445 Bacterial
459	24	85.7	604	4	ABBS8756	Abbs8756 Drosophil	532	24	85.7	933	2	AAW98599	Aaw98599 H. pylori
460	24	85.7	604	4	ABBS9056	Abbs9056 Drosophil	533	24	85.7	933	6	ABU30840	Abu30840 Protein e
461	24	85.7	605	7	ABO78170	Ab878170 Pseudomon	534	24	85.7	946	2	ABR62797	AbR62797 VISA Stap
462	24	85.7	608	6	ABU02715	Abu02715 S. pneumo	535	24	85.7	946	2	AAy35060	Aay35060 Chlamydia

536	24	85.7	960	5	AAU75476	Aau75476 S. aureus	609	23	82.1	17	5	ABB04505	Abb04505 Alternati
537	24	85.7	972	8	ADN40548	Adn40548 Candida a	610	23	82.1	23	9	AEA04762	Aea04762 ZAP CCH
538	24	85.7	974	8	ADN40552	Adn40552 Candida a	611	23	82.1	55	4	AU62850	Au62850 Propionib
539	24	85.7	989	3	AAg47166	Aag47166 Arabidops	612	23	82.1	55	6	ABM59369	Abm59369 Propionib
540	24	85.7	989	3	ABO68689	Abob68689 Pseudomon	613	23	82.1	78	7	ABO62969	Abob62969 Klebsiell
541	24	85.7	1004	4	ABB60899	Abbb60899 Drosophil	614	23	82.1	82	4	AAO6363	Aao06363 Human foe
542	24	85.7	1013	4	ABG06132	Abg06132 Novel hum	615	23	82.1	82	4	AAO6363	Aao06363 Human foe
543	24	85.7	1018	3	AG47165	Aag47165 Arabidops	616	23	82.1	83	4	AAO6363	Aao06363 Human foe
544	24	85.7	1033	5	ABP74111	Abp74111 Human TRI	617	23	82.1	99	4	AAU49597	Aau49597 Propionib
545	24	85.7	1033	8	ADK70510	Adk70510 Respirato	618	23	82.1	99	6	ABM46116	Abm46116 Propionib
546	24	85.7	1042	4	ABB66302	Abbb66302 Drosophil	619	23	82.1	100	3	AAU54270	Aau54270 Human pan
547	24	85.7	1042	4	ABB96654	Abbb96654 Putative	620	23	82.1	101	2	AAU54270	Aau54270 Human pan
548	24	85.7	1069	4	ABG13177	Abg13177 Novel hum	621	23	82.1	103	7	ADP05232	Adp05232 Bacterial
549	24	85.7	1075	3	AG47164	Aag47164 Arabidops	622	23	82.1	115	4	ABG07479	Abg07479 Novel hum
550	24	85.7	1085	6	ABU31244	Abu31244 Protein e	623	23	82.1	139	6	ABU31895	Abu31895 Protein e
551	24	85.7	1085	6	ABO28426	Abob28426 Protein e	624	23	82.1	141	7	ADCO0666	Adco0666 Enteroha
552	24	85.7	1097	4	ABG25655	Abg25655 Novel hum	625	23	82.1	146	2	AAW73397	Aaw73397 Human sec
553	24	85.7	1142	2	AAU25140	Aau25140 JAK1. 3/2	626	23	82.1	154	4	ABG17732	Abg17732 Novel hum
554	24	85.7	1142	2	AAU25140	Aau25140 JAK1. 3/2	627	23	82.1	163	7	ABO63618	Abob63618 Klebsiell
555	24	85.7	1142	3	AAU25140	Aau25140 JAK1. 3/2	628	23	82.1	169	4	AAU25140	Aau25140 JAK1. 3/2
556	24	85.7	1142	4	AAU25140	Aau25140 JAK1. 3/2	629	23	82.1	169	7	ABO62195	Abob62195 Secreted
557	24	85.7	1142	4	AAU25140	Aau25140 JAK1. 3/2	630	23	82.1	183	2	AAU25140	Aau25140 JAK1. 3/2
558	24	85.7	1142	4	AAU25140	Aau25140 JAK1. 3/2	631	23	82.1	183	3	AAU25140	Aau25140 JAK1. 3/2
559	24	85.7	1142	7	ADP14187	Adp14187 Human src	632	23	82.1	183	4	AAU25140	Aau25140 JAK1. 3/2
560	24	85.7	1142	7	ADP45066	Adp45066 Human kin	633	23	82.1	183	4	AAU25140	Aau25140 JAK1. 3/2
561	24	85.7	1142	8	ADP79175	Adp79175 Human jak	634	23	82.1	183	4	AAU25140	Aau25140 JAK1. 3/2
562	24	85.7	1142	9	ADP80353	Adp80353 Human jak	635	23	82.1	183	4	AAU25140	Aau25140 JAK1. 3/2
563	24	85.7	1142	9	ADP80353	Adp80353 Human jak	636	23	82.1	183	5	ABO90318	Abob90318 Human pol
564	24	85.7	1153	3	ABO15199	Abob15199 Human jan	637	23	82.1	183	5	ABO15199	Abob15199 Human jan
565	24	85.7	1153	3	ABO15199	Abob15199 Human jan	638	23	82.1	183	5	ABO15199	Abob15199 Human jan
566	24	85.7	1153	5	ABG60307	Abg60307 Lymphona	639	23	82.1	183	8	ADL30802	Adl30802 Human pro
567	24	85.7	1153	8	ADP79175	Adp79175 Human jak	640	23	82.1	183	8	ADP79175	Adp79175 Human jak
568	24	85.7	1153	8	ADP79175	Adp79175 Human jak	641	23	82.1	183	8	ADP79175	Adp79175 Human jak
569	24	85.7	1153	8	ADP79175	Adp79175 Human jak	642	23	82.1	183	8	ADP79175	Adp79175 Human jak
570	24	85.7	1154	5	ABG60308	Abg60308 Lymphona	643	23	82.1	192	4	ABM12325	Abm12325 Human sec
571	24	85.7	1154	5	ABG60308	Abg60308 Lymphona	644	23	82.1	192	4	ABM12325	Abm12325 Human sec
572	24	85.7	1154	8	ADQ97890	Adq97890 Human can	645	23	82.1	193	6	AAE33247	Aae33247 Human G-p
573	24	85.7	1170	8	ADQ97890	Adq97890 Human can	646	23	82.1	193	6	AAE33247	Aae33247 Human G-p
574	24	85.7	1174	8	ABG25659	Abg25659 Novel hum	647	23	82.1	200	4	ABG19232	Abg19232 Novel hum
575	24	85.7	1200	3	ABE19313	Abel19313 Amino aci	648	23	82.1	202	5	ABM55150	Abm55150 Lactococc
576	24	85.7	1214	9	ABE27322	Abel27322 Pinus rad	649	23	82.1	203	8	ADK67487	Adk67487 Plant ful
577	24	85.7	1221	5	ABP73765	Abp73765 Candida a	650	23	82.1	205	7	ABM85710	Abm85710 Mouse pro
578	24	85.7	1224	4	ABE64966	Abbe64966 Drosophil	651	23	82.1	213	9	ABE41859	Abe41859 L. pneumo
579	24	85.7	1233	8	ADN20989	Adn20989 Bacterial	652	23	82.1	214	4	AAE65832	Aae65832 Human G p
580	24	85.7	1234	6	ABU38409	Abu38409 Protein e	653	23	82.1	220	9	ABE38622	Abe38622 L. pneumo
581	24	85.7	1234	6	ABU38409	Abu38409 Protein e	654	23	82.1	223	7	ADH88125	Adh88125 Enterococ
582	24	85.7	1236	6	ADJ39092	Adj39092 Pseudomon	655	23	82.1	229	2	AAW22028	Aaw22028 Cryptospo
583	24	85.7	1239	6	ABU41544	Abu41544 Protein e	656	23	82.1	239	3	AAE29031	Aae29031 Arabidops
584	24	85.7	1245	6	ABJ18937	Abj18937 Pathogen	657	23	82.1	243	4	AAE59380	Aae59380 Protein t
585	24	85.7	1248	7	ABE62789	Abel62789 MRSA GTP	658	23	82.1	243	6	AAE33248	Aae33248 Human G-p
586	24	85.7	1263	6	ADA89466	Ada89466 Staphyloc	659	23	82.1	251	3	AAE29030	Aae29030 Arabidops
587	24	85.7	1263	6	ABM73319	Abm73319 Staphyloc	660	23	82.1	256	6	ABP97090	Abp97090 Human G p
588	24	85.7	1264	7	ABO81518	Abob81518 Pseudomon	661	23	82.1	258	6	ABU00590	Abu00590 S. pneumo
589	24	85.7	1365	7	ADJ70240	Adj70240 Human hea	662	23	82.1	258	6	ABM72323	Abm72323 Staphyloc
590	24	85.7	1434	6	ABE52635	Abel52635 Protein s	663	23	82.1	258	8	ADK47592	Adk47592 Streptoco
591	24	85.7	1434	7	ADK64752	Adk64752 Disease c	664	23	82.1	263	8	ABM80875	Abm80875 Tumour-as
592	24	85.7	1462	7	ABM88208	Abm88208 Rice abio	665	23	82.1	263	8	ADR94333	Adr94333 Novel S.
593	24	85.7	1878	4	ABE61852	Abbe61852 Drosophil	666	23	82.1	263	9	ABM58203	Abm58203 Streptoco
594	24	85.7	1895	4	ABB70088	Abbb70088 Drosophil	667	23	82.1	287	7	ADJ71062	Adj71062 Human hea
595	24	85.7	2000	8	ADN04333	Adn04333 Antipsori	668	23	82.1	291	4	AAE78278	Aae78278 Rat PTP-S
596	24	85.7	2000	8	ADP24104	Adp24104 PRO polyp	669	23	82.1	294	5	ABM06003	Abm06003 Human can
597	24	85.7	2286	8	ADT04699	Adt04699 Human DNA	670	23	82.1	294	5	ABM06003	Abm06003 Human can
598	24	85.7	2309	4	ABE66232	Abbe66232 Drosophil	671	23	82.1	298	6	ABM65767	Abm65767 Propionib
599	24	85.7	2472	7	ADP55353	Adp55353 Human Pro	672	23	82.1	299	4	AAU50496	Aau50496 Propionib
600	24	85.7	2472	7	ADP55353	Adp55353 Human Pro	673	23	82.1	299	6	ABM47015	Abm47015 Propionib
601	24	85.7	2477	7	ABR84742	Abbr84742 Human spe	674	23	82.1	308	8	ADK96458	Adk96458 Plant ful
602	24	85.7	2477	7	ADJ68432	Adj68432 Human hea	675	23	82.1	312	2	AAE15352	Aae15352 Protein d
603	24	85.7	5147	4	ABM59831	Abm59831 Drosophil	676	23	82.1	316	8	ADY06697	Ady06697 Plant ful
604	24	85.7	16368	9	ABM67171	Abm67171 Photorhab	677	23	82.1	334	3	ADK76322	Adk76322 Plant ful
605	24	82.1	5	5	AEA45978	Aea45978 Apolipop	678	23	82.1	342	3	AAE29029	Aae29029 Arabidops
606	24	82.1	7	7	AAU46270	Aau46270 H11 bindi	679	23	82.1	342	6	ABU47684	Abu47684 Protein e
607	23	82.1	7	7	AAU46270	Aau46270 H11 bindi	680	23	82.1	344	6	ABU47684	Abu47684 Protein e
608	23	82.1	8	8	ADN65503	Adn65503 HLA bindi	681	23	82.1	344	6	ABU47688	Abu47688 Protein e

682	23	82.1	345	2	AAY34671	Aay34671 Chlamydia	755	23	82.1	714	5	AAU79801	Aau79801 Human G-p
683	23	82.1	346	7	ABO60702	Aboc60702 Klebsiell	756	23	82.1	714	6	AAE33236	Aae33236 Human G-p
684	23	82.1	349	4	AAG75571	Aag75571 Human col	757	23	82.1	720	8	ADS42419	Ads42419 Bacterial
685	23	82.1	359	7	ABM66936	Abm66936 Rice abio	758	23	82.1	736	4	AAU35880	Aau35880 Helicobac
686	23	82.1	364	3	AAG39023	Aag39023 Arabidops	759	23	82.1	736	4	AAU35700	Aau35700 Helicobac
687	23	82.1	364	4	AAE00430	Aae00430 Schizosac	760	23	82.1	736	6	ABU30700	Abu30700 Proteine
688	23	82.1	368	8	ADS21993	Ads21993 Bacterial	761	23	82.1	747	7	ADES5002	Ade55002 Rat Prote
689	23	82.1	369	7	ADB85132	Adb85132 Rat prote	762	23	82.1	751	4	AAU78945	Aam78945 Human pro
690	23	82.1	372	3	AAV95654	Aav95654 Arabidops	763	23	82.1	751	4	AAU78945	Aam78945 Human pro
691	23	82.1	372	3	AAV95654	Aav95654 Arabidops	764	23	82.1	751	4	AAU78945	Aam78945 Human pro
692	23	82.1	378	8	ADX90026	Adx90026 Plant ful	765	23	82.1	776	9	AEA04751	Aea04751 CCCH-type
693	23	82.1	388	3	AAG39022	Aag39022 Arabidops	766	23	82.1	801	5	ABP69054	Abp69054 Human pol
694	23	82.1	388	9	AEB27122	Aeb27122 Pinus rad	767	23	82.1	801	5	AAU09864	Aau09864 Novel hum
695	23	82.1	389	6	AAE33240	Aae33240 Human G-p	768	23	82.1	802	4	AAU79929	Aam79929 Human hea
696	23	82.1	406	3	AAG13720	Aag13720 Arabidops	769	23	82.1	802	4	AAU79929	Aam79929 Human pro
697	23	82.1	407	3	AAG13719	Aag13719 Arabidops	770	23	82.1	808	5	ABP70068	Abp70068 Human NOV
698	23	82.1	409	8	ADM57191	Adm57191 A thalian	771	23	82.1	841	2	AAW34985	Aaw34985 Archaeabac
699	23	82.1	411	5	ABU50661	Abu50661 Helicobac	772	23	82.1	841	5	AAU79400	Aau79400 Human G-p
700	23	82.1	411	5	ABU51857	Abu51857 Helicobac	773	23	82.1	847	6	AAE33237	Aae33237 Human G-p
701	23	82.1	411	5	ABU51857	Abu51857 Helicobac	774	23	82.1	861	5	ABP07686	Abp07686 Human GTP
702	23	82.1	411	7	ADJ68665	Adj68665 Human hea	775	23	82.1	862	5	ABB47321	Abb47321 Listeria
703	23	82.1	411	7	ADP65187	Adp65187 Human pyr	776	23	82.1	885	3	AAV90238	Aav90238 Mature Ch
704	23	82.1	411	8	ADOS5105	Ados5105 Protein #	777	23	82.1	890	9	ADY17127	Ady17127 PRO polyyp
705	23	82.1	411	8	ADS92975	Ads92975 Pyruvate	778	23	82.1	910	4	AAE12023	Aae12023 Human G-p
706	23	82.1	411	9	AEA62668	Aea62668 Mitochond	779	23	82.1	910	5	AAU79399	Aau79399 Human G-p
707	23	82.1	414	5	ABU51458	Abu51458 Helicobac	780	23	82.1	910	5	AAE29238	Aae29238 Human 7TM
708	23	82.1	431	5	ABU51976	Abu51976 Helicobac	781	23	82.1	910	5	AAE14515	Aae14515 Human nov
709	23	82.1	433	4	AAU29789	Aau29789 Novel hum	782	23	82.1	910	6	ABR48167	AbR48167 Human bla
710	23	82.1	436	3	AAG39021	Aag39021 Arabidops	783	23	82.1	910	6	ABU56632	Abu56632 Lung canc
711	23	82.1	437	5	ABU51187	Abu51187 Helicobac	784	23	82.1	910	6	ABU09573	Abu09573 Human pro
712	23	82.1	440	5	ABU51847	Abu51847 Helicobac	785	23	82.1	910	7	ADB75297	AdB75297 Prostate
713	23	82.1	441	5	ABU50816	Abu50816 Helicobac	786	23	82.1	910	7	ADN39890	Adn39890 Cancer/an
714	23	82.1	441	5	ABU51234	Abu51234 Helicobac	787	23	82.1	910	7	ADN39890	Adn39890 Cancer/an
715	23	82.1	441	5	ABU51111	Abu51111 Helicobac	788	23	82.1	910	8	ADO28971	Ado28971 Human nov
716	23	82.1	445	5	ABU51111	Abu51111 Helicobac	789	23	82.1	914	2	AAW88429	Aaw88429 Chlamydia
717	23	82.1	451	2	AAE27721	Aae27721 Mouse per	790	23	82.1	921	5	ABP64873	Abp64873 Human pro
718	23	82.1	452	6	AAE33246	Aae33246 Human G-p	791	23	82.1	928	2	AAW88418	Aaw88418 Chlamydia
719	23	82.1	453	5	ABU50802	Abu50802 Helicobac	792	23	82.1	928	3	AAV90237	Aav90237 Chlamydia
720	23	82.1	473	4	AAU25322	Aau25322 Human pro	793	23	82.1	928	5	ABN90573	Abn90573 Chlamydia
721	23	82.1	483	3	AAG35481	Aag35481 Arabidops	794	23	82.1	942	5	ABP64872	Abp64872 Human pro
722	23	82.1	485	3	AAV69385	Aav69385 Amino aci	795	23	82.1	944	5	ABP39507	Abp39507 Staphyloc
723	23	82.1	485	3	AAV69392	Aav69392 Amino aci	796	23	82.1	953	8	ADJ66498	Adj66498 K1A1284
724	23	82.1	485	7	ADN39158	Adn39158 Cancer/an	797	23	82.1	972	6	ABU19453	Abu19453 Protein e
725	23	82.1	495	4	AAW78993	Aaw78993 Human pro	798	23	82.1	988	2	AAW56107	Aaw56107 S. pombe
726	23	82.1	495	7	ADB74254	Adb74254 Mycobacte	799	23	82.1	997	8	ADO28979	Ado28979 Mouse nov
727	23	82.1	498	7	ADSO7867	Adso7867 Novel pro	800	23	82.1	1009	8	ADY06602	Ady06602 Plant ful
728	23	82.1	498	8	ADQ79754	Adq79754 Human gal	801	23	82.1	1010	5	AAU15275	Aau15275 Human lar
729	23	82.1	499	6	ADA13315	Ada13315 Human fir	802	23	82.1	1011	6	ABU26071	Abu26071 Aspergill
730	23	82.1	502	2	AAV35329	Aav35329 Chlamydia	803	23	82.1	1024	5	ABU07504	Abu07504 Human GTP
731	23	82.1	514	4	AAW79977	Aaw79977 Human pro	804	23	82.1	1066	6	ABJ25532	Abj25532 Aspergill
732	23	82.1	515	9	ADZ35951	Adz35951 Sesame cy	805	23	82.1	1066	6	ABJ26132	Abj26132 Aspergill
733	23	82.1	526	5	ABU50684	Abu50684 Helicobac	806	23	82.1	1116	7	ADK64164	Adk64164 Disease t
734	23	82.1	536	3	AAV76007	Aav76007 Murine Ri	807	23	82.1	1148	7	ADP70436	Adp70436 Orphan re
735	23	82.1	536	3	AAV55946	Aav55946 Skin cell	808	23	82.1	1218	4	AAU03495	Aau03495 Drosophil
736	23	82.1	536	5	ABB72146	Abb72146 Murine pr	809	23	82.1	1218	4	ABB58777	Abb58777 Drosophil
737	23	82.1	538	5	AAU79803	Aau79803 Novel hum	810	23	82.1	1220	7	ADG90657	Adg90657 Hepatic s
738	23	82.1	540	6	ABP97077	Abp97077 Human G p	811	23	82.1	1403	7	ADG90649	Adg90649 Hepatic s
739	23	82.1	540	9	AEB11710	Aeb11710 Rat prote	812	23	82.1	1455	7	ADG90647	Adg90647 Hepatic s
740	23	82.1	541	5	ABBS7066	Abbs7066 Mouse isc	813	23	82.1	1682	7	ADE60401	Ade60401 Human Pro
741	23	82.1	552	3	AAG35480	Aag35480 Arabidops	814	23	82.1	1704	7	ADG90651	Adg90651 Hepatic s
742	23	82.1	554	2	AAK05271	Aak05271 Amino aci	815	23	82.1	1771	7	ADG90648	Adg90648 Hepatic s
743	23	82.1	589	5	AAU09863	Aau09863 Novel hum	816	23	82.1	1799	6	ABU34866	Abu34866 Protein e
744	23	82.1	593	8	ADN18083	Adn18083 Bacterial	817	23	82.1	1867	7	ADG90660	Adg90660 Hepatic s
745	23	82.1	598	5	AAU79802	Aau79802 Human G-p	818	23	82.1	1887	7	ADG90646	Adg90646 Hepatic s
746	23	82.1	598	5	AAE14516	Aae14516 Human nov	819	23	82.1	1899	7	ADG90662	Adg90662 Hepatic s
747	23	82.1	598	6	ABP97076	Abp97076 Human G p	820	23	82.1	1899	7	ADG90659	Adg90659 Hepatic s
748	23	82.1	609	4	ABBS7871	Abbs7871 Drosophil	821	23	82.1	1906	7	ADG90661	Adg90661 Hepatic s
749	23	82.1	621	3	AAG35479	Aag35479 Arabidops	822	23	82.1	1909	7	ADG90650	Adg90650 Hepatic s
750	23	82.1	641	5	ABP70069	Abp70069 Human NOV	823	23	82.1	1934	7	ADG90656	Adg90656 Hepatic s
751	23	82.1	642	8	ADO62467	Ado62467 Transcrip	824	23	82.1	2016	4	ABG66424	Abg66424 Drosophil
752	23	82.1	685	2	AAV35056	Aav35056 Chlamydia	825	23	82.1	2016	6	ABG73274	Abg73274 D. melano
753	23	82.1	753	8	ADN17958	Adn17958 Bacterial	826	23	82.1	2062	5	AAU99400	Aau99400 Human tum
754	23	82.1	702	8	ADR08827	Adr08827 Human pro	827	23	82.1	2067	6	ABU11831	Abu11831 Human MDD

828	23	82.1	2103	6	ABU35729	Abu35729 Protein e	901	22	78.6	140	9	ADZ73244	Adz73244 Human inc
829	22	78.6	7	4	AAM45436	Aam45436 H11 bindi	902	22	78.6	141	9	AEA21760	Aea21760 Porcine I
830	22	78.6	11	2	AAW08376	Aaw08376 Rat brain	903	22	78.6	143	4	AAO06601	Aao06601 Human pol
831	22	78.6	11	2	AAW73649	Aaw73649 Rat adeno	904	22	78.6	143	6	ADA57424	Ada57424 Human sec
832	22	78.6	12	3	AAW98096	Aay98096 Improved	905	22	78.6	143	6	ADA41302	Ada41302 Human sec
833	22	78.6	17	2	AAW90323	Abp62282 Human ant	906	22	78.6	146	8	ADY06817	Ady06817 Plant ful
834	22	78.6	18	5	ABP62282	Abp62282 Human imm	907	22	78.6	147	7	ADM04415	Adm04415 Human pro
835	22	78.6	18	8	ADK52485	Adk52485 Human kal	908	22	78.6	148	6	ABR53826	Abx53826 Protein s
836	22	78.6	19	8	ADQ92387	Adq92387 Human hul	909	22	78.6	148	7	ADK64990	Adk64990 Disease t
837	22	78.6	19	8	ADQ92381	Adq92381 Human hul	910	22	78.6	149	9	ABE36492	Aeb36492 L. pneumo
838	22	78.6	19	8	ADQ92383	Adq92383 Human hul	911	22	78.6	151	5	ABP43528	Abp43528 Human sec
839	22	78.6	19	8	ADQ80570	Adq80570 TNF-alpha	912	22	78.6	151	5	ADL07470	Adl07470 Human p28
840	22	78.6	19	8	ADQ80572	Adq80572 TNF-alpha	913	22	78.6	151	8	ADQ65391	Adq65391 Novel hum
841	22	78.6	19	8	ADQ80576	Adq80576 TNF-alpha	914	22	78.6	151	8	ADX89778	Adx89778 Plant ful
842	22	78.6	20	7	ADR40526	Adk40526 KDR & VEG	915	22	78.6	155	7	ASG69892	Asg69892 Pseudomon
843	22	78.6	20	7	ADR40526	Adk40526 KDR & VEG	916	22	78.6	155	7	ASG69892	Asg69892 Pseudomon
844	22	78.6	21	7	ADG99513	Adg99513 Cancer-re	917	22	78.6	165	4	ABG20263	Abg20263 Novel hum
845	22	78.6	27	4	ABG11067	Abg11067 Novel hum	918	22	78.6	168	2	AAW55521	Aaw55521 H. pylori
846	22	78.6	38	8	ADJ57561	Adj57561 Human CD9	919	22	78.6	169	7	ABO81527	Abw081527 Pseudomon
847	22	78.6	41	4	AAW92900	Aam92900 Human dig	920	22	78.6	171	5	ABG71402	Abg71402 Protein k
848	22	78.6	50	5	ABP42531	Abp42531 Human ova	921	22	78.6	174	8	ADI43378	Adi43378 Plant tra
849	22	78.6	56	4	AAU47514	Aau47514 Propionib	922	22	78.6	175	6	ABM69537	Abm69537 Photorhab
850	22	78.6	56	6	ABM44033	Abm44033 Propionib	923	22	78.6	176	4	ABG23145	Abg23145 Novel hum
851	22	78.6	62	4	ABG23138	Abg23138 Novel hum	924	22	78.6	185	4	ABG23139	Abg23139 Novel hum
852	22	78.6	62	7	ADF60406	Adf60406 Human con	925	22	78.6	187	4	ABG16394	Abg16394 Novel hum
853	22	78.6	63	5	ABF03513	Abp03513 Human ORF	926	22	78.6	193	4	AAW73162	Aaw73162 Human pro
854	22	78.6	64	3	ABG32054	Abg32054 Human sec	927	22	78.6	196	4	ABG23143	Abg23143 Novel hum
855	22	78.6	65	4	AAW87346	Aam87346 Human imm	928	22	78.6	197	3	AAW07530	Aaw07530 Arabidops
856	22	78.6	67	4	AAU43935	Aau43935 Propionib	929	22	78.6	197	4	ABB60548	Abb60548 Drosophil
857	22	78.6	67	6	ABM40454	Abm40454 Propionib	930	22	78.6	197	4	ABG95550	Abg95550 Human pro
858	22	78.6	67	7	ADF06982	Adf06982 Bacterial	931	22	78.6	200	4	ABG23144	Abg23144 Novel hum
859	22	78.6	68	2	AAW55401	Aaw55401 H. pylori	932	22	78.6	200	7	ABO80286	Abw080286 Pseudomon
860	22	78.6	69	3	AAW303208	Aag303208 Human sec	933	22	78.6	203	4	ABW70102	Abw70102 Drosophil
861	22	78.6	69	5	ABP53094	Abp53094 Human cyp	934	22	78.6	208	7	ADD30326	Add30326 Plant yie
862	22	78.6	69	9	ADZ88827	Adz88827 Breast ep	935	22	78.6	208	8	ADI44251	Adi44251 Plant tra
863	22	78.6	71	4	ABW15829	Abw15829 Human ner	936	22	78.6	209	4	AAG76051	Aag76051 Human col
864	22	78.6	72	3	AAQ33869	Aaq33869 Arabidops	937	22	78.6	215	9	ABW41312	Aeb41312 L. pneumo
865	22	78.6	77	4	AAU21269	Aau21269 Human nov	938	22	78.6	216	7	ABG63021	Abg63021 Klebsiell
866	22	78.6	77	4	ABG23134	Abg23134 Novel hum	939	22	78.6	217	4	ABG72852	Abg72852 Human olf
867	22	78.6	79	2	AAW35951	Aaw35951 Human CD9	940	22	78.6	217	4	ABG29722	Abg29722 Novel hum
868	22	78.6	79	6	AAW05058	Abu05058 Human exp	941	22	78.6	218	7	ADB95096	Adb95096 A. thalia
869	22	78.6	81	4	AAW74332	Aag74332 Human col	942	22	78.6	222	3	ADX24108	Adx24108 Mouse lat
870	22	78.6	82	5	ABP09945	Abp09945 Human ORF	943	22	78.6	222	8	ADX71184	Adx71184 Plant ful
871	22	78.6	83	4	AAO09648	Aao09648 Human pol	944	22	78.6	223	3	AAW24109	Aaw24109 Rat latex
872	22	78.6	85	3	AAW44637	Aam44637 Propionib	945	22	78.6	226	2	AAW15483	Aaw15483 Human p28
873	22	78.6	88	4	AAW90557	Aam90557 Human imm	946	22	78.6	226	2	AAW02430	Aay02430 Human gan
874	22	78.6	88	9	ABE94380	Aeb94380 Human SWI	947	22	78.6	226	7	ADE54537	Ades4537 Human Pro
875	22	78.6	93	5	ADK35325	Adk35325 Novel hum	948	22	78.6	226	7	ADE57693	Ades7693 Rat Prote
876	22	78.6	96	4	ABG29561	Abg29561 Novel hum	949	22	78.6	226	7	ADN95767	Adn95767 Rat Prote
877	22	78.6	96	8	ADY13570	Ady13570 Plant ful	950	22	78.6	226	7	ADN95764	Adn95764 Human BBC
878	22	78.6	102	8	ADN18715	Adn18715 Bacterial	951	22	78.6	226	8	ADN37256	Adn37256 Amino aci
879	22	78.6	105	7	ADC97044	Adc97044 E. faeciu	952	22	78.6	226	8	ADP25087	Adp25087 PRO polyyp
880	22	78.6	106	3	AAW57460	Aag57460 Arabidops	953	22	78.6	226	8	ADX77264	Adx77264 Plant ful
881	22	78.6	106	5	ABP09677	Abp09677 Human ORF	954	22	78.6	227	2	AAW86834	Aaw86834 Human CD9
882	22	78.6	106	6	ADW06798	Adw06798 Alloiococ	955	22	78.6	227	5	ABW78366	Abw78366 Amino aci
883	22	78.6	113	3	AAW57459	Aag57459 Arabidops	956	22	78.6	227	5	AAE14636	Aae14636 Human CD9
884	22	78.6	114	4	ABG19974	Abg19974 Novel hum	957	22	78.6	227	6	ABU05057	Abu05057 Human exp
885	22	78.6	118	7	ADL12112	Adl12112 Pseudomon	958	22	78.6	227	6	ABU05060	Abu05060 Human exp
886	22	78.6	118	7	ADL12112	Adl12112 Pseudomon	959	22	78.6	227	7	ABW00436	Abw00436 Human CD9
887	22	78.6	119	4	AAW23094	Aaw23094 Novel hum	960	22	78.6	227	7	ADK69862	Adk69862 Human CD9
888	22	78.6	122	6	ADA35859	Ada35859 Acinetoba	961	22	78.6	227	8	ADI19366	Adi19366 Human CD9
889	22	78.6	123	7	ADW64080	Adw64080 Human pro	962	22	78.6	227	9	AEA89005	Aea89005 Human CD9
890	22	78.6	127	5	ABP62174	Abp62174 Human imm	963	22	78.6	228	2	AAW27525	Aaw27525 Metastaei
891	22	78.6	127	7	ADW41862	Adw41862 Human ant	964	22	78.6	228	4	ABW44581	Abw44581 Human wou
892	22	78.6	134	6	ABU30639	Abu30639 Protein e	965	22	78.6	228	6	ABU05059	Abu05059 Human exp
893	22	78.6	134	6	ADW06800	Adw06800 Alloiococ	966	22	78.6	228	6	ABU05052	Abu05052 Human exp
894	22	78.6	135	4	AAO01764	Aao01764 Human pol	967	22	78.6	228	6	ABU05048	Abu05048 Human exp
895	22	78.6	136	8	ADW65803	Adw65803 Plant ful	968	22	78.6	228	6	ABU05056	Abu05056 Human exp
896	22	78.6	136	9	ABW91577	Abw91577 M. xanthu	969	22	78.6	228	6	ABU05049	Abu05049 Human exp
897	22	78.6	139	3	AAW07790	Aaw07790 C-jun N-t	970	22	78.6	228	6	ABU05050	Abu05050 Human exp
898	22	78.6	139	3	AAW07800	Aaw07800 Amino aci	971	22	78.6	228	6	ABU05053	Abu05053 Human exp
899	22	78.6	140	3	AAW64689	Aaw64689 Human 5'	972	22	78.6	228	7	ABW01519	Abw01519 Protein #
900	22	78.6	140	8	ADU72253	Adu72253 Signal pe	973	22	78.6	228	7	ADW89037	Adw89037 TAT278. 1

974 22 78.6 228 7 ADG32002 Human hom  
975 22 78.6 228 8 ADJ57558 Human CD9  
976 22 78.6 228 8 ADL26782 Human CD9  
977 22 78.6 228 8 ADL82853 Human PRO  
978 22 78.6 228 8 ADP23088 PRO polyp  
979 22 78.6 228 8 ADR73450 Human CD9  
980 22 78.6 228 9 ADV70263 Tumor-agg  
981 22 78.6 228 8 ADV97163 Human CD9  
982 22 78.6 228 9 ADY19604 PRO polyp  
983 22 78.6 228 9 ADY14362 PRO polyp  
984 22 78.6 228 9 AEB38016 L. pneumo  
985 22 78.6 228 9 AEB98450 Human CD9  
986 22 78.6 228 9 ADH86512 Enterococ  
987 22 78.6 231 2 AAY02431 Mouse gan  
988 22 78.6 231 2 AAY02432 Rat ganly  
989 22 78.6 231 4 ABB64761 Drosoephil  
990 22 78.6 232 7 ADE54535 Rat Prote  
991 22 78.6 232 6 ABU41450 Protein e  
992 22 78.6 235 4 AAB47423 EpsO. 10/  
993 22 78.6 237 5 ABG68915 Lawsonia  
994 22 78.6 238 8 ADX87449 Plant ful  
995 22 78.6 239 7 ADM26171 Hyperther  
996 22 78.6 240 5 AAU93102 Arabidops  
997 22 78.6 240 7 ADD30939 Plant yie  
998 22 78.6 240 7 ADE37245 Plant yie  
999 22 78.6 240 8 ADI41919 Plant tra  
1000 22 78.6 240 8 ADS43251 Bacterial

# ALIGNMENTS

RESULT 1  
AAB81979  
ID AAB81979 standard; peptide; 5 AA.  
XX  
AC AAB81979;  
DT 03-JUL-2001 (first entry)  
XX  
DE Ganglioside GD3 specific antibody related peptide SEQ ID NO: 3.  
XX  
KW Ganglioside; GD3; complementarity determining region; CDR; antibody;  
KW cancer.  
XX  
OS Mus musculus.  
XX  
PN WO200123432-A1.  
XX  
PD 05-APR-2001.  
XX  
PF 29-SEP-2000; 2000WO-JP006774.  
XX  
PR 30-SEP-1999; 99JP-00278291.  
PR 06-APR-2000; 2000JP-00105088.  
XX  
PA (KYOW ) KYOWA HAKKO KOGYO KK.  
XX  
PI Hanai N, Shitara K, Nakamura K, Niwa R;  
XX  
DR WPI; 2001-266143/27.  
XX  
PT New human type complementation-determining region-transplanted antibody  
PT and derivatives against ganglioside GD3; useful in diagnosis and therapy  
PT of e.g. tumors, with low antigenicity, little side effects but potent  
PT activity in cancer.  
XX  
PS Claim 5; Page 141; 183pp; Japanese.  
XX  
CC The present invention describes a monoclonal antibody which can react  
CC specifically with ganglioside GD3. The antibody and its derivatives are  
CC useful in the diagnosis and therapy of tumours, particularly cancer  
CC diagnosis. The present sequence is a protein used in the exemplification

CC of the invention  
XX  
SQ Sequence 5 AA;  
Query Match 100.0%; Score 28; DB 4; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 HYAMS 5  
DB 1 HYAMS 5  
RESULT 2  
ABU11004  
ID ABU11004 standard; peptide; 5 AA.  
XX  
AC ABU11004;  
XX  
DT 04-FEB-2003 (first entry)  
XX  
DE Modified ganglioside GD3 antibody associated peptide #1.  
XX  
KW Ganglioside GD3; anti-ganglioside GD3 antibody; tumour; melanoma.  
XX  
OS Mus musculus.  
XX  
PN WO200278739-A1.  
XX  
PD 10-OCT-2002.  
XX  
PF 29-MAR-2002; 2002WO-JP003170.  
XX  
PR 29-MAR-2001; 2001JP-00097483.  
XX  
PA (KYOW ) KYOWA HAKKO KOGYO KK.  
XX  
PI Shitara K, Niwa R, Kanazawa J, Asada M;  
XX  
DR WPI; 2003-067410/06.  
XX  
PT Drugs containing genetically-modified antibody against ganglioside GD3,  
PT its fragment, immunocompetent cell activators or/and antitumor agents in  
PT combination, applicable in treating malignant tumor like melanoma.  
XX  
PS Claim 6; Page 98; 121pp; Japanese.  
XX  
CC The invention describes drugs contain a genetically-modified antibody  
CC against ganglioside GD3 or its fragment and at least 1 of a substance  
CC capable of activating immunocompetent cells and a substance having an  
CC antitumor activity in combination. The drugs can be used to treat tumour  
CC like melanoma and can provide a treatment with enhanced therapeutic  
CC effect and little side-reactions, particularly to relieve problems of  
CC side-effects during the conventional single administration. This sequence  
CC represents a peptide associated with the anti- ganglioside GD3 antibody  
XX  
SQ Sequence 5 AA;  
Query Match 100.0%; Score 28; DB 6; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 HYAMS 5  
DB 1 HYAMS 5  
RESULT 3  
ADZ57810  
ID ADZ57810 standard; peptide; 5 AA.  
XX  
AC ADZ57810;  
XX



DT 30-JUN-2005 (first entry)  
 XX Ganglioside GD3 binding antibody associated CDR1 SEQ ID NO 14.  
 DE cytostatic; antibody engineering; cancer; neoplasm; ganglioside; GD3;  
 KW pharmaceutical.  
 KW Mus musculus.  
 OS WO2005035577-A1.  
 PN 21-APR-2005.  
 XX 08-OCT-2004; 2004WO-JP015314.  
 XX 08-OCT-2003; 2003JP-00350161.  
 XX (KYOWA) KYOWA HAKKO KOGYO KK.  
 XX Iida S, Satoh M, Urakubo M, Wakitani M, Uchida K, Niwa R;  
 PI Shitara K;  
 XX WPI; 2005-346195/35.  
 DR Antibody composition for treating ganglioside GD3 associated disease e.g.  
 XX cancer, comprises genetically modified antibody molecule, which  
 PT specifically binds to ganglioside GD3 and has N-glycoside-binding sugar  
 PT chain in its Fc domain.  
 XX Claim 8; SEQ ID NO 14; 124pp; Japanese.  
 PS The invention describes an antibody composition (I), comprising a  
 CC genetically modified antibody molecule which specifically binds to  
 CC ganglioside GD3 and has an N-glycoside-binding complex sugar chain in its  
 CC Fc domain, where the N-glycoside-binding complex sugar chain is a sugar  
 CC chain having no fucose attached to N-acetylglucosamine at the reducing  
 CC end of the sugar chain. Also described are: a transformant (II) capable  
 CC of producing (I), obtained by introducing DNA that encodes the antibody  
 CC molecule which specifically binds with ganglioside GD3, to a host cell;  
 CC producing (I), involving cultivating (I) in a culture medium, such that  
 CC C1 (sic) is produced and accumulated in the culture, extracting and  
 CC purifying C1 from the culture medium; a pharmaceutical (III) containing  
 CC C1 as an active ingredient; and a therapeutic agent (A1) for ganglioside  
 CC GD3 associated disease, comprising C1 as an active ingredient. (I) is  
 CC useful for treating GD3 associated disease, which involves administering  
 CC (I), where the GD3 associated diseases is cancer. (A1) is also useful for  
 CC treating GD3 associated disease. (II) is useful for producing (I). (I) is  
 CC useful for manufacturing a therapeutic agent for GD3 associated disease.  
 CC This sequence represents a ganglioside GD3 binding antibody associated  
 CC peptide.  
 XX Sequence 5 AA;  
 SQ Query Match 100.0%; Score 28; DB 9; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 HYAMS 5  
 DB |||||  
 1 HYAMS 5  
 RESULT 4  
 AAB14979  
 ID AAB14979 standard; protein; 119 AA.  
 XX AAB14979;  
 AC AAB14979;  
 XX 01-DEC-2000 (first entry)  
 DT Staphylococcus aureus phosphopantethienyl transferase protein Acps.  
 DE Acps; phosphopantethienyl transferase; antibacterial;  
 KW

KW Helicobacter pylori; stomach cancer; ulcer; gastritis.  
 XX Staphylococcus aureus.  
 OS WO200040594-A1.  
 PN 13-JUL-2000.  
 XX 13-DEC-1999; 99WO-US029464.  
 XX 08-JAN-1999; 99US-00227700.  
 XX (SMIK) SMITHKLINE BEECHAM CORP.  
 XX Pearson SC;  
 PI WPI; 2000-465946/40.  
 DR N-PSDB; AAA73679.  
 XX New isolated Staphylococcus aureus polypeptide, referred to as Acps, for  
 PT treating or diagnosing individuals with a disease in need of enhanced or  
 PT inhibited activity or expression of the polypeptide.  
 XX Claim 1; Page 3; 38pp; English.  
 PS The present sequence is the Staphylococcus aureus phosphopantethienyl  
 CC transferase family protein Acps. The DNA encoding this sequence was  
 CC isolated from a Staphylococcus aureus DNA library. The Acps protein and  
 CC its agonists, antagonists or nucleic acids may be used to treat  
 CC individuals that are in need of enhanced or inhibited activity or  
 CC expression of the protein, or an immunological response to it. They may  
 CC also be used to detect and treat microbial diseases, such as Helicobacter  
 CC pylori infections that cause stomach cancer, ulcers and gastritis  
 XX Sequence 119 AA;  
 SQ Query Match 100.0%; Score 28; DB 3; Length 119;  
 Best Local Similarity 100.0%; Pred. No. 95;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 HYAMS 5  
 DB |||||  
 106 HYAMS 110  
 RESULT 5  
 AAB81985  
 ID AAB81985 standard; protein; 119 AA.  
 XX AAB81985;  
 AC AAB81985;  
 XX 03-JUL-2001 (first entry)  
 DT Ganglioside GD3 specific antibody related protein SEQ ID NO: 9.  
 XX Ganglioside; GD3; complementarity determining region; CDR; antibody;  
 KW cancer.  
 XX Synthetic.  
 OS WO200123432-A1.  
 PN 05-APR-2001.  
 PD 29-SEP-2000; 2000WO-JP006774.  
 XX 30-SEP-1999; 99JP-00278291.  
 PR 06-APR-2000; 2000JP-00105088.  
 XX (KYOWA) KYOWA HAKKO KOGYO KK.  
 XX Hanai N, Shitara K, Nakamura K, Niwa R;  
 PI



DR WPI; 2001-266143/27.  
XX  
PT New human type complementation-determining region-transplanted antibody  
PT and derivatives against ganglioside GD3, useful in diagnosis and therapy  
PT of e.g. tumors, with low antigenicity, little side effects but potent  
PT activity in cancer.  
XX  
PS Claim 20; Page 142-143; 183pp; Japanese.  
XX  
CC The present invention describes a monoclonal antibody which can react  
CC specifically with ganglioside GD3. The antibody and its derivatives are  
CC useful in the diagnosis and therapy of tumours, particularly cancer  
CC diagnosis. The present sequence is a protein used in the exemplification  
CC of the invention  
XX  
SQ Sequence 119 AA;  
  
Query Match 100.0%; Score 28; DB 4; Length 119;  
Best Local Similarity 100.0%; Pred. No. 95;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 HYAMS 5  
DB 31 HYAMS 35  
  
RESULT 6  
AAB81989  
ID AAB81989 standard; protein; 119 AA.  
XX  
AC AAB81989;  
XX  
DT 03-JUL-2001 (first entry)  
XX  
DE Ganglioside GD3 specific antibody related protein SEQ ID NO: 55.  
XX  
KW Ganglioside; GD3; complementarity determining region; CDR; antibody;  
KW cancer.  
XX  
OS Mus musculus.  
XX  
PN WO200123432-A1.  
XX  
PD 05-APR-2001.  
XX  
PF 29-SEP-2000; 2000WO-JP006774.  
XX  
PR 30-SEP-1999; 99JP-00278291.  
PR 06-APR-2000; 2000JP-00105088.  
XX  
PA (KYOW ) KYOWA HAKKO KOGYO KK.  
XX  
PI Hanai N, Shitara K, Nakamura K, Niwa R;  
XX  
WPI; 2001-266143/27.  
XX  
PT New human type complementation-determining region-transplanted antibody  
PT and derivatives against ganglioside GD3, useful in diagnosis and therapy  
PT of e.g. tumors, with low antigenicity, little side effects but potent  
PT activity in cancer.  
XX  
PS Claim 10; Page 173-174; 183pp; Japanese.  
XX  
CC The present invention describes a monoclonal antibody which can react  
CC specifically with ganglioside GD3. The antibody and its derivatives are  
CC useful in the diagnosis and therapy of tumours, particularly cancer  
CC diagnosis. The present sequence is a protein used in the exemplification  
CC of the invention  
XX  
SQ Sequence 119 AA;  
  
Query Match 100.0%; Score 28; DB 4; Length 119;  
Best Local Similarity 100.0%; Pred. No. 95;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 HYAMS 5  
DB 31 HYAMS 35  
  
RESULT 7  
ABU11012  
ID ABU11012 standard; protein; 119 AA.  
XX  
AC ABU11012;  
XX  
DT 04-FEB-2003 (first entry)  
XX  
DE Modified ganglioside GD3 antibody associated protein #5.  
XX  
KW Ganglioside GD3; anti-ganglioside GD3 antibody; tumour; melanoma.  
XX  
OS Mus musculus.  
XX  
PN WO200278739-A1.  
XX  
PD 10-OCT-2002.  
XX  
PF 29-MAR-2002; 2002WO-JP003170.  
XX  
PR 29-MAR-2001; 2001JP-00097483.  
XX  
PA (KYOW ) KYOWA HAKKO KOGYO KK.  
XX  
PI Shitara K, Niwa R, Kanazawa J, Asada M;  
XX  
WPI; 2003-067410/06.  
XX  
PT Drugs containing genetically-modified antibody against ganglioside GD3,  
PT its fragment, immunocompetent cell activators or/and antitumor agents in  
PT combination, applicable in treating malignant tumor like melanoma.  
XX  
PS Claim 7; Page 112-113; 121pp; Japanese.  
XX  
CC The invention describes drugs contain a genetically-modified antibody  
CC against ganglioside GD3 or its fragment and at least 1 of a substance  
CC capable of activating immunocompetent cells and a substance having an  
CC antitumor activity in combination. The drugs can be used to treat tumour  
CC like melanoma and can provide a treatment with enhanced therapeutic  
CC effect and little side-reactions, particularly to relieve problems of  
CC side-effects during the conventional single administration. This sequence  
CC represents a protein associated with the anti- ganglioside GD3 antibody  
XX  
SQ Sequence 119 AA;  
  
Query Match 100.0%; Score 28; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 95;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 HYAMS 5  
DB 31 HYAMS 35  
  
RESULT 8  
ABU11010  
ID ABU11010 standard; protein; 119 AA.  
XX  
AC ABU11010;  
XX  
DT 04-FEB-2003 (first entry)  
XX  
DE Modified ganglioside GD3 antibody associated protein #3.  
XX  
KW Ganglioside GD3; anti-ganglioside GD3 antibody; tumour; melanoma.  
XX

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OS Synthetic.
XX WO200278739-A1.
PN
XX 10-OCT-2002.
PD
XX
XX 29-MAR-2002; 2002WO-JP003170.
XX
XX
XX 29-MAR-2001; 2001JP-00097483.
PR
XX (KYOW ) KYOWA HAKKO KOGYO KK.
PA
XX Shitara K, Niwa R, Kanazawa J, Asada M;
PI
XX WPI; 2003-067410/06.
DR
XX
XX
PT Drugs containing genetically-modified antibody against ganglioside GD3,
PT its fragment, immunocompetent cell activators or/and anticumor agents in
PT combination, applicable in treating malignant tumor like melanoma.
XX
XX Claim 8; Page 99; 121pp; Japanese.
PS
XX
XX The invention describes drugs contain a genetically-modified antibody
CC against ganglioside GD3 or its fragment and at least 1 of a substance
CC capable of activating immunocompetent cells and a substance having an
CC antitumor activity in combination. The drugs can be used to treat tumour
CC like melanoma and can provide a treatment with enhanced therapeutic
CC effect and little side-reactions, particularly to relieve problems of
CC side-effects during the conventional single administration. This sequence
CC represents a protein associated with the anti- ganglioside GD3 antibody
XX
XX Sequence 119 AA;
SQ
Query Match 100.0%; Score 28; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HYAMS 5
DB 31 HYAMS 35
RESULT 9
ABR83239
ID ABR83239 standard; protein; 119 AA.
XX
AC ABR83239;
XX
DT 30-SEP-2003 (first entry)
XX
DE S. aureus acyl carrier protein synthase acps protein SEQ ID NO:34.
XX
KW Crystallised recombinant polypeptide; Staphylococcus aureus; vaccine;
KW Streptococcus pneumoniae; Helicobacter pylori; Pseudomonas aeruginosa;
KW membrane biosynthesis; crystal form; antibacterial; crystal structure;
KW immunological response; vaccination; ftsZ; fabZ; fabG; acps; murD; murC;
KW fabH; tagD; obg.
XX
OS Staphylococcus aureus.
XX
XX WO2003027139-A2.
PN
XX
XX 03-APR-2003.
XX
XX 24-SEP-2002; 2002WO-CA001443.
XX
XX 24-SEP-2001; 2001US-0324449P.
PR
XX 24-SEP-2001; 2001US-0324504P.
PR
XX 01-OCT-2001; 2001US-0326269P.
PR
XX 03-OCT-2001; 2001US-0326887P.
PR
XX 24-OCT-2001; 2001US-0339560P.
PR
XX 25-OCT-2001; 2001US-0337471P.
PR
XX 26-OCT-2001; 2001US-0340000P.
XX

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PR 26-OCT-2001; 2001US-0340002P.
PR 26-OCT-2001; 2001US-0340027P.
PR 18-DEC-2001; 2001US-0341767P.
PR 21-DEC-2001; 2001US-0344307P.
PR 27-DEC-2001; 2001US-0343946P.
XX
XX (AFFI-) AFFINIUM PHARM INC.
XX
XX Edwards A, Dharamsi A, Vedadi M, Alam MZ, Awrey D, Beattie B;
PI Canadien V, Domagala M, Houston S, Kanagarajah D, Li Q, Mansoury K;
PI McDonald M, Necakov S, Ng I, Pinder B, Sheldrick B, Vallee F;
PI Viola C, Wrezel O;
XX
XX WPI; 2003-441048/41.
DR N-PSDB; ACF06198.
XX
XX Novel crystallized recombinant polypeptides from Staphylococcus aureus,
PT Streptococcus pneumoniae and Helicobacter pylori and which are involved
PT in membrane biosynthesis, useful as targets for pathogenic bacteria.
XX
XX Claim 84; Fig 29; 312pp; English.
PS
XX
XX The present invention describes a crystallised recombinant polypeptide
CC (I) comprising amino acid sequence of polypeptides from Staphylococcus
CC aureus, Streptococcus pneumoniae, Helicobacter pylori and Pseudomonas
CC aeruginosa and which are involved in membrane biosynthesis, or amino acid
CC sequences having at least 90 % identity with the polypeptide sequence,
CC where the polypeptide is in crystal form. (I) has antibacterial activity
CC and can be used in vaccines. (I) is useful for designing a modulator for
CC the prevention or treatment of S. aureus, H. pylori, S. pneumoniae, and
CC P. aeruginosa-related disease or disorder. (I) is also useful for
CC identifying small molecules that bind to a recombinant polypeptide. The
CC structural and functional information of (I) aid in the discovery and
CC design of therapeutic and diagnostic molecules. The crystal structure is
CC useful to make a structural or computer model of the polypeptide, complex
CC or its portion. (I) can be used for inducing an immunological response in
CC an individual and as an antigen for vaccination of a host to produce
CC specific antibodies which protect against invasion of bacteria, for
CC example by blocking adherence of bacteria to damaged tissue. ACF06185 to
CC ACF06232 and ABR83203 to ABR83333 represent sequences used in the
CC exemplification of the present invention
XX
XX Sequence 119 AA;
SQ
Query Match 100.0%; Score 28; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HYAMS 5
DB 106 HYAMS 110
RESULT 10
ABR83238
ID ABR83238 standard; protein; 119 AA.
XX
XX ABR83238;
AC
XX
XX 30-SEP-2003 (first entry)
XX
XX S. aureus acyl carrier protein synthase acps protein SEQ ID NO:32.
XX
XX Crystallised recombinant polypeptide; Staphylococcus aureus; vaccine;
KW Streptococcus pneumoniae; Helicobacter pylori; Pseudomonas aeruginosa;
KW membrane biosynthesis; crystal form; antibacterial; crystal structure;
KW immunological response; vaccination; ftsZ; fabZ; fabG; acps; murD; murC;
KW fabH; tagD; obg.
XX
OS Staphylococcus aureus.
XX
XX WO2003027139-A2.
PN
XX
XX

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PD 03-APR-2003.
XX
XX
XX 24-SEP-2002; 2002WO-CA001443.
XX
XX 24-SEP-2001; 2001US-0324449P.
XX 24-SEP-2001; 2001US-0324504P.
XX 01-OCT-2001; 2001US-0326269P.
XX 03-OCT-2001; 2001US-0326887P.
XX 24-OCT-2001; 2001US-0339560P.
XX 25-OCT-2001; 2001US-0337471P.
XX 26-OCT-2001; 2001US-0340000P.
XX 26-OCT-2001; 2001US-0340002P.
XX 26-OCT-2001; 2001US-0340027P.
XX 18-DEC-2001; 2001US-0341767P.
XX 21-DEC-2001; 2001US-0344307P.
XX 27-DEC-2001; 2001US-0343946P.
XX
XX (AFFI-) AFFINIUM PHARM INC.
XX
XX Edwards A, Dharamsi A, Vedadi M, Alam MZ, Awrey D, Beattie B;
XX Canadian V, Domagala M, Houston S, Kanagarajah D, Li Q, Mansoury K;
XX McDonald M, Necakov S, Ng I, Pinder B, Sheldrick B, Vallee F;
XX Viola C, Wrezel O;
XX
XX WPI; 2003-441048/41.
XX N-PSDB; ACP06197.
XX
XX Novel crystallized recombinant polypeptides from Staphylococcus aureus,
XX Streptococcus pneumoniae and Helicobacter pylori and which are involved
XX in membrane biosynthesis, useful as targets for pathogenic bacteria.
XX
XX Claim 84; Fig 27; 312pp; English.
XX
XX The present invention describes a crystallised recombinant polypeptide
XX (I) comprising amino acid sequence of polypeptides from Staphylococcus
XX aureus, Streptococcus pneumoniae, Helicobacter pylori and Pseudomonas
XX aeruginosa and which are involved in membrane biosynthesis, or amino acid
XX sequences having at least 90 % identity with the polypeptide sequence,
XX where the polypeptide is in crystal form. (I) has antibacterial activity
XX and can be used in vaccines. (I) is useful for designing a modulator for
XX the prevention or treatment of S. aureus, H. pylori, S. pneumoniae, and
XX P. aeruginosa-related disease or disorder. (I) is also useful for
XX identifying small molecules that bind to a recombinant polypeptide. The
XX structural and functional information of (I) aid in the discovery and
XX design of therapeutic and diagnostic molecules. The crystal structure is
XX useful to make a structural or computer model of the polypeptide, complex
XX or its portion. (I) can be used for inducing an immunological response in
XX an individual and as an antigen for vaccination of a host to produce
XX specific antibodies which protect against invasion of bacteria, for
XX example by blocking adherence of bacteria to damaged tissue. ACP06185 to
XX ACP06232 and ABR83203 to ABR83333 represent sequences used in the
XX exemplification of the present invention
XX
XX Sequence 119 AA;
SQ
Query Match 100.0%; Score 28; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HYAMS 5
DB 106 HYAMS 110
RESULT 11
ABU16272
ID ABU16272 standard; protein; 119 AA.
XX
XX AC ABU16272;
XX
XX 19-JUN-2003 (first entry)
XX
XX Protein encoded by Prokaryotic essential gene #1799.
XX
XX Antisense; prokaryotic essential gene; cell proliferation; drug design.
XX
XX Staphylococcus aureus.
XX
XX WO200277183-A2.
XX
XX 03-OCT-2002.
XX
XX 21-MAR-2002; 2002WO-US009107.
XX
XX 21-MAR-2001; 2001US-00815242.
XX 06-SEP-2001; 2001US-00948993.
XX 25-OCT-2001; 2001US-0342923P.
XX 08-FEB-2002; 2002US-00072851.
XX 06-MAR-2002; 2002US-0362699P.
XX
XX (ELIT-) ELITRA PHARM INC.
XX
XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
XX Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX
XX WPI; 2003-029926/02.
XX N-PSDB; ACA20142.
XX
XX New antisense nucleic acids, useful for identifying proteins or screening
XX for homologous nucleic acids required for cellular proliferation to
XX isolate candidate molecules for rational drug discovery programs.
XX
XX Claim 25; SEQ ID NO 44196; 1766pp; English.
XX
XX The invention relates to an isolated nucleic acid comprising any one of
XX the 6213 antisense sequences given in the specification where expression
XX of the nucleic acid inhibits proliferation of a cell. Also included are:
XX (1) a vector comprising a promoter operably linked to the nucleic acid
XX encoding a polypeptide whose expression is inhibited by the antisense
XX nucleic acid; (2) a host cell containing the vector; (3) an isolated
XX polypeptide or its fragment whose expression is inhibited by the
XX antisense nucleic acid; (4) an antibody capable of specifically binding
XX the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
XX proliferation or the activity of a gene in an operon required for
XX proliferation; (7) identifying a compound that influences the activity of
XX the gene product or that has an activity against a biological pathway
XX required for proliferation, or that inhibits cellular proliferation; (8)
XX identifying a gene required for cellular proliferation or the biological
XX pathway in which a proliferation-required gene or its gene product lies
XX or a gene on which the test compound that inhibits proliferation of an
XX organism acts; (9) manufacturing an antibiotic; (10) profiling a
XX compound's activity; (11) a culture comprising strains in which the gene
XX product is overexpressed or underexpressed; (12) determining the extent
XX to which each of the strains is present in a culture or collection of
XX strains; or (13) identifying the target of a compound that inhibits the
XX proliferation of an organism. The antisense nucleic acids are useful for
XX identifying proteins or screening for homologous nucleic acids required
XX for cellular proliferation to isolate candidate molecules for rational
XX drug discovery programs, or for screening homologous nucleic acids
XX required for proliferation in cells other than S. aureus, S. typhimurium,
XX K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of
XX the target prokaryotic essential genes. Note: The sequence data for this
XX patent did not form part of the printed specification, but was obtained
XX in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 119 AA;
SQ
Query Match 100.0%; Score 28; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HYAMS 5
DB 106 HYAMS 110

```

RESULT 12  
 ABU43645  
 ID ABU43645 standard; protein; 119 AA.  
 XX  
 AC ABU43645;  
 XX  
 DT 19-JUN-2003 (first entry)  
 XX  
 DE Protein encoded by Prokaryotic essential gene #29172.  
 XX  
 KW Antisense; prokaryotic essential gene; cell proliferation; drug design.  
 XX  
 OS Staphylococcus haemolyticus.  
 XX  
 PN WO200277183-A2.  
 XX  
 PD 03-OCT-2002.  
 XX  
 XX 21-MAR-2002; 2002WO-US009107.  
 XX  
 PR 21-MAR-2001; 2001US-00815242.  
 PR 06-SEP-2001; 2001US-00948993.  
 PR 25-OCT-2001; 2001US-0342923P.  
 PR 08-FEB-2002; 2002US-00072851.  
 PR 06-MAR-2002; 2002US-0362699P.  
 XX  
 PA (ELIT-) ELITRA PHARM INC.  
 XX  
 XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;  
 PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;  
 XX  
 DR WPI; 2003-029926/02.  
 DR N-PSDB; ACA47515.  
 XX  
 PT New antisense nucleic acids, useful for identifying proteins or screening  
 PT for homologous nucleic acids required for cellular proliferation to  
 PT isolate candidate molecules for rational drug discovery programs.  
 XX  
 PS Claim 25; SEQ ID NO 71569; 1766pp; English.  
 CC The invention relates to an isolated nucleic acid comprising any one of  
 CC the 6213 antisense sequences given in the specification where expression  
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:  
 CC (1) a vector comprising a promoter operably linked to the nucleic acid  
 CC encoding a polypeptide whose expression is inhibited by the antisense  
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated  
 CC polypeptide or its fragment whose expression is inhibited by the  
 CC antisense nucleic acid; (4) an antibody capable of specifically binding  
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
 CC proliferation or the activity of a gene in an operon required for  
 CC proliferation; (7) identifying a compound that influences the activity of  
 CC the gene product or that has an activity against a biological pathway  
 CC required for proliferation, or that inhibits cellular proliferation; (8)  
 CC identifying a gene required for cellular proliferation or the biological  
 CC pathway in which a proliferation-required gene or its gene product lies  
 CC or a gene on which the test compound that inhibits proliferation of an  
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a  
 CC compound's activity; (11) a culture comprising strains in which the gene  
 CC product is overexpressed or underexpressed; (12) determining the extent  
 CC to which each of the strains is present in a culture or collection of  
 CC strains; or (13) identifying the target of a compound that inhibits the  
 CC proliferation of an organism. The antisense nucleic acids are useful for  
 CC identifying proteins or screening for homologous nucleic acids required  
 CC for cellular proliferation to isolate candidate molecules for rational  
 CC drug discovery programs, or for screening homologous nucleic acids  
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,  
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of  
 CC the target prokaryotic essential genes. Note: The sequence data for this  
 CC patent did not form part of the printed specification, but was obtained  
 CC in electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences

SQ Sequence 119 AA;  
 Query Match 100.0%; Score 28; DB 6; Length 119;  
 Best Local Similarity 100.0%; Pred. No. 95;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 HVAMS 5  
 DB 107 HYAMS 111  
 XX  
 RESULT 13  
 ABW71799  
 ID ABW71799 standard; protein; 119 AA.  
 XX  
 AC ABW71799;  
 XX  
 DT 20-NOV-2003 (first entry)  
 XX  
 DE Staphylococcus aureus protein #1039.  
 XX  
 KW Antibacterial; vaccine; gene therapy; infection; sepsis; diagnosis;  
 KW enzymatic assay; antibiotic target.  
 XX  
 OS Staphylococcus aureus.  
 XX  
 PN WO200294868-A2.  
 XX  
 PD 28-NOV-2002.  
 XX  
 PF 27-MAR-2002; 2002WO-IB002637.  
 XX  
 PR 27-MAR-2001; 2001GB-00007661.  
 XX  
 PA (CHIR-) CHIRON SPA.  
 XX  
 PI Masignani V, Mora M, Scarselli M;  
 XX  
 DR WPI; 2003-120786/11.  
 DR N-PSDB; ACF73359.  
 XX  
 PT New Staphylococcus aureus protein, useful as a vaccine for treating or  
 PT preventing Staphylococcal infection, specifically an infection caused by  
 PT *S. aureus*, e.g. sepsis.  
 XX  
 PS Claim 1; SEQ ID NO 2078; 49pp; English.  
 CC The invention relates to novel genes and encoded proteins from  
 CC Staphylococcus aureus. A composition comprising the *S. aureus* protein, a  
 CC nucleic acid encoding the protein, or an antibody to the protein, is  
 CC useful as a pharmaceutical, particularly as a vaccine for treating or  
 CC preventing infection due to Staphylococcus bacteria, specifically an  
 CC infection caused by *S. aureus*. The composition is particularly useful for  
 CC treating or preventing sepsis in a patient. The composition can also be  
 CC used for diagnostics. The protein is also used in an assay for enzymatic  
 CC studies and as a target for antibiotics. This sequence represents one of  
 CC the novel *S. aureus* proteins of the invention  
 XX  
 SQ Sequence 119 AA;  
 Query Match 100.0%; Score 28; DB 6; Length 119;  
 Best Local Similarity 100.0%; Pred. No. 95;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 HVAMS 5  
 DB 106 HYAMS 110  
 XX  
 RESULT 14  
 ADW94782  
 ID ADW94782 standard; protein; 119 AA.  
 XX

AC ADW94782;  
XX 21-APR-2005 (first entry)  
XX Proliferation-required gene dpj protein, SEQ ID 722.  
DE  
XX  
XX Cell proliferation; microorganism; dpj.  
XX Staphylococcus aureus.  
OS  
XX US2005026189-A1.  
PN  
XX  
XX 03-FEB-2005.  
XX  
XX 28-MAY-2004; 2004US-00857625.  
PF  
XX 29-MAY-2003; 2003US-0474768P.  
PR  
XX (WANG/) WANG L.  
PA (ZAMU/) ZAMUDIO C.  
XX  
XX Wang L, Zamudio C;  
PI  
XX WPI; 2005-151156/16.  
DR  
XX N-PSDB; ADW94490.  
DR  
XX  
XX Predicting operons of prokaryotes, by segregating consecutive genes of  
PT organism, into bins based on their orientation, performing composite  
PT operon prediction analysis, associating genes between operon boundaries  
PT as putative operons.  
XX  
XX Example 7; SEQ ID NO 722; 116pp; English.  
XX  
XX The present invention relates to a method (M1) for predicting operons of  
CC target prokaryotes. The method comprises identifying consecutive genes of  
CC an organism's genome, determining the orientation of a gene in the genome  
CC relative to its flanking genes, segregating the genes into bins based on  
CC their orientation, performing composite operon prediction analysis,  
CC determining operon boundaries by identifying gene pairs with confidence  
CC scores below specific threshold and associating genes between boundaries  
CC as putative operons. Also claimed is a computer-based system (I) for  
CC carrying out (M1). (M1) is useful for identifying a gene that is required  
CC for proliferation of a microorganism and in cell-based assays. ADW94067-  
CC ADW94260 are proliferation-required operons from Staphylococcus aureus,  
CC predicted using the method of the invention. ADW94261-ADW94610 are  
CC proliferation-required genes, and ADW94611-ADW94884 are the encoded  
CC proteins, from the predicted operons of the invention. Note: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format directly from USPTO at  
CC seqdata.uspto.gov/sequence.html?DocID=20050026189.  
XX  
XX Sequence 119 AA;  
SQ  
Query Match 100.0%; Score 28; DB 9; Length 119;  
Best Local Similarity 100.0%; Pred. No. 95;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 HYAMS 5  
DB 106 HYAMS 110  
RESULT 15  
ADZ57816  
ID ADZ57816 standard; protein; 119 AA.  
XX  
XX ADZ57816;  
XX  
XX 30-JUN-2005 (first entry)  
XX  
XX Ganglioside GD3 binding antibody associated protein SEQ ID NO 20.  
DE  
XX cytostatic; antibody engineering; cancer; neoplasm; ganglioside; GD3;  
KW

KW pharmaceutical.  
XX  
XX Mus musculus.  
XX  
XX WO2005035577-A1.  
PN  
XX 21-APR-2005.  
PD  
XX 08-OCT-2004; 2004WO-JP015314.  
PF  
XX 08-OCT-2003; 2003JP-00350161.  
PR  
XX (KYOW ) KYOWA HAKKO KOGYO KK.  
XX  
XX Iida S, Satoh M, Urakubo M, Wakitani M, Uchida K, Niwa R;  
PI Shitara K;  
PI  
XX WPI; 2005-346195/35.  
DR  
XX  
XX Antibody composition for treating ganglioside GD3 associated disease e.g.  
PT cancer, comprises genetically modified antibody molecule, which  
PT specifically binds to ganglioside GD3 and has N-glycoside-binding sugar  
PT chain in its Fc domain.  
XX  
XX Claim 13; SEQ ID NO 20; 124pp; Japanese.  
XX  
XX The invention describes an antibody composition (I), comprising a  
CC genetically modified antibody molecule which specifically binds to  
CC ganglioside GD3 and has an N-glycoside-binding complex sugar chain in its  
CC Fc domain, where the N-glycoside-binding complex sugar chain is a sugar  
CC chain having no fucose attached to N-acetylglucosamine at the reducing  
CC end of the sugar chain. Also described are: a transformant (II) capable  
CC of producing (I), obtained by introducing DNA that encodes the antibody  
CC molecule which specifically binds with ganglioside GD3, to a host cell;  
CC producing (I), involving cultivating (I) in a culture medium, such that  
CC C1 (sic) is produced and accumulated in the culture, extracting and  
CC purifying C1 from the culture medium; a pharmaceutical (III) containing  
CC C1 as an active ingredient; and a therapeutic agent (A1) for ganglioside  
CC GD3 associated disease, comprising C1 as an active ingredient. (I) is  
CC useful for treating GD3 associated disease, which involves administering  
CC (I), where the GD3 associated disease is cancer. (A1) is also useful for  
CC treating GD3 associated disease. (II) is useful for producing (I). (I) is  
CC useful for manufacturing a therapeutic agent for GD3 associated disease.  
CC This sequence represents a ganglioside GD3 binding antibody associated  
CC protein.  
XX  
XX Sequence 119 AA;  
SQ  
Query Match 100.0%; Score 28; DB 9; Length 119;  
Best Local Similarity 100.0%; Pred. No. 95;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 HYAMS 5  
DB 31 HYAMS 35  
RESULT 16  
ADZ57818  
ID ADZ57818 standard; protein; 119 AA.  
XX  
XX ADZ57818;  
XX  
XX 30-JUN-2005 (first entry)  
XX  
XX Ganglioside GD3 binding antibody associated protein SEQ ID NO 22.  
DE  
XX cytostatic; antibody engineering; cancer; neoplasm; ganglioside; GD3;  
KW pharmaceutical.  
XX  
XX Synthetic.  
XX  
XX WO2005035577-A1.  
PN

```

XX PD 21-APR-2005.
XX XX
XX PF 08-OCT-2004; 2004WO-JP015314.
XX XX
XX PR 08-OCT-2003; 2003JP-00350161.
XX XX
XX PA (KYOW ) KYOWA HAKKO KOGYO KK.
XX XX
XX PI Iida S, Satoh M, Urakubo M, Wakitani M, Uchida K, Niwa R;
XX PI Shitara K;
XX XX
XX DR WPI; 2005-346195/35.
XX XX
XX PT Antibody composition for treating ganglioside GD3 associated disease e.g.
XX PT cancer, comprises genetically modified antibody molecule, which
XX PT specifically binds to ganglioside GD3 and has N-glycoside-binding sugar
XX PT chain in its Fc domain.
XX PS Claim 19; SEQ ID NO 22; 124pp; Japanese.
XX CC The invention describes an antibody composition (I), comprising a
XX CC genetically modified antibody molecule which specifically binds to
XX CC ganglioside GD3 and has an N-glycoside-binding complex sugar chain in its
XX CC Fc domain, where the N-glycoside-binding complex sugar chain is a sugar
XX CC chain having no fucose attached to N-acetylglucosamine at the reducing
XX CC end of the sugar chain. Also described are: a transformant (II) capable
XX CC of producing (I), obtained by introducing DNA that encodes the antibody
XX CC molecule which specifically binds with ganglioside GD3, to a host cell;
XX CC producing (I), involving cultivating (I) in a culture medium, such that
XX CC Cl (sic) is produced and accumulated in the culture, extracting and
XX CC purifying Cl from the culture medium; a pharmaceutical (III) containing
XX CC Cl as an active ingredient; and a therapeutic agent (A1) for ganglioside
XX CC GD3 associated disease, comprising Cl as an active ingredient. (I) is
XX CC useful for treating GD3 associated disease, which involves administering
XX CC (I), where the GD3 associated diseases is cancer. (A1) is also useful for
XX CC treating GD3 associated disease. (II) is useful for producing (I). (I) is
XX CC useful for manufacturing a therapeutic agent for GD3 associated disease.
XX CC This sequence represents a ganglioside GD3 binding antibody associated
XX CC protein.
XX SQ Sequence 119 AA;

Query Match 100.0%; Score 28; DB 9; Length 119;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HVAMS 5
DB |||||
31 HYAMS 35

RESULT 17
ADZ57821
ID ADZ57821 standard; protein; 119 AA.
XX
XX AC ADZ57821;
XX
XX DT 30-JUN-2005 (first entry)
XX
XX DE Ganglioside GD3 binding antibody associated protein SEQ ID NO 25.
XX
XX KW cytostatic; antibody engineering; cancer; neoplasm; ganglioside; GD3;
XX KW pharmaceutical.
XX OS Synthetic.
XX XX WO2005035577-A1.
XX PN
XX PD 21-APR-2005.
XX XX
XX PF 08-OCT-2004; 2004WO-JP015314.
XX XX

PR 08-OCT-2003; 2003JP-00350161.
XX XX
XX PA (KYOW ) KYOWA HAKKO KOGYO KK.
XX XX
XX PI Iida S, Satoh M, Urakubo M, Wakitani M, Uchida K, Niwa R;
XX PI Shitara K;
XX XX
XX DR WPI; 2005-346195/35.
XX XX
XX PT Antibody composition for treating ganglioside GD3 associated disease e.g.
XX PT cancer, comprises genetically modified antibody molecule, which
XX PT specifically binds to ganglioside GD3 and has N-glycoside-binding sugar
XX PT chain in its Fc domain.
XX PS Claim 24; SEQ ID NO 25; 124pp; Japanese.
XX CC The invention describes an antibody composition (I), comprising a
XX CC genetically modified antibody molecule which specifically binds to
XX CC ganglioside GD3 and has an N-glycoside-binding complex sugar chain in its
XX CC Fc domain, where the N-glycoside-binding complex sugar chain is a sugar
XX CC chain having no fucose attached to N-acetylglucosamine at the reducing
XX CC end of the sugar chain. Also described are: a transformant (II) capable
XX CC of producing (I), obtained by introducing DNA that encodes the antibody
XX CC molecule which specifically binds with ganglioside GD3, to a host cell;
XX CC producing (I), involving cultivating (I) in a culture medium, such that
XX CC Cl (sic) is produced and accumulated in the culture, extracting and
XX CC purifying Cl from the culture medium; a pharmaceutical (III) containing
XX CC Cl as an active ingredient; and a therapeutic agent (A1) for ganglioside
XX CC GD3 associated disease, comprising Cl as an active ingredient. (I) is
XX CC useful for treating GD3 associated disease, which involves administering
XX CC (I), where the GD3 associated diseases is cancer. (A1) is also useful for
XX CC treating GD3 associated disease. (II) is useful for producing (I). (I) is
XX CC useful for manufacturing a therapeutic agent for GD3 associated disease.
XX CC This sequence represents a ganglioside GD3 binding antibody associated
XX CC protein.
XX SQ Sequence 119 AA;

Query Match 100.0%; Score 28; DB 9; Length 119;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HVAMS 5
DB |||||
31 HYAMS 35

RESULT 18
AAR33256
ID AAR33256 standard; protein; 130 AA.
XX
XX AC AAR33256;
XX
XX DT 25-MAR-2003 (revised)
XX DT 12-JUL-1993 (first entry)
XX
XX DE Rat immunoglobulin H chain variable region of pM641HA3.
XX
XX KW Promoter; variable; region; rat; immunoglobulin; heavy; H; chain;
XX KW humanised; chimeric; antibody; expression vector.
XX OS Rattus rattus.
XX
XX FH Key Location/Qualifiers
XX FT Peptide 1..10
XX FT /note= "Signal peptide"
XX FT Protein 11..130
XX FT /note= "Mature protein"
XX
XX PN EP533199-A2.
XX PD 24-MAR-1993.
XX XX

```

PF 18-SEP-1992; 92EP-00116026.  
 XX  
 PR 18-SEP-1991; 91JP-00238375.  
 XX  
 XX (KYOW ) KYOWA HAKKO KOGYO CO LTD.  
 PA  
 PI Shitara K, Hanai N, Hasegawa M, Miyaji H, Kuwana Y;  
 XX  
 DR WPI: 1993-095510/12.  
 DR N-PSDB; AAQ33257.  
 XX  
 XX Humanised chimeric antibody prodn. against ganglioside GD3 - for treating  
 PT cancers, such as melanoma, neuroblastoma, etc.  
 PS Claim 6; Page 29-30; 63pp; English.  
 XX  
 CC The sequences given in AAR33256-57 represent rat heavy and light chain  
 CC variable regions respectively. The DNA sequences encoding these proteins  
 CC were used in the construction of humanised chimeric antibody expression  
 CC vectors. In these humanised antibodies none of the amino acids of the non  
 CC -human animal Ab variable region have been changed. (Updated on 25-MAR-  
 CC 2003 to correct PN field.)  
 XX  
 SQ Sequence 130 AA;  
 Query Match 100.0%; Score 28; DB 2; Length 130;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 HYAMS 5  
 Db |||||  
 41 HYAMS 45  
 RESULT 19  
 AAR53341  
 ID AAR53341 standard; protein; 130 AA.  
 XX  
 AC AAR53341;  
 XX  
 DT 18-NOV-1994 (first entry)  
 XX  
 DE KM641 L chain variable region.  
 XX  
 DE Monoclonal antibody; Ab; ganglioside GM2; chimera; chimeric antibody;  
 KW expression vector; heavy; light; chain; hypervariable region; CDR;  
 KW constant region; hybridoma; Ig; immunoglobulin; promoter; enhancer.  
 XX  
 OS Mus musculus.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..10  
 FT /label= sig\_peptide  
 XX  
 PN AU9346181-A.  
 XX  
 PD 17-MAR-1994.  
 XX  
 PF 07-SEP-1993; 93AU-00046181.  
 XX  
 PR 07-SEP-1992; 92JP-00238452.  
 XX  
 PA (KYOW ) KYOWA HAKKO KOGYO KK.  
 XX  
 PI Nakamura K, Koike M, Shitara K, Hanai N, Kuwana Y, Hasegawa M;  
 XX  
 DR WPI: 1994-126857/16.  
 DR N-PSDB; AAQ45439.  
 XX  
 XX Humanised antibody specific for ganglioside GM2 - used for producing a  
 PT cytotoxic effect on cancers such as melanoma, neuroblastoma and glioma.  
 XX  
 PS Example 2; Page 116-117; 191pp; English.

XX Example 2 describes the construction of the vector pCh1641HA1 for  
 CC chimeric human antibody H chain expression. mRNA from mouse anti-GD3  
 CC monoclonal Ab KM641-producing cells was isolated and KM641 H and L chain  
 CC cDNAs isolated. The base sequences of the Ig variable regions in KM641 H  
 CC chain cDNA (pKM641HA3) and KM641 L chain cDNA (pKM641HA2) are given in  
 CC AAQ45438-39. A KM641-derived chimeric human Ab H chain expression vector  
 CC was constructed by joining the H chain variable region gene from  
 CC pKM641HA3 to a vector for chimeric human Ab H chain expression using the  
 CC synthetic DNAs given in AAQ63439 and AAQ63440  
 XX  
 SQ Sequence 130 AA;  
 Query Match 100.0%; Score 28; DB 2; Length 130;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 HYAMS 5  
 Db |||||  
 41 HYAMS 45  
 RESULT 20  
 AAY28369  
 ID AAY28369 standard; protein; 130 AA.  
 XX  
 AC AAY28369;  
 XX  
 DT 04-NOV-1999 (first entry)  
 XX  
 DE pKM641 HA3 immunoglobulin heavy chain.  
 XX  
 DE antibody; nucleotide; genomic; hypervariable region; chimeric;  
 KW light chain; amino acid.  
 XX  
 OS Mus sp.  
 XX  
 PN US5939532-A.  
 XX  
 PD 17-AUG-1999.  
 XX  
 PF 07-JUN-1995; 95US-00483528.  
 XX  
 PR 07-SEP-1993; 93US-00116778.  
 XX  
 PA (KYOW ) KYOWA HAKKO KOGYO KK.  
 XX  
 PI Nakamura K, Hanai N, Kuwana Y, Hasegawa M, Koike M, Shitara K;  
 XX  
 DR WPI: 1999-468416/39.  
 DR N-PSDB; AAX99482.  
 XX  
 PT Chimeric human antibody expression vectors.  
 XX  
 PS Example 1; Col 99-101; 188pp; English.  
 XX  
 CC This immunoglobulin region was isolated from pKM641HA3. This sequence has  
 CC no methionine initiation codon and the leader sequence was partly  
 CC lacking. The chimeric human antibodies are useful in the treatment of  
 CC cancer, especially that which is of neural ectodermal origin. In contrast  
 CC to prior art constructs based on mouse monoclonal antibodies, the  
 CC chimeric human antibodies do not cause anti-mouse immunoglobulin  
 CC production. The chimeric human antibodies have a prolonged half-life and  
 CC a reduced frequency of adverse effects when compared to mouse monoclonal  
 CC antibodies  
 XX  
 SQ Sequence 130 AA;  
 Query Match 100.0%; Score 28; DB 2; Length 130;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 HYAMS 5

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Db          |||||
            41 HYAMS 45

RESULT 21
AAB01627
ID  AAB01627 standard; protein; 130 AA.
XX
XX  AAB01627;
AC
XX  07-DEC-2000 (first entry)
XX
XX  Murine immunoglobulin heavy chain variable region.
DE
XX  Mouse; immunoglobulin; H chain; heavy chain; variable region; cancer;
KW  humanised antibody.
XX
XX  Mus sp.
OS
XX
XX  Key Location/Qualifiers
FH  1..10
FT  Peptide /label= signal_peptide
FT  Protein 11..130
FT  /label= mature_immunoglobulin_heavy_chain_variable_region
XX
XX  EP1013761-A2.
XX
XX  28-JUN-2000.
PD
XX
XX  18-SEP-1992; 99EP-00124345.
XX
XX  18-SEP-1991; 91JP-00238375.
XX  18-SEP-1992; 92EP-00116026.
XX
XX  (KYOW ) KYOWA HAKKO KOGYO KK.
XX
XX  Shitara K, Hanai N, Hasegawa M, Miyaji H, Kuwana Y;
XX  WPI; 2000-402204/35.
DR  N-PSDB; AAA51003.
XX
XX  New humanized chimera antibody KM-871 useful for treating cancer,
PT  comprises variable region of mouse monoclonal antibody, reactive with
PT  ganglioside and human antibody constant region.
XX
XX  Claim 14; Page 27-28; 65pp; English.
XX
XX  The present sequence is a murine immunoglobulin heavy chain variable
CC  region from plasmid KM-641. The coding sequence was used in the creation
CC  of an expression vector, along with the sequence for a human antibody, to
CC  produce humanised chimaeric antibodies, which can be used to treat
CC  cancer. Humanised chimaeric antibodies are more effective than mouse
CC  antibodies as they do not provoke a reaction in the human and side
CC  effects, such as the formation of anti-mouse immunoglobulin antibody and
CC  the rapid half-life of the immunoglobulins, do not occur
XX
XX  Sequence 130 AA;
SQ
Query Match 100.0%; Score 28; DB 3; Length 130;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5
    |||||
Db 41 HYAMS 45

RESULT 22
AAB81977
ID  AAB81977 standard; protein; 138 AA.
XX
XX  AAB81977;
AC
XX

```

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DT 03-JUL-2001 (first entry)
XX
XX  Ganglioside GD3 specific antibody related protein SEQ ID NO: 1.
DE
XX  Ganglioside; GD3; complementarity determining region; CDR; antibody;
KW  cancer.
XX
XX  Mus musculus.
XX
XX  WO200123432-A1.
PN
XX  05-APR-2001.
PD
XX  29-SEP-2000; 2000WO-JP006774.
XX
XX  30-SEP-1999; 99JP-00278291.
XX  06-APR-2000; 2000JP-00105088.
PR
XX  (KYOW ) KYOWA HAKKO KOGYO KK.
XX
XX  Hanai N, Shitara K, Nakamura K, Niwa R;
PI
XX  WPI; 2001-266143/27.
XX
XX  New human type complementation-determining region-transplanted antibody
PT  and derivatives against ganglioside GD3. The antibody and its derivatives are
PT  useful in the diagnosis and therapy of tumours, particularly cancer
PT  of e.g. tumors, with low antigenicity, little side effects but potent
PT  activity in cancer.
XX
XX  Example 1; Page 138-139; 183pp; Japanese.
XX
XX  The present invention describes a monoclonal antibody which can react
CC  specifically with ganglioside GD3. The antibody and its derivatives are
CC  useful in the diagnosis and therapy of tumours, particularly cancer
CC  diagnosis. The present sequence is a protein used in the exemplification
CC  of the invention
XX
XX  Sequence 138 AA;
SQ
Query Match 100.0%; Score 28; DB 4; Length 138;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5
    |||||
Db 50 HYAMS 54

RESULT 23
ABU11002
ID  ABU11002 standard; protein; 138 AA.
XX
XX  ABU11002;
AC
XX
XX  04-FEB-2003 (first entry)
DT
XX
XX  Modified ganglioside GD3 antibody associated protein #1.
DE
XX  Ganglioside GD3; anti-ganglioside GD3 antibody; tumour; melanoma.
XX
XX  Mus musculus.
OS
XX  WO200278739-A1.
XX
XX  10-OCT-2002.
PD
XX
XX  29-MAR-2002; 2002WO-JP003170.
XX
XX  29-MAR-2001; 2001JP-00097483.
XX
XX  (KYOW ) KYOWA HAKKO KOGYO KK.
XX
XX  Shitara K, Niwa R, Kanazawa J, Asada M;
PI

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XX WPI; 2003-067410/06.  
 XX Drugs containing genetically-modified antibody against ganglioside GD3,  
 PT its fragment, immunocompetent cell activators or/and antitumor agents in  
 PT combination, applicable in treating malignant tumor like melanoma.  
 XX  
 PS Example 3; Page 97; 121pp; Japanese.  
 XX  
 CC The invention describes drugs contain a genetically-modified antibody  
 CC against ganglioside GD3 or its fragment and at least 1 of a substance  
 CC capable of activating immunocompetent cells and a substance having an  
 CC antitumor activity in combination. The drugs can be used to treat tumour  
 CC like melanoma and can provide a treatment with enhanced therapeutic  
 CC effect and little side-reactions, particularly to relieve problems of  
 CC side-effects during the conventional single administration. This sequence  
 CC represents a protein associated with the anti- ganglioside GD3 antibody  
 XX  
 SQ Sequence 138 AA;  
 Query Match 100.0%; Score 28; DB 6; Length 138;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 HYAMS 5  
 Db 50 HYAMS 54  
 |||||  
 RESULT 24  
 ABG28979  
 ID ABG28979 standard; protein; 156 AA.  
 XX  
 AC ABG28979;  
 XX  
 DT 18-FEB-2002 (first entry)  
 XX  
 DE Novel human diagnostic protein #28970.  
 XX  
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic;  
 KW food supplement; medical imaging; diagnostic; genetic disorder.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200175067-A2.  
 XX  
 PD 11-OCT-2001.  
 XX  
 PF 30-MAR-2001; 2001WO-US008631.  
 XX  
 PR 31-MAR-2000; 2000US-00540217.  
 PR 23-AUG-2000; 2000US-00649167.  
 XX  
 PA (HYSE-) HYSEQ INC.  
 XX  
 PI Drmanac RT, Liu C, Tang YT;  
 XX  
 XX WPI; 2001-639362/73.  
 DR N-PSDB; AAS93166.  
 XX  
 PT New isolated polynucleotide and encoded polypeptides, useful in  
 PT diagnostics, forensics, gene mapping, identification of mutations  
 PT responsible for genetic disorders or other traits and to assess  
 PT biodiversity.  
 XX  
 PS Claim 20; SEQ ID NO 59338; 103pp; English.  
 XX  
 CC The invention relates to isolated polynucleotide (I) and polypeptide (II)  
 CC sequences. (II) is useful as hybridisation probes, polymerase chain  
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,  
 CC and in recombinant production of (II). The polynucleotides are also used  
 CC in diagnostics as expressed sequence tags for identifying expressed  
 CC genes. (I) is useful in gene therapy techniques to restore normal

CC activity of (II) or to treat disease states involving (II). (II) is  
 CC useful for generating antibodies against it, detecting or quantitating a  
 CC polypeptide in tissue, as molecular weight markers and as a food  
 CC supplement. (II) and its binding partners are useful in medical imaging  
 CC of sites expressing (II). (I) and (II) are useful for treating disorders  
 CC involving aberrant protein expression or biological activity. The  
 CC polypeptide and polynucleotide sequences have applications in  
 CC diagnostics, forensics, gene mapping, identification of mutations  
 CC and responsible for genetic disorders or other traits to assess biodiversity  
 CC and to produce other types of data and products dependent on DNA and  
 CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic  
 CC amino acid sequences of the invention. Note: The sequence data for this  
 CC patent did not appear in the printed specification, but was obtained in  
 CC electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 156 AA;  
 Query Match 100.0%; Score 28; DB 4; Length 156;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 HYAMS 5  
 Db 49 HYAMS 53  
 |||||  
 RESULT 25  
 AAB96839  
 ID AAB96839 standard; protein; 280 AA.  
 XX  
 AC AAB96839;  
 XX  
 DT 29-OCT-2001 (first entry)  
 XX  
 DE Putative P. abyssi periplasmic serine protease.  
 XX  
 KW Hyperthermophilic archaeon; hyperthermophilic protein.  
 XX  
 OS Pyrococcus abyssi.  
 XX  
 PN FR2792851-A1.  
 XX  
 PD 27-OCT-2000.  
 XX  
 PF 21-APR-1999; 99FR-00005034.  
 XX  
 PR 21-APR-1999; 99FR-00005034.  
 XX  
 PA (CNRS ) CNRS CENT NAT RECH SCI.  
 XX (IPRE-) IFREMER INST FR RECH EXPL MER.  
 XX  
 PI Forterre P, Thierry JC, Prieur D, Dietrich J, Lecompte O;  
 PI Querellou J, Weissenbach J, Saurin W, Heilig R;  
 XX  
 DR WPI; 2001-126236/14.  
 XX  
 XX New nucleotide sequences isolated from Pyrococcus abyssi encode proteins  
 PT useful in industry.  
 PS  
 PS Claim 7; Page 1634; 1657pp; French.  
 XX  
 CC The present invention relates to the genomic sequence of Pyrococcus  
 CC abyssi (see AAF8431 and AAH41223-7) and P. abyssi proteins. P. abyssi is  
 CC a hyperthermophilic archaeon, which is isolated from deep-sea  
 CC hydrothermal vents. The present sequence is one such P. abyssi protein.  
 CC The proteins of the present invention have various potential industrial  
 CC uses, since the proteins are stable at very high temperatures, some up to  
 CC 110 degrees centigrade. Note: This patent is in the same patent family as  
 CC WO200005082, which contains additional sequences as shown in AAB99132-  
 CC AAB99143, AAH75903-AAH75920 and AAG66436  
 XX  
 SQ Sequence 280 AA;

Query Match 100.0%; Score 28; DB 4; Length 280;  
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HVAMS 5  
 DB 126 HVAMS 130

RESULT 26  
 ADS21217  
 ID ADS21217 standard; protein; 280 AA.  
 XX  
 AC ADN46873;  
 XX  
 DT 01-JUL-2004 (first entry)  
 XX  
 DE Thermococcus kodakaraensis KOD1 protein sequence SeqID751.  
 XX  
 KW gene disruption; gene targeting; marker gene; transformation;  
 KW homologous recombination; hyperthermostable archaeobacterium; KOD1;  
 KW gene structure; gene function; enzyme activity; medicine;  
 KW forensic science; food; drug inspection; molecular biology; immunology.  
 XX  
 OS Thermococcus kodakaraensis.  
 XX  
 PN WO2004022736-A1.  
 XX  
 PD 18-MAR-2004.  
 XX  
 PF 29-AUG-2003; 2003WO-IB003597.  
 XX  
 PR 30-AUG-2002; 2002JP-00319011.  
 XX  
 PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.  
 XX  
 PI Imanaka T, Atomi H;  
 XX  
 DR WPI; 2004-257583/24.  
 XX  
 PT Method for disrupting targeted gene in genome of organism particularly  
 PT thermotable bacterium and with genome chips for analysis, applicable in  
 PT studying gene structure and functions.  
 XX  
 PS Claim 9; SEQ ID NO 751; 598pp; Japanese.  
 XX  
 CC This invention relates to a novel method for targeting disruption of an  
 CC arbitrary gene in a genome of an organism which comprises providing the  
 CC whole sequential data of the genome of such organism, selecting at least  
 CC 1 arbitrary region in the sequence, providing a vector that contains a  
 CC sequence homologous with the selected region and a marker gene,  
 CC transformation, and homologous recombination. The genome is preferably  
 CC the genome of a hyperthermostable archaeobacterium, particularly  
 CC Thermococcus kodakaraensis KOD1. The method is for targeting the  
 CC disruption of a gene in the genome of an organism, which is applicable in  
 CC studying gene structure and functions as well as enzyme activities of  
 CC encoded proteins and useful in medicine, forensic science, food or drug  
 CC inspection, molecular biology and immunology. With this method, the  
 CC disruption of a gene at an arbitrary position in a genome can be achieved  
 CC efficiently and reliably. The present sequence is that of a protein  
 CC encoded by the genome of Thermococcus kodakaraensis which was derived  
 CC using the method of the invention. Note: The sequence data for this  
 CC patent did not form part of the printed specification, but was obtained  
 CC in electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 280 AA;

Query Match 100.0%; Score 28; DB 8; Length 280;  
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HVAMS 5  
 DB 126 HVAMS 130

RESULT 27  
 ADS21217  
 ID ADS21217 standard; protein; 412 AA.  
 XX  
 AC ADS21217;  
 XX  
 DT 02-DEC-2004 (first entry)  
 XX  
 DE Bacterial polypeptide #10250.  
 XX  
 KW Recombinant DNA construct; transformed plant; improved plant property;  
 KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;  
 KW pathogen tolerance; pest tolerance; plant disease resistance;  
 KW cell cycle pathway modification; plant growth regulator; carbohydrate;  
 KW homologous recombination; seed oil yield; protein yield; lignin; galactomannan;  
 KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;  
 KW bacterial polypeptide.  
 XX  
 OS Bacteria.  
 XX  
 PN US2003233675-A1.  
 XX  
 PD 18-DEC-2003.  
 XX  
 PF 20-FEB-2003; 2003US-00369493.  
 XX  
 PR 21-FEB-2002; 2002US-0360039P.  
 XX  
 PA (CAOY/) CAO Y.  
 PA (HINK/) HINKLE G J.  
 PA (SLAT/) SLATER S C.  
 PA (CHEN/) CHEN X.  
 PA (GOLD/) GOLDMAN B S.  
 XX  
 PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;  
 XX  
 DR WPI; 2004-061375/06.  
 XX  
 PT New recombinant DNA construct comprising a promoter positioned to provide  
 PT for expression of a polynucleotide encoding a polypeptide from a  
 PT microbial source, useful for producing plants with improved properties.  
 XX  
 PS Claim 1; SEQ ID NO 10250; 122pp; English.  
 XX  
 CC The invention relates to a recombinant DNA construct comprising a  
 CC promoter functional in a plant cell, where the promoter is positioned to  
 CC provide for expression of a polynucleotide encoding a polypeptide from a  
 CC microbial source. The invention also relates to a transformed plant  
 CC comprising the recombinant DNA construct and a method of producing a  
 CC transformed plant having an improved property. The plant is a crop plant  
 CC such as maize or soybean. The method of producing a transformed plant  
 CC having an improved property comprises transforming a plant with the  
 CC recombinant DNA construct and growing the transformed plant, where the  
 CC polynucleotide or polypeptide is useful for improving plant properties.  
 CC The recombinant DNA construct is useful for producing plants with  
 CC improved plant properties, e.g. improved cold, heat or drought tolerance,  
 CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,  
 CC increased resistance to plant disease, better growth rate by modification  
 CC of the cell cycle pathway with plant growth regulators, increased rate of  
 CC homologous recombination, modified seed oil or protein yield and/or  
 CC content, improved yield by modification of carbohydrate, nitrogen or  
 CC phosphorus use and/or uptake, by modification of photosynthesis or by  
 CC providing improved plant growth and development under at least one stress  
 CC condition, improved lignin production or improved galactomannan  
 CC production. This sequence represents a bacterial polypeptide used in the  
 CC scope of the invention. Note: The sequence data for this patent did not  
 CC form part of the printed specification but was obtained in electronic  
 CC format from USPTO at seqdata.uspto.gov/sequence.html.

XX SQ Sequence 412 AA;  
Query Match 100.0%; Score 28; DB 8; Length 412;  
Best Local Similarity 100.0%; Pred. No. 3.7e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 HYAMS 5  
|||||  
DB 390 HYAMS 394

RESULT 28  
ADS64477  
ID ADS64477 standard; protein; 424 AA.  
XX AC  
XX ADS64477;  
XX DT 16-DEC-2004 (first entry)  
XX DE Pseudomonas aeruginosa Na+/H+ antiporter protein.  
XX KW Salt tolerance; salt overly sensitive protein; SOS; plant agriculture;  
KW abiotic stress; gene therapy; plant protectant; chinese hamster;  
KW Na+/H+ antiporter.  
XX OS Pseudomonas aeruginosa.  
XX OS US2004186276-A1.  
XX PN 23-SEP-2004.  
XX PD  
XX PF 02-JAN-2004; 2004US-00749386.  
XX PR 04-APR-2000; 2000US-0194648P.  
XX PR 04-APR-2001; 2001US-00824734.  
XX PA (UYAR-) UNIV ARIZONA STATE.  
XX PI Zhu J, Shi H, Ishitani M, Stevenson B;  
XX WPI; 2004-689242/67.  
XX DR New isolated polynucleotide encoding a salt overly sensitive (SOS1)  
PT protein, useful in plant agriculture, in particular for reducing abiotic  
PT stress and increasing the salt tolerance in plants.  
XX PS Disclosure; SEQ ID NO 4; 37pp; English.  
XX CC The invention relates to nucleic acids and proteins related to salt  
CC tolerance in plants. The invention is particularly directed to salt  
CC overly sensitive (SOS) proteins and nucleic acids encoding such proteins.  
CC The methods and compositions of the present invention are useful in plant  
CC agriculture, in particular for reducing abiotic stress and increasing the  
CC salt tolerance in plants. The invention is also useful in gene therapy.  
CC The present sequence is the Pseudomonas aeruginosa Na+/H+ antiporter  
CC protein. This sequence is related to the invention.  
XX SQ Sequence 424 AA;  
Query Match 100.0%; Score 28; DB 8; Length 424;  
Best Local Similarity 100.0%; Pred. No. 3.8e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 HYAMS 5  
|||||  
DB 272 HYAMS 276

RESULT 29  
ABM91663  
ID ABM91663 standard; protein; 496 AA.  
XX

AC ABM91663;  
XX 02-JUN-2005 (first entry)  
XX M. xanthus protein sequence, seq id 10862.  
DE Transgenic plant; DNA replication; gene regulation; gene expression.  
XX KW Myxococcus xanthus.  
XX OS US6833447-B1.  
XX PN 21-DEC-2004.  
XX PD 10-JUL-2001; 2001US-00902540.  
XX PF 10-JUL-2000; 2000US-0217883P.  
XX PR (MONS ) MONSANTO TECHNOLOGY LLC.  
XX PA Goldman BS, Hinkle GJ, Slater SC, Wiegand RC;  
XX PI WPI; 2005-028716/03.  
XX DR New substantially purified Myxococcus xanthus nucleic acid molecule  
XX encoding a nitrite reductase, useful for determining gene expression,  
XX PT identifying mutations in a gene of interest, and for constructing  
XX PT mutations in a gene of interest.  
XX PS Example 2; SEQ ID NO 10862; 25pp; English.  
XX CC The invention relates to a substantially purified nucleic acid molecule  
CC encoding a nitrite reductase of SEQ ID NO. 11936. Further disclosed is a  
CC recombinant DNA construct for expression of a nitrite reductase gene in a  
CC plant cell, and a plant cell comprising the recombinant DNA construct.  
CC The nucleic acid is useful for determining gene expression, identifying  
CC mutations in a gene of interest, and for constructing mutations in a gene  
CC of interest. Sequences given in records for SEQ IDs 9692-16825 represent  
CC a group of 7134 Myxococcus xanthus proteins and peptides. Note: The  
CC sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from USPTO  
XX SQ Sequence 496 AA;  
Query Match 100.0%; Score 28; DB 9; Length 496;  
Best Local Similarity 100.0%; Pred. No. 4.6e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 HYAMS 5  
|||||  
DB 225 HYAMS 229

RESULT 30  
ABO71592  
ID ABO71592 standard; protein; 514 AA.  
XX AC ABO71592;  
XX DT 29-JUL-2004 (first entry)  
XX DE Pseudomonas aeruginosa polypeptide #3767.  
XX KW Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.  
XX OS Pseudomonas aeruginosa.  
XX OS US6551795-B1.  
XX PN 22-APR-2003.  
XX PD 18-FEB-1999; 99US-00252991.  
XX PF

PR 18-FEB-1998; 98US-0074788P.  
PR 27-JUL-1998; 98US-0094190P.  
XX (GENO-) GENOME THERAPEUTICS CORP.  
PA Rubenfield MJ, Nolling J, Deloughery C, Bush D;  
PI WPI; 2003-615309/58.  
XX N-PSDB; AB005163.  
DR Novel isolated nucleic acid encoding *Pseudomonas aeruginosa* polypeptide,  
XX useful as molecular targets for diagnostics, prophylaxis and treatment of  
PT pathological conditions resulting from bacterial infection.  
PT  
XX  
PS Disclosure; SEQ ID NO 20338; 455pp; English.  
XX  
CC The invention relates to *Pseudomonas aeruginosa* polypeptides and the  
CC polynucleotides encoding them. The sequences are useful in diagnosis and  
CC therapy of pathological conditions, as molecular targets for diagnostics,  
CC prophylaxis and treatment of pathological conditions resulting from a  
CC bacterial infection, for evaluating a compound, such as a polypeptide,  
CC for the ability to bind a *P. aeruginosa* nucleic acid, as components of  
CC effective antibacterial targets, as targets for antibacterial drugs,  
CC including anti-*P. aeruginosa* drugs, as templates for recombinant  
CC production of *P. aeruginosa*-derived peptides or polypeptides, as target  
CC components for diagnosis and/or treatment of *P. aeruginosa*-caused  
CC infection, and in detection of *P. aeruginosa* sequences or other sequences  
CC of *Pseudomonas* species using biochip technology. Sequences ABO67826-  
CC ABO84396 represent *P. aeruginosa* polypeptides of the invention. Note: The  
CC sequence data for this patent did not form part of the printed  
CC specification but was obtained in electronic format from USPTO at  
CC seqdata.uspto.gov/sequence.html  
XX  
SQ Sequence 514 AA;  
  
Query Match 100.0%; Score 28; DB 7; Length 514;  
Best Local Similarity 100.0%; Pred. No. 4.7e+02; Indels 0; Gaps 0;  
Matches 5; Conservative 0; Mismatches 0;  
  
QY 1 HYAMS 5  
|||  
Db 362 HYAMS 366  
  
RESULT 31  
AAB81987  
ID AAB81987 standard; protein; 582 AA.  
XX  
AC AAB81987;  
XX  
DT 03-JUL-2001 (first entry)  
XX  
DE Ganglioside GD3 specific antibody related protein SEQ ID NO: 53.  
XX  
KW Ganglioside; GD3; complementarity determining region; CDR; antibody;  
KW cancer.  
XX  
OS Synthetic.  
XX  
WO200123432-A1.  
XX  
PD 05-APR-2001.  
XX  
PF 29-SEP-2000; 2000WO-JP006774.  
XX  
PR 30-SEP-1999; 99JP-00278291.  
XX  
PR 06-APR-2000; 2000JP-00105088.  
XX  
PA (KYOW ) KYOWA HAKKO KOGYO KK.  
XX  
PI Hanai N, Shitara K, Nakamura K, Niwa R;  
XX  
DR WPI; 2001-266143/27.  
  
New human type complementation-determining region-transplanted antibody  
and derivatives against ganglioside GD3, useful in diagnosis and therapy  
of e.g. tumors, with low antigenicity, little side effects but potent  
activity in cancer.  
  
Query Match 100.0%; Score 28; DB 4; Length 582;  
Best Local Similarity 100.0%; Pred. No. 5.4e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 HYAMS 5  
|||  
Db 31 HYAMS 35  
  
RESULT 32  
AAB81991  
ID AAB81991 standard; protein; 582 AA.  
XX  
AC AAB81991;  
XX  
DT 03-JUL-2001 (first entry)  
XX  
DE Ganglioside GD3 specific antibody related protein SEQ ID NO: 57.  
XX  
KW Ganglioside; GD3; complementarity determining region; CDR; antibody;  
KW cancer.  
XX  
OS Synthetic.  
XX  
WO200123432-A1.  
XX  
PD 05-APR-2001.  
XX  
PF 29-SEP-2000; 2000WO-JP006774.  
XX  
PR 30-SEP-1999; 99JP-00278291.  
XX  
PR 06-APR-2000; 2000JP-00105088.  
XX  
PA (KYOW ) KYOWA HAKKO KOGYO KK.  
XX  
PI Hanai N, Shitara K, Nakamura K, Niwa R;  
XX  
DR WPI; 2001-266143/27.  
  
New human type complementation-determining region-transplanted antibody  
and derivatives against ganglioside GD3, useful in diagnosis and therapy  
of e.g. tumors, with low antigenicity, little side effects but potent  
activity in cancer.  
  
Query Match 100.0%; Score 28; DB 4; Length 582;  
Best Local Similarity 100.0%; Pred. No. 5.4e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 HYAMS 5  
|||  
Db 31 HYAMS 35  
  
RESULT 33  
AAB81991  
ID AAB81991 standard; protein; 582 AA.  
XX  
AC AAB81991;  
XX  
DT 03-JUL-2001 (first entry)  
XX  
DE Ganglioside GD3 specific antibody related protein SEQ ID NO: 57.  
XX  
KW Ganglioside; GD3; complementarity determining region; CDR; antibody;  
KW cancer.  
XX  
OS Synthetic.  
XX  
WO200123432-A1.  
XX  
PD 05-APR-2001.  
XX  
PF 29-SEP-2000; 2000WO-JP006774.  
XX  
PR 30-SEP-1999; 99JP-00278291.  
XX  
PR 06-APR-2000; 2000JP-00105088.  
XX  
PA (KYOW ) KYOWA HAKKO KOGYO KK.  
XX  
PI Hanai N, Shitara K, Nakamura K, Niwa R;  
XX  
DR WPI; 2001-266143/27.

XX New human type complementation-determining region-transplanted antibody  
PT and derivatives against ganglioside GD3, useful in diagnosis and therapy  
PT of e.g. tumors, with low antigenicity, little side effects but potent  
PT activity in cancer.  
XX  
PS Claim 41; Page 168-172; 183pp; Japanese.  
XX  
XX The present invention describes a monoclonal antibody which can react  
CC specifically with ganglioside GD3. The antibody and its derivatives are  
CC useful in the diagnosis and therapy of tumors, particularly cancer  
CC diagnosis. The present sequence is a protein used in the exemplification  
CC of the invention  
XX  
SQ Sequence 582 AA;  
  
Query Match 100.0%; Score 28; DB 4; Length 582;  
Best Local Similarity 100.0%; Pred. No. 5.4e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 HYAMS 5  
|||  
Db 31 HYAMS 35  
  
RESULT 32  
AAB81991  
ID AAB81991 standard; protein; 582 AA.  
XX  
AC AAB81991;  
XX  
DT 03-JUL-2001 (first entry)  
XX  
DE Ganglioside GD3 specific antibody related protein SEQ ID NO: 57.  
XX  
KW Ganglioside; GD3; complementarity determining region; CDR; antibody;  
KW cancer.  
XX  
OS Synthetic.  
XX  
WO200123432-A1.  
XX  
PD 05-APR-2001.  
XX  
PF 29-SEP-2000; 2000WO-JP006774.  
XX  
PR 30-SEP-1999; 99JP-00278291.  
XX  
PR 06-APR-2000; 2000JP-00105088.  
XX  
PA (KYOW ) KYOWA HAKKO KOGYO KK.  
XX  
PI Hanai N, Shitara K, Nakamura K, Niwa R;  
XX  
DR WPI; 2001-266143/27.  
  
New human type complementation-determining region-transplanted antibody  
and derivatives against ganglioside GD3, useful in diagnosis and therapy  
of e.g. tumors, with low antigenicity, little side effects but potent  
activity in cancer.  
  
Query Match 100.0%; Score 28; DB 4; Length 582;  
Best Local Similarity 100.0%; Pred. No. 5.4e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 HYAMS 5  
|||  
Db 31 HYAMS 35  
  
RESULT 33  
AAB81991  
ID AAB81991 standard; protein; 582 AA.  
XX  
AC AAB81991;  
XX  
DT 03-JUL-2001 (first entry)  
XX  
DE Ganglioside GD3 specific antibody related protein SEQ ID NO: 57.  
XX  
KW Ganglioside; GD3; complementarity determining region; CDR; antibody;  
KW cancer.  
XX  
OS Synthetic.  
XX  
WO200123432-A1.  
XX  
PD 05-APR-2001.  
XX  
PF 29-SEP-2000; 2000WO-JP006774.  
XX  
PR 30-SEP-1999; 99JP-00278291.  
XX  
PR 06-APR-2000; 2000JP-00105088.  
XX  
PA (KYOW ) KYOWA HAKKO KOGYO KK.  
XX  
PI Hanai N, Shitara K, Nakamura K, Niwa R;  
XX  
DR WPI; 2001-266143/27.  
  
New human type complementation-determining region-transplanted antibody  
and derivatives against ganglioside GD3, useful in diagnosis and therapy  
of e.g. tumors, with low antigenicity, little side effects but potent  
activity in cancer.  
  
Query Match 100.0%; Score 28; DB 4; Length 582;  
Best Local Similarity 100.0%; Pred. No. 5.4e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 HYAMS 5  
|||  
Db 31 HYAMS 35  
  
RESULT 34  
AAB81991  
ID AAB81991 standard; protein; 582 AA.  
XX  
AC AAB81991;  
XX  
DT 03-JUL-2001 (first entry)  
XX  
DE Ganglioside GD3 specific antibody related protein SEQ ID NO: 57.  
XX  
KW Ganglioside; GD3; complementarity determining region; CDR; antibody;  
KW cancer.  
XX  
OS Synthetic.  
XX  
WO200123432-A1.  
XX  
PD 05-APR-2001.  
XX  
PF 29-SEP-2000; 2000WO-JP006774.  
XX  
PR 30-SEP-1999; 99JP-00278291.  
XX  
PR 06-APR-2000; 2000JP-00105088.  
XX  
PA (KYOW ) KYOWA HAKKO KOGYO KK.  
XX  
PI Hanai N, Shitara K, Nakamura K, Niwa R;  
XX  
DR WPI; 2001-266143/27.

```
QY      1 HYAMS 5
Db      |||||
        31 HYAMS 35

RESULT 33
AAM79111
ID  AAM79111 standard; protein; 1268 AA.
XX
AC  AAM79111;
XX
DT  06-NOV-2001 (first entry)
XX
DE  Human protein SEQ ID NO 1773.
XX
KW  Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW  vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW  tissue growth factor; immunomodulatory; cancer; leukaemia;
KW  nervous system disorder; arthritis; inflammation.
XX
OS  Homo sapiens.
XX
PN  WO200157190-A2.
XX
PD  09-AUG-2001.
XX
PF  05-FEB-2001; 2001WO-US004098.
XX
PR  03-FEB-2000; 2000US-00496914.
PR  27-APR-2000; 2000US-00560875.
PR  20-JUN-2000; 2000US-00598075.
PR  19-JUL-2000; 2000US-00620325.
PR  01-SEP-2000; 2000US-00634936.
PR  15-SEP-2000; 2000US-00663561.
PR  20-OCT-2000; 2000US-00693325.
PR  30-NOV-2000; 2000US-00728422.
XX
PA  (HYSE-) HYSEQ INC.
XX
PI  Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y;
PI  Ma Y, Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
PI  Xue AJ, Yang Y, Wejhrman T, Goodrich R;
XX
DR  WPI: 2001-476283/51.
DR  N-PSDB; AAK52244.
XX
PT  Nucleic acids encoding polypeptides with cytokine-like activities, useful
PT  in diagnosis and gene therapy.
XX
PS  Claim 20; Page 4124-4126; 6221pp; English.
XX
CC  The invention relates to polynucleotides (AAK51456-AAK53435) and the
CC  encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to
CC  cytokine, cell proliferation or cell differentiation or which may induce
CC  production of other cytokines in other cell populations. The
CC  polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC  peptide therapy. The polypeptides have various cytokine-like activities,
CC  e.g. stem cell growth factor activity, haematopoiesis regulating
CC  activity, tissue growth factor activity, immunomodulatory activity and
CC  activin/inhibin activity and may be useful in the diagnosis and/or
CC  treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC  inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111
CC  (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the
CC  sequence listing were missing at the time of publication
XX
SQ  Sequence 1268 AA;

Query Match      100.0%; Score 28; DB 4; Length 1268;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 HYAMS 5
Db      |||||
        182 HYAMS 186

RESULT 34
ADX06569
ID  ADX06569 standard; protein; 1268 AA.
XX
AC  ADX06569;
XX
DT  21-APR-2005 (first entry)
XX
DE  Cyclin-dependent kinase modulation biomarker SEQ ID NO 1134.
XX
KW  cytostatic; cyclin-dependent kinase; cdk; biomarker.
XX
OS  Homo sapiens.
XX
PN  WO2005012875-A2.
XX
PD  10-FEB-2005.
XX
PF  29-JUL-2004; 2004WO-US024424.
XX
PR  29-JUL-2003; 2003US-0490890P.
XX
PA  (BRIM ) BRISTOL-MYERS SQUIBB CO.
XX
PI  Li M, Rupnow BA, Webster KR, Jackson DG, Wong TW;
XX
DR  WPI: 2005-163068/17.
DR  N-PSDB; ADX06568.
XX
PT  Biomarkers useful for predicting or determining the response of a mammal
PT  to a cancer treatment comprising administration of a modulator of cyclin-
PT  dependent kinase activity.
XX
PS  Claim 5; SEQ ID NO 1134; 141pp; English.
XX
CC  This invention describes a novel method of predicting or determining
CC  whether a mammal will respond or is responding to an anti-cancer agent
CC  that modulates cyclin-dependent kinase (cdk) activity. The method
CC  comprises measuring the level of one or more biomarkers selected from
CC  2774 biomarkers given in the specification (nucleotide sequence SEQ ID
CC  NO:1246 (Genbank EST W28729) is especially preferred). The method of the
CC  invention is utilized in a kit for determining or predicting whether
CC  patient would be susceptible or resistant to treatment by an agent
CC  modulating cdk activity. The invention also describes a method for
CC  utilizing individualized genetic profiles for treating diseases and
CC  disorders based on patient's response and molecular level, specialized
CC  microarrays comprising the biomarkers described, antibodies directed
CC  against the biomarkers and a cell culture model to identify biomarkers.
CC  The cdk modulator is preferably N-5-[(5-(1,1-Dimethylethyl)-2-
CC  oxazolyl)methyl]thio]-2-thiazolyl-4-piperidine carboxamide, 0.5-L-
CC  tartaric acid salt. Note: The sequence data for this patent did not form
CC  part of the printed specification, but was obtained in electronic format
CC  directly from WIPO at ftp.wipo.int/pub/published_pct_sequences. This
CC  sequence represents a biomarker used in the method of the invention.
XX
SQ  Sequence 1268 AA;

Query Match      100.0%; Score 28; DB 9; Length 1268;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 HYAMS 5
Db      |||||
        182 HYAMS 186

RESULT 35
AAM80095
ID  AAM80095 standard; protein; 1270 AA.
```



OS Homo sapiens.  
 PN WO200147944-A2.  
 XX  
 PD 05-JUL-2001.  
 XX  
 PF 28-DEC-2000; 2000WO-US035498.  
 XX  
 PR 28-DEC-1999; 99US-0173419P.  
 PR 27-DEC-2000; 2000US-00173419.  
 XX  
 PA (CURA-) CURAGEN CORP.  
 XX  
 PI Shimkets RA, Leach M;  
 XX  
 DR WPI; 2001-465210/50.  
 XX  
 PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,  
 PT oncogenes and histones, useful for diagnosing and treating, e.g. cancer,  
 PT autoimmune diseases and infections.  
 XX  
 PS Disclosure; Page 3779; 4143pp; English.  
 XX  
 CC The present invention relates to oligonucleotides (see AAL26793-AAL34659)  
 CC encoding polymorphic variants of proteins related to amylases, amyloid  
 CC proteins, angiotensin, apoptosis related proteins, cadherin, cyclin,  
 CC polymerase, oncogenes, histones, kinases, colony stimulating factors,  
 CC complement related proteins, cytochromes, kinesins, cytokines,  
 CC interferons, interleukins, G-protein coupled receptors and thioesterases.  
 CC The present sequence is a peptide encoded by one such oligonucleotide.  
 CC The oligonucleotides and the peptides encoded by them may be used in the  
 CC prevention, diagnosis and treatment of diseases associated with  
 CC inappropriate expression of the proteins listed above. Disorders that may  
 CC be prevented, diagnosed and/or treated include multifactorial diseases  
 CC with a genetic component, such as autoimmune diseases (e.g. rheumatoid  
 CC arthritis, multiple sclerosis, diabetes, systemic lupus erythematosus  
 CC and Grave's disease), inflammation, cancer (e.g. cancers of the bladder,  
 CC brain, breast, colon and kidney, leukaemia), diseases of the nervous  
 CC system and an infection of pathogenic organisms  
 XX  
 SQ Sequence 14 AA;  
 Query Match 89.3%; Score 25; DB 4; Length 14;  
 Best Local Similarity 80.0%; Pred. No. 47;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 HYAMS 5  
 Db 1 HYALS 5  
 RESULT 38  
 ID AAB34620  
 AC AAB34620 standard; protein; 50 AA.  
 XX  
 DT 26-JAN-2001 (first entry)  
 XX  
 DE Human secreted protein sequence encoded by gene 44 SEQ ID NO:104.  
 XX  
 KW Human; secreted protein; diagnosis; immunosuppressive; antiarthritic;  
 KW antirheumatic; antiproliferative; neurostatic; cardiac; vasotropic;  
 KW cerebroprotective; neurotropic; neuroprotective; antibacterial; virucide;  
 KW fungicide; ophthalmological; gene therapy; autoimmune disease; neoplasm;  
 KW hyperproliferative disorder; cancer; cardiovascular disorder; infection;  
 KW cerebrovascular disorder; angiogenesis; nervous system disorder;  
 KW ocular disorder; wound healing; skin aging; food additive; preservative.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200056751-A1.  
 XX

PD 28-SEP-2000.  
 XX  
 PF 09-MAR-2000; 2000WO-US006013.  
 XX  
 PR 19-MAR-1999; 99US-0125360P.  
 PR 11-JUN-1999; 99US-0138626P.  
 PR 03-DEC-1999; 99US-0168662P.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI Rosen CA, Ruben SM, Komatsoulis G;  
 XX  
 DR WPI; 2000-579482/54.  
 DR N-PSDB; AAC59781.  
 XX  
 PT Isolated nucleic acid molecule encoding a human secreted protein is used  
 PT in preventing, treating or ameliorating a medical condition.  
 XX  
 PS Claim 11; Page 387; 419pp; English.  
 XX  
 CC The polynucleotide sequences given in AAC59738 to AAC59787 encode the  
 CC human secreted proteins given in AAB34577 to AAB34626. AAB34627 to  
 CC AAB34686 represent human secreted polypeptide sequences and proteins  
 CC homologous to them, which are given in the exemplification of the present  
 CC invention. Human secreted proteins have activities based on the tissues  
 CC and cells the genes are expressed in. Example of activities include:  
 CC antiarthritic; immunosuppressive; antirheumatic; antiproliferative;  
 CC neurostatic; cardiac; vasotropic; cerebroprotective; neurotropic;  
 CC cerebroprotective; antibacterial; virucide; fungicide; and  
 CC ophthalmological. The polynucleotides and proteins can be used to  
 CC prevent, treat or ameliorate a medical condition in e.g. humans, mice,  
 CC rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used  
 CC in diagnosing a pathological condition or susceptibility to a  
 CC pathological condition. Disorders which are diagnosed or treated include  
 CC autoimmune diseases, hyperproliferative disorders e.g. neoplasms and  
 CC cancers of the breast or liver, cardiovascular disorders, cerebrovascular  
 CC disorders, angiogenesis, nervous system disorders, infections caused by  
 CC bacteria, viruses and fungi and ocular disorders. The proteins can also  
 CC be used to aid wound healing and epithelial cell proliferation, to  
 CC prevent skin aging due to sunburn, to maintain organs before  
 CC transplantation, for supporting cell culture of primary tissues, to  
 CC regenerate tissues and in chemotaxis. The proteins can also be used as a  
 CC food additive or preservative to increase or decrease storage  
 CC capabilities. AAC59729 to AAC59737 and AAB34576 represent sequences used  
 CC in the exemplification of the present invention  
 XX  
 SQ Sequence 50 AA;  
 Query Match 89.3%; Score 25; DB 3; Length 50;  
 Best Local Similarity 80.0%; Pred. No. 1.9e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 HYAMS 5  
 Db 36 HYAMT 40  
 RESULT 39  
 ID AAO03185  
 AC AAO03185 standard; protein; 76 AA.  
 XX  
 AC AAO03185;  
 XX  
 DT 06-NOV-2001 (first entry)  
 XX  
 DE Human polypeptide SEQ ID NO 17077.  
 XX  
 KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;  
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;  
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;  
 KW nervous system disorders; arthritis; inflammation.  
 XX  
 OS Homo sapiens.





XX The present invention describes an isolated polynucleotide (I) of  
 CC *Alloiooccus otitidis* genomic DNA, which encodes an antigenic protein.  
 CC *Alloiooccus otitidis* is a Gram-positive bacterium. Also described: (1)  
 CC an isolated polypeptide that is encoded by the polynucleotide (I); (2) an  
 CC expression vector comprising the novel isolated polynucleotide (I); its  
 CC complement, degenerate variant or fragment; (3) a genetically engineered  
 CC host cell, transfected, transformed or infected with the vector of (2);  
 CC (4) an antibody specific for the polypeptide of (1); (5) an immunogenic  
 CC composition comprising the polypeptide, its complement, biological  
 CC equivalent or fragment, or the polynucleotide that is comprised in the  
 CC expression vector; (6) a pharmaceutical composition comprising the  
 CC polypeptide of (1) and a carrier; (7) a protein chip comprising an array  
 CC of the polypeptides of (1), their biological equivalent or fragment; (8)  
 CC immunising against *Alloiooccus otitidis* by administering to a host the  
 CC immunogenic composition; (9) detecting and/or identifying *Alloiooccus*  
 CC *otitidis* in the biological sample; (10) a kit comprising a container  
 CC containing the novel polynucleotide, its degenerate variant or fragment,  
 CC or the antibody of (4); and (11) producing a polypeptide by culturing the  
 CC genetically engineered host cell under conditions suitable to produce the  
 CC polypeptide from the culture. (I) can be used in gene therapy. The  
 CC polynucleotides, polypeptides, antibodies and compositions of the present  
 CC invention can be used for treating and diagnosing diseases, drug  
 CC screening assays and monitoring of effects during drug clinical trials.  
 CC The polynucleotides are useful for expressing and detecting *Alloiooccus*  
 CC *otitidis*. The present sequence represents an *Alloiooccus otitidis*  
 CC antigen protein from the present invention.

XX SQ Sequence 113 AA;

Query Match 89.3%; Score 25; DB 6; Length 113;  
 Best Local Similarity 80.0%; Pred. No. 4.6e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5  
 Db |||:|  
 74 HVALS 78

RESULT 42

AAG81907  
 ID AAG81907 standard; protein; 116 AA.

XX AAG81907;  
 XX  
 XX 03-SEP-2001 (first entry)  
 XX  
 XX S. epidermidis open reading frame protein sequence SEQ ID NO:908.  
 XX  
 XX Staphylococcus epidermidis SR1 strain; infection; diagnosis; vaccination;  
 KW endocarditis.  
 KW

XX Staphylococcus epidermidis.

XX WO2001134809-A2.

XX 17-MAY-2001.

XX 09-NOV-2000; 2000WO-US030782.

XX 09-NOV-1999; 99US-0164258P.

XX (GLAX ) GLAXO GROUP LTD.

XX Kimmerly WJ;

XX WPI; 2001-316495/33.

DR N-PSDB; AAG82757.

XX Nucleic acids encoding polypeptides from *Staphylococcus epidermidis*,  
 PT useful for vaccinating against infections, e.g. endocarditis.

XX Claim 18; Page 271; 2189pp; English.

XX AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides  
 CC (II), given in AAG81454 to AAG83120, from *Staphylococcus epidermidis*. (I)  
 CC and (II) can have antibacterial activity and therefore can be used in  
 CC vaccination. The nucleic acids (I) may be used to produce the S.  
 CC epidermidis polypeptides (II) via the production of vectors containing  
 CC them which are used to produce hosts cells which express the  
 CC polypeptides. The polypeptides (II) (and/or nucleic acids) may then be  
 CC used to vaccinate subjects and to raise antibodies against the bacteria.  
 CC The polypeptides may also be used to assay for other inhibitors of their  
 CC activity and therefore identify compounds that may be used for the  
 CC treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to  
 CC AAH55090 represent specifically claimed S. epidermidis genomic DNA  
 CC polynucleotide sequences from the present invention. AAH55091 to AAH55098  
 CC represent oligonucleotide sequences and primers which are used in the  
 CC exemplification of the present invention. N.B. The present invention  
 CC specifically claims all the polynucleotide sequences given in the  
 CC sequence listing of the present specification, however the sequence  
 CC listing only goes up to SEQ ID NO:4454 so even though sequences are given  
 CC in the disclosure for SEQ ID NO:4465 to 4472, no sequences are present  
 CC for SEQ ID NO:4455 to 4464

XX SQ Sequence 116 AA;

Query Match 89.3%; Score 25; DB 4; Length 116;  
 Best Local Similarity 80.0%; Pred. No. 4.7e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5  
 Db |||:|  
 34 HYAMT 38

RESULT 43

ABU49557  
 ID ABU49557 standard; protein; 126 AA.

XX AC ABU49557;

XX 19-JUN-2003 (first entry)

XX Protein encoded by Prokaryotic essential gene #35084.

XX Antisense; prokaryotic essential gene; cell proliferation; drug design.

XX *Vibrio cholerae*.

XX WO200277183-A2.

XX 03-OCT-2002.

XX 21-MAR-2002; 2002WO-US009107.

XX 21-MAR-2001; 2001US-00815242.

PR 06-SEP-2001; 2001US-00948993.

PR 25-OCT-2001; 2001US-0342923P.

PR 08-FEB-2002; 2002US-00072851.

PR 06-MAR-2002; 2002US-0362699P.

XX (ELIT-) ELITRA PHARM INC.

XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;

PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

XX WPI; 2003-029926/02.

DR N-PSDB; ACAS3427.

XX New antisense nucleic acids, useful for identifying proteins or screening  
 PT for homologous nucleic acids required for cellular proliferation to  
 PT isolate candidate molecules for rational drug discovery programs.

XX Claim 25; SEQ ID NO 77481; 1766pp; English.

CC The invention relates to an isolated nucleic acid comprising any one of  
 CC the 6213 antisense sequences given in the specification where expression  
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:  
 CC (1) a vector comprising a promoter operably linked to the nucleic acid  
 CC encoding a polypeptide whose expression is inhibited by the antisense  
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated  
 CC polypeptide or its fragment whose expression is inhibited by the  
 CC antisense nucleic acid; (4) an antibody capable of specifically binding  
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
 CC proliferation or the activity of a gene in an operon required for  
 CC proliferation; (7) identifying a compound that influences the activity of  
 CC the gene product or that has an activity against a biological pathway  
 CC required for proliferation, or that inhibits cellular proliferation; (8)  
 CC identifying a gene required for cellular proliferation or the biological  
 CC pathway in which a proliferation-required gene or its gene product lies  
 CC or a gene on which the test compound that inhibits proliferation of an  
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a  
 CC product's activity; (11) a culture comprising strains in which the gene  
 CC product is overexpressed or underexpressed; (12) determining the extent  
 CC to which each of the strains is present in a culture or collection of  
 CC strains; or (13) identifying the target of a compound that inhibits the  
 CC proliferation of an organism. The antisense nucleic acids are useful for  
 CC identifying proteins or screening for homologous nucleic acids required  
 CC for cellular proliferation to isolate candidate molecules for rational  
 CC drug discovery programs, or for screening homologous nucleic acids  
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,  
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of  
 CC the target prokaryotic essential genes. Note: The sequence data for this  
 CC patent did not form part of the printed specification, but was obtained  
 CC in electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 126 AA;

Query Match 89.3%; Score 25; DB 6; Length 126;

Best Local Similarity 80.0%; Pred. No. 5.2e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5

Db 115 HYAMA 119

RESULT 44

ADB07674

ID ADB07674 standard; protein; 133 AA.

XX ADB07674;

XX 20-NOV-2003 (first entry)

XX Alloiooccus otitis antigenic protein SEQ ID NO:1614.

XX Alloiooccus otitis; antigenic protein; immunogenic; immunisation;  
 KW gene therapy; Gram-positive bacterium; infection.

XX Alloiooccus otitis.

XX WO2003048304-A2.

XX 12-JUN-2003.

XX 25-NOV-2002; 2002WO-US036123.

XX 29-NOV-2001; 2001US-0333777P.

XX 18-NOV-2002; 2002US-0426742P.

XX (AMHP ) WYETH HOLDINGS CORP.

XX Fletcher LD, Mcmichael JC, Russell DP, Zagursky RJ;

XX WPI; 2003-505284/47.

DR N-PSDB; ADB07673.

XX

PT New Alloiooccus otitis polynucleotides and polypeptides, useful for  
 PT treating and diagnosing diseases, drug screening assays and monitoring of  
 PT effects during drug clinical trials.

XX Claim 33; SEQ ID NO 1614; 1019pp; English.

CC The present invention describes an isolated polynucleotide (1) of  
 CC Alloiooccus otitis genomic DNA, which encodes an antigenic protein.  
 CC Alloiooccus otitis is a Gram-positive bacterium. Also described: (1)  
 CC an isolated polypeptide that is encoded by the polynucleotide (1); (2) an  
 CC expression vector comprising the novel isolated polynucleotide (1); its  
 CC complement, degenerate variant or fragment; (3) a genetically engineered  
 CC host cell, transfected, transformed or infected with the vector of (2);  
 CC (4) an antibody specific for the polypeptide of (1); (5) an immunogenic  
 CC composition comprising the polypeptide, its complement, biological  
 CC equivalent or fragment, or the polynucleotide that is comprised in the  
 CC expression vector; (6) a pharmaceutical composition comprising the  
 CC polypeptide of (1) and a carrier; (7) a protein chip comprising an array  
 CC of the polypeptides of (1), their biological equivalent or fragment; (8)  
 CC immunising against Alloiooccus otitis by administering to a host the  
 CC immunogenic composition; (9) detecting and/or identifying Alloiooccus  
 CC otitis in the biological sample; (10) a kit comprising a container  
 CC containing the novel polynucleotide, its degenerate variant or fragment,  
 CC or the antibody of (4); and (11) producing a polypeptide by culturing the  
 CC genetically engineered host cell under conditions suitable to produce the  
 CC polypeptide from the culture. (1) can be used in gene therapy. The  
 CC polynucleotides, polypeptides, antibodies and compositions of the present  
 CC invention can be used for treating and diagnosing diseases, drug  
 CC screening assays and monitoring of effects during drug clinical trials.  
 CC The polynucleotides are useful for expressing and detecting Alloiooccus  
 CC otitis. The present sequence represents an Alloiooccus otitis  
 CC antigen protein from the present invention.

XX Sequence 133 AA;

Query Match 89.3%; Score 25; DB 6; Length 133;

Best Local Similarity 80.0%; Pred. No. 5.5e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5

Db 74 HYALS 78

RESULT 45

ADB07668

ID ADB07668 standard; protein; 134 AA.

XX ADB07668;

XX 20-NOV-2003 (first entry)

XX Alloiooccus otitis antigenic protein SEQ ID NO:1608.

XX Alloiooccus otitis; antigenic protein; immunogenic; immunisation;  
 KW gene therapy; Gram-positive bacterium; infection.

XX Alloiooccus otitis.

XX WO2003048304-A2.

XX 12-JUN-2003.

XX 25-NOV-2002; 2002WO-US036123.

XX 29-NOV-2001; 2001US-0333777P.

XX 18-NOV-2002; 2002US-0426742P.

XX (AMHP ) WYETH HOLDINGS CORP.

XX Fletcher LD, Mcmichael JC, Russell DP, Zagursky RJ;

XX



PR 19-MAY-2000; 2000US-0205515P.  
PR 07-JUN-2000; 2000US-0209467P.  
PR 28-JUN-2000; 2000US-0214886P.  
PR 30-JUN-2000; 2000US-0215135P.  
PR 07-JUL-2000; 2000US-0216647P.  
PR 07-JUL-2000; 2000US-0216880P.  
PR 11-JUL-2000; 2000US-0217487P.  
PR 11-JUL-2000; 2000US-0217496P.  
PR 14-JUL-2000; 2000US-0218290P.  
PR 26-JUL-2000; 2000US-0220963P.  
PR 26-JUL-2000; 2000US-0220964P.  
PR 14-AUG-2000; 2000US-0224518P.  
PR 14-AUG-2000; 2000US-0224519P.  
PR 14-AUG-2000; 2000US-0225213P.  
PR 14-AUG-2000; 2000US-0225214P.  
PR 14-AUG-2000; 2000US-0225266P.  
PR 14-AUG-2000; 2000US-0225267P.  
PR 14-AUG-2000; 2000US-0225268P.  
PR 14-AUG-2000; 2000US-0225270P.  
PR 14-AUG-2000; 2000US-0225447P.  
PR 14-AUG-2000; 2000US-0225757P.  
PR 14-AUG-2000; 2000US-0225758P.  
PR 14-AUG-2000; 2000US-0225759P.  
PR 18-AUG-2000; 2000US-0226279P.  
PR 22-AUG-2000; 2000US-0226681P.  
PR 22-AUG-2000; 2000US-0226686P.  
PR 22-AUG-2000; 2000US-0227182P.  
PR 23-AUG-2000; 2000US-0227009P.  
PR 30-AUG-2000; 2000US-0228924P.  
PR 01-SEP-2000; 2000US-0229287P.  
PR 01-SEP-2000; 2000US-0229343P.  
PR 01-SEP-2000; 2000US-0229344P.  
PR 01-SEP-2000; 2000US-0229345P.  
PR 05-SEP-2000; 2000US-0229509P.  
PR 06-SEP-2000; 2000US-0230437P.  
PR 06-SEP-2000; 2000US-0230438P.  
PR 08-SEP-2000; 2000US-0231242P.  
PR 08-SEP-2000; 2000US-0231243P.  
PR 08-SEP-2000; 2000US-0231244P.  
PR 08-SEP-2000; 2000US-0231413P.  
PR 08-SEP-2000; 2000US-0231414P.  
PR 08-SEP-2000; 2000US-0232080P.  
PR 08-SEP-2000; 2000US-0232081P.  
PR 12-SEP-2000; 2000US-0231968P.  
PR 14-SEP-2000; 2000US-0232397P.  
PR 14-SEP-2000; 2000US-0232398P.  
PR 14-SEP-2000; 2000US-0232399P.  
PR 14-SEP-2000; 2000US-0232400P.  
PR 14-SEP-2000; 2000US-0232401P.  
PR 14-SEP-2000; 2000US-0233063P.  
PR 14-SEP-2000; 2000US-0233064P.  
PR 14-SEP-2000; 2000US-0233065P.  
PR 21-SEP-2000; 2000US-0234223P.  
PR 21-SEP-2000; 2000US-0234274P.  
PR 25-SEP-2000; 2000US-0234997P.  
PR 25-SEP-2000; 2000US-0234998P.  
PR 26-SEP-2000; 2000US-0235484P.  
PR 27-SEP-2000; 2000US-0235834P.  
PR 27-SEP-2000; 2000US-0235836P.  
PR 29-SEP-2000; 2000US-0236327P.  
PR 29-SEP-2000; 2000US-0236367P.  
PR 29-SEP-2000; 2000US-0236368P.  
PR 29-SEP-2000; 2000US-0236369P.  
PR 29-SEP-2000; 2000US-0236370P.  
PR 02-OCT-2000; 2000US-0236802P.  
PR 02-OCT-2000; 2000US-0237037P.  
PR 02-OCT-2000; 2000US-0237038P.  
PR 02-OCT-2000; 2000US-0237039P.  
PR 02-OCT-2000; 2000US-0237040P.  
PR 13-OCT-2000; 2000US-0239835P.  
PR 13-OCT-2000; 2000US-0239937P.  
PR 20-OCT-2000; 2000US-0240960P.  
PR 20-OCT-2000; 2000US-0241221P.  
PR 20-OCT-2000; 2000US-0241785P.  
PR 20-OCT-2000; 2000US-0241786P.  
PR 20-OCT-2000; 2000US-0241787P.  
PR 20-OCT-2000; 2000US-0241808P.  
PR 20-OCT-2000; 2000US-0241809P.  
PR 20-OCT-2000; 2000US-0241826P.  
PR 01-NOV-2000; 2000US-0244617P.  
PR 08-NOV-2000; 2000US-0246474P.  
PR 08-NOV-2000; 2000US-0246475P.  
PR 08-NOV-2000; 2000US-0246476P.  
PR 08-NOV-2000; 2000US-0246477P.  
PR 08-NOV-2000; 2000US-0246478P.  
PR 08-NOV-2000; 2000US-0246523P.  
PR 08-NOV-2000; 2000US-0246524P.  
PR 08-NOV-2000; 2000US-0246525P.  
PR 08-NOV-2000; 2000US-0246526P.  
PR 08-NOV-2000; 2000US-0246527P.  
PR 08-NOV-2000; 2000US-0246528P.  
PR 08-NOV-2000; 2000US-0246532P.  
PR 08-NOV-2000; 2000US-0246609P.  
PR 08-NOV-2000; 2000US-0246610P.  
PR 08-NOV-2000; 2000US-0246611P.  
PR 08-NOV-2000; 2000US-0246613P.  
PR 17-NOV-2000; 2000US-0249207P.  
PR 17-NOV-2000; 2000US-0249208P.  
PR 17-NOV-2000; 2000US-0249209P.  
PR 17-NOV-2000; 2000US-0249210P.  
PR 17-NOV-2000; 2000US-0249211P.  
PR 17-NOV-2000; 2000US-0249212P.  
PR 17-NOV-2000; 2000US-0249213P.  
PR 17-NOV-2000; 2000US-0249214P.  
PR 17-NOV-2000; 2000US-0249215P.  
PR 17-NOV-2000; 2000US-0249216P.  
PR 17-NOV-2000; 2000US-0249217P.  
PR 17-NOV-2000; 2000US-0249218P.  
PR 17-NOV-2000; 2000US-0249244P.  
PR 17-NOV-2000; 2000US-0249245P.  
PR 17-NOV-2000; 2000US-0249254P.  
PR 17-NOV-2000; 2000US-0249256P.  
PR 17-NOV-2000; 2000US-0249257P.  
PR 17-NOV-2000; 2000US-0249297P.  
PR 17-NOV-2000; 2000US-0249299P.  
PR 17-NOV-2000; 2000US-0249300P.  
PR 01-DEC-2000; 2000US-0250160P.  
PR 01-DEC-2000; 2000US-0250391P.  
PR 05-DEC-2000; 2000US-0251030P.  
PR 05-DEC-2000; 2000US-0251988P.  
PR 06-DEC-2000; 2000US-0256719P.  
PR 06-DEC-2000; 2000US-0251479P.  
PR 08-DEC-2000; 2000US-0251856P.  
PR 08-DEC-2000; 2000US-0251868P.  
PR 08-DEC-2000; 2000US-0251869P.  
PR 08-DEC-2000; 2000US-0251989P.  
PR 08-DEC-2000; 2000US-0251990P.  
PR 11-DEC-2000; 2000US-0254097P.  
PR 05-JAN-2001; 2001US-02559678P.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
PI Rosen CA, Baraah SC, Ruben SM;  
XX  
XX WPI; 2001-465460/50.  
DR N-PSDB; AAS27290.  
XX  
PT Novel polypeptides useful for diagnosing, treating, preventing and/or  
PT prognosing disorders related to the proteins, including cancers, immune  
PT disorders and neuronal disorders.  
XX  
PS Claim 1; SEQ ID NO 938; 880pp; English.  
XX  
XX The invention relates to novel isolated polypeptides (I), and  
CC polynucleotides (II). (I), (II) and the antibody to (I) are useful for  
CC diagnosing, preventing and treating diseases including immune system

CC disorders (e.g. congenital and acquired immunodeficiencies, autoimmune  
CC disorders (e.g. rheumatoid arthritis), inflammatory conditions, organ  
CC transplant rejections and graft versus host disease, infectious diseases  
CC (e.g. hepatitis C), bleeding disorders, haemoglobin abnormalities and  
CC other blood-related disorders (sickle cell anaemia), myeloproliferative  
CC disorders, primary haematopoietic disorders, hyperproliferative disorders  
CC (e.g. Gaucher's disease and cancer), neurodegenerative disorders (e.g.  
CC Alzheimer's disease, Parkinson's disease), chromosomal abnormalities  
CC (Down syndrome), ischaemic injury (e.g. stroke), renal disorders (e.g.  
CC glomerulonephritis), cardiovascular disorders (e.g. arrhythmia),  
CC respiratory disorders, dermatological disorders, in wound healing,  
CC epithelial cell proliferation, endocrine disorders (e.g. Addison's  
CC disease), reproductive system disorders, gastrointestinal disorder  
CC (inflammatory disorders), liver disorders (cirrhosis), as stimulators of  
CC B-cell responsiveness to pathogens, activators of T-cells, to induce  
CC higher affinity antibodies, and as a means to induce tumour proliferation  
CC in pathologies e.g. acquired immune deficiency syndrome (AIDS). AAU17059-  
CC AAU17693 represent novel signal transduction pathway protein, amino acid  
CC sequences of the invention  
XX

Query Match 89.3%; Score 25; DB 4; Length 150;  
Best Local Similarity 80.0%; Pred. No. 6.3e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HYAMS 5  
Db 65 HYALS 69

RESULT 48  
ADB94081  
ID ADB94081 standard; protein; 150 AA.

AC ADB94081;

DT 04-DEC-2003 (first entry)

DE Human novel protein #315.

KW human; autoimmune disease; Parkinson's disease; silicosis;  
KW gastrointestinal disease; atherosclerosis; haemophilia; thrombocytopenia;  
KW immunosuppressive agent; adjuvant; enhance immune response;  
KW higher affinity antibody induction;  
KW increased serum immunoglobulin concentration.

OS Homo sapiens.

XX US2002168711-A1.

XX 14-NOV-2002.

XX 17-JAN-2001; 2001US-00764868.

XX 31-JAN-2000; 2000US-0179065P.

XX 04-FEB-2000; 2000US-0180628P.

XX 28-JUN-2000; 2000US-0214886P.

XX 07-JUL-2000; 2000US-0216647P.

XX 07-JUL-2000; 2000US-0216880P.

XX 11-JUL-2000; 2000US-0217487P.

XX 11-JUL-2000; 2000US-0217496P.

XX 14-JUL-2000; 2000US-0218290P.

XX 26-JUL-2000; 2000US-0220963P.

XX 26-JUL-2000; 2000US-0220964P.

XX 14-AUG-2000; 2000US-0224518P.

XX 14-AUG-2000; 2000US-0225267P.

XX 14-AUG-2000; 2000US-0225268P.

XX 14-AUG-2000; 2000US-0225270P.

XX 14-AUG-2000; 2000US-0225447P.

XX 14-AUG-2000; 2000US-0225757P.

XX 22-AUG-2000; 2000US-0225758P.

XX 22-AUG-2000; 2000US-0226686P.

PR 30-AUG-2000; 2000US-0228924P.  
PR 01-SEP-2000; 2000US-0229287P.  
PR 01-SEP-2000; 2000US-0229343P.  
PR 01-SEP-2000; 2000US-0229344P.  
PR 01-SEP-2000; 2000US-0229345P.  
PR 05-SEP-2000; 2000US-0229509P.  
PR 05-SEP-2000; 2000US-0229513P.  
PR 08-SEP-2000; 2000US-0231413P.  
PR 21-SEP-2000; 2000US-0234223P.  
PR 21-SEP-2000; 2000US-0234274P.  
PR 25-SEP-2000; 2000US-0234997P.  
PR 27-SEP-2000; 2000US-0235834P.  
PR 29-SEP-2000; 2000US-0236327P.  
PR 29-SEP-2000; 2000US-0236367P.  
PR 29-SEP-2000; 2000US-0236368P.  
PR 29-SEP-2000; 2000US-0236369P.  
PR 29-SEP-2000; 2000US-0236370P.  
PR 02-OCT-2000; 2000US-0236802P.  
PR 02-OCT-2000; 2000US-0237037P.  
PR 02-OCT-2000; 2000US-0237038P.  
PR 02-OCT-2000; 2000US-0237039P.  
PR 13-OCT-2000; 2000US-0237040P.  
PR 20-OCT-2000; 2000US-0239935P.  
PR 20-OCT-2000; 2000US-0240960P.  
PR 20-OCT-2000; 2000US-0241785P.  
PR 20-OCT-2000; 2000US-0241809P.  
PR 01-NOV-2000; 2000US-0244617P.  
PR 17-NOV-2000; 2000US-0249299P.  
PR 08-DEC-2000; 2000US-0251856P.  
PR 08-DEC-2000; 2000US-0251868P.  
PR 08-DEC-2000; 2000US-0251869P.

(ROSE/) ROSEN C A.

(RUBE/) RUBEN S M.

(BARA/) BARASH S C.

Rosen CA, Ruben SM, Barash SC;

WPI; 2003-719985/68.

N-PSDB; ADB93458.

New isolated polypeptide useful for diagnosing and treating  
immunosuppressive conditions such as autoimmune disease and Parkinson's  
disease.

Claim 11; SEQ ID NO 938; 345pp; English.

The invention relates to an isolated polypeptide. The polypeptide is  
useful for diagnosing a pathological condition or a susceptibility to a  
pathological condition in a subject, by determining the presence or  
amount of expression of the polypeptide in a biological sample and  
diagnosing a pathological condition or a susceptibility to a pathological  
condition based on the presence or amount of expression of the  
polypeptide. The polypeptide is also useful for identifying a binding  
partner to the polypeptide, which involves contacting the polypeptide  
with a binding partner and determining whether the binding partner  
effects an activity of the polypeptide. The polypeptide or the nucleic  
acid encoding the polypeptide is useful for preventing, treating, or  
ameliorating a medical condition, which involves administering the  
polypeptide or the nucleic acid to a mammalian subject. The nucleic acid  
is useful for diagnosing a pathological condition or a susceptibility to  
a pathological condition in a subject, which involves determining the  
presence or absence of a mutation in the nucleic acid, and diagnosing a  
pathological condition or susceptibility to a pathological condition  
based on the presence or absence of the mutation. The polypeptide, the  
nucleic acid and an antibody to the polypeptide are useful for treating  
autoimmune disease, Parkinson's disease, silicosis, gastrointestinal  
disease, atherosclerosis, haemophilia, thrombocytopenia. The polypeptide,  
the nucleic acid and the antibody are useful as immunosuppressive agents,  
as adjuvants to enhance immune responses, and as agents to induce higher  
affinity antibodies and increase serum immunoglobulin concentrations. The  
present sequence represents the amino acid sequence of a novel human  
protein. Note: The sequence data for this patent did not form part of the

CC printed specification but was obtained in electronic format direct from  
CC USPTO at seqdata.uspto.gov/sequence.html?DocID=20020169711.

XX  
SQ Sequence 150 AA;

Query Match 89.3%; Score 25; DB 7; Length 150;  
Best Local Similarity 80.0%; Pred. No. 6.3e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5  
|||:|  
Db 65 HYALS 69

## RESULT 49

ABG21786  
ID ABG21786 standard; protein; 164 AA.

XX  
AC ABG21786;

XX  
DT 18-FEB-2002 (first entry)

XX  
DE Novel human diagnostic protein #21777.

XX  
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;  
KW Food supplement; medical imaging; diagnostic; genetic disorder.

XX  
OS Homo sapiens.

XX  
PN WO200175067-A2.

XX  
PD 11-OCT-2001.

XX  
PF 30-MAR-2001; 2001WO-US008631.

XX  
PR 31-MAR-2000; 2000US-00540217.

XX  
PR 23-AUG-2000; 2000US-00649167.

XX  
PA (HYSE-) HYSEQ INC.

XX  
PI Drmanac RT, Liu C, Tang YT;

XX  
DR WPI; 2001-639362/73.

XX  
DR N-PSDB; AAS85973.

XX  
PT New isolated polynucleotide and encoded polypeptides, useful in  
PT diagnostics, forensics, gene mapping, identification of mutations  
PT responsible for genetic disorders or other traits and to assess  
PT biodiversity.

XX  
PS Claim 20; SEQ ID NO 52145; 103pp; English.

XX  
CC The invention relates to isolated polynucleotide (I) and polypeptide (II)  
CC sequences. (I) is useful as hybridisation probes, polymerase chain  
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,  
CC and in recombinant production of (II). The polynucleotides are also used  
CC in diagnostics as expressed sequence tags for identifying expressed  
CC genes. (I) is useful in gene therapy techniques to restore normal  
CC activity of (II) or to treat disease states involving (II). (II) is  
CC useful for generating antibodies against it, detecting or quantitating a  
CC polypeptide in tissue, as molecular weight markers and as a food  
CC supplement. (II) and its binding partners are useful in medical imaging  
CC of sites expressing (II). (I) and (II) are useful for treating disorders  
CC involving aberrant protein expression or biological activity. The  
CC polypeptide and polynucleotide sequences have applications in  
CC diagnostics, forensics, gene mapping, identification of mutations  
CC responsible for genetic disorders or other traits to assess biodiversity  
CC and to produce other types of data and products dependent on DNA and  
CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic  
CC amino acid sequences of the invention. Note: The sequence data for this  
CC patent did not appear in the printed specification, but was obtained in  
CC electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences

XX  
SQ Sequence 164 AA;

Query Match 89.3%; Score 25; DB 4; Length 164;  
Best Local Similarity 80.0%; Pred. No. 6.9e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5  
|||:|  
Db 18 HYALS 22

## RESULT 50

AAG66027  
ID AAG66027 standard; protein; 180 AA.

XX  
AC AAG66027;

XX  
DT 27-FEB-2002 (first entry)

XX  
DE Ryk protein extracellular domain and WIF domain.

XX  
KW Ryk protein; angiogenesis; variant; receptor tyrosine kinase; cytostatic;  
KW antidiabetic; ophthalmological; cardiac; vulnary; antiangiogenic;  
KW gene therapy; Wnt inhibitory factor; WIF.

XX  
OS Homo sapiens.

XX  
PN WO200185789-A2.

XX  
PD 15-NOV-2001.

XX  
PF 09-MAY-2001; 2001WO-US015043.

XX  
PR 10-MAY-2000; 2000US-00568783.

XX  
PA (FARB ) BAYER CORP.

XX  
PI Rocznia S, Dubois-Stringfellow NA, Zolotorev A;

XX  
DR WPI; 2002-049443/06.

XX  
DR N-PSDB; AAI67765.

XX  
PT Modulating angiogenesis at a site, for treating or preventing cancer,  
PT metastasis, diabetic retinopathy, cardiovascular disease, wound by  
PT supplying composition comprising variant Ryk protein to the site.

XX  
PS Claim 27; Fig 3; 81pp; English.

XX  
CC The invention relates to modulating angiogenesis at a site by supplying a  
CC composition comprising a variant Ryk protein (I) (a member of the  
CC receptor tyrosine kinase family), or modulating formation of cells into  
CC capillary-like structures by contacting the cells with a composition  
CC comprising (I). The method is useful modulating angiogenesis at a site  
CC (preferably, within a human) or modulating the formation of cells  
CC (endothelial cells of human origin) into capillary-like structure. The  
CC (I) is useful for preventing, treating or ameliorating a medical  
CC condition e.g., cancer, metastasis, diabetic retinopathy, macular  
CC degeneration, cardiovascular disease, wound, pregnancy, or a clinical  
CC regulation of placental vascularization in an individual. The variant  
CC protein is supplied to the individual as a source of polynucleotide  
CC encoding the protein and expressing the protein in vivo. (I) is used as  
CC an immunogen to produce an antibody against it. The antibodies are useful  
CC for modulating angiogenesis at a site. Polynucleotides encoding (I) is  
CC useful in gene therapy technique for treating above mentioned medical  
CC conditions. The present sequence represents the amino acid sequence of  
CC the extracellular domain of Ryk protein consisting the Wnt inhibitory  
CC factor (WIF) domain

XX  
SQ Sequence 180 AA;

Query Match 89.3%; Score 25; DB 5; Length 180;

Best Local Similarity 80.0%; Pred. No. 7.7e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5  
|||:  
Db 77 HYALS 81

Search completed: April 6, 2006, 09:03:39  
Job time : 71.1186 secs

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 6, 2006, 08:56:41 ; Search time 5 Seconds  
(without alignments)  
96.217 Million cell updates/sec

Title: US-10-089-500-3

Perfect score: 28

Sequence: 1 HYAMS 5

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

PIR 80:\*

1: PIR1:\*

2: PIR2:\*

3: PIR3:\*

4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query %	Match	Length	DB	ID	Description
1	28	100.0	119	2	E89999	-----	holo-ACP synthase
2	28	100.0	143	2	A71051	-----	hypothetical prote
3	28	100.0	146	2	AD3630	-----	pseudoazurin [limpo
4	28	100.0	185	2	T37007	-----	probable aminoglyc
5	28	100.0	280	2	E75216	-----	hypothetical prote
6	28	100.0	280	2	C71453	-----	hypothetical prote
7	28	100.0	284	2	C72320	-----	conserved hypothet
8	28	100.0	286	2	A64317	-----	hypothetical prote
9	28	100.0	288	2	A70371	-----	conserved hypothet
10	28	100.0	291	2	H69356	-----	conserved hypothet
11	28	100.0	292	2	F64486	-----	hypothetical prote
12	28	100.0	295	2	H75229	-----	hypothetical prote
13	28	100.0	297	2	AB2284	-----	hypothetical prote
14	28	100.0	424	2	C83159	-----	Na+/H+ antiporter
15	28	100.0	839	2	S62963	-----	hypothetical prote
16	25	89.3	126	2	F82072	-----	holo-(acyl-carrier
17	25	89.3	216	2	JL0090	-----	ependymin precursor
18	25	89.3	221	2	S63682	-----	hypothetical prote
19	25	89.3	273	2	C82182	-----	hypothetical prote
20	25	89.3	283	2	T15932	-----	hypothetical prote
21	25	89.3	287	2	T23325	-----	hypothetical prote
22	25	89.3	287	2	T23324	-----	hypothetical prote
23	25	89.3	310	2	T43158	-----	probable GRP-bindi
24	25	89.3	312	2	H89884	-----	hypothetical prote
25	25	89.3	314	2	T23675	-----	hypothetical prote
26	25	89.3	313	2	T43299	-----	probable GRP-bindi
27	25	89.3	324	2	T50249	-----	conserved hypothet
28	25	89.3	325	2	A86202	-----	hypothetical prote
29	25	89.3	333	2	S15238	-----	O-antigen acetylas

30	25	89.3	338	2	E75301	-----	conserved hypothet
31	25	89.3	352	1	BVECHD	-----	molybdenum transpo
32	25	89.3	352	2	A80595	-----	molybdenum transpo
33	25	89.3	352	2	B85579	-----	ATP-binding compon
34	25	89.3	352	2	A90728	-----	ATP-binding compon
35	25	89.3	359	2	AB0844	-----	membrane-bound lye
36	25	89.3	361	2	B85918	-----	membrane-bound lye
37	25	89.3	361	2	A65050	-----	membrane-bound lye
38	25	89.3	361	2	F91073	-----	membrane-bound lye
39	25	89.3	367	2	H83088	-----	membrane-bound lye
40	25	89.3	394	2	AB1068	-----	probable membrane
41	25	89.3	399	2	F87356	-----	hypothetical prote
42	25	89.3	406	2	G85775	-----	hypothetical prote
43	25	89.3	406	2	C90927	-----	selenocysteine lya
44	25	89.3	406	2	H64925	-----	aminotransferase n
45	25	89.3	420	2	B87201	-----	hypothetical prote
46	25	89.3	420	2	A70796	-----	probable cycloprop
47	25	89.3	442	2	B81418	-----	adenylosuccinate l
48	25	89.3	468	2	A5476	-----	protein kinase (EC
49	25	89.3	516	2	H82756	-----	conserved hypothet
50	25	89.3	541	2	AC2392	-----	hypothetical prote
51	25	89.3	559	2	A12227	-----	hypothetical prote
52	25	89.3	593	2	A47186	-----	receptor protein t
53	25	89.3	594	2	I58386	-----	receptor tyrosine
54	25	89.3	594	2	I56248	-----	receptor tyrosine
55	25	89.3	607	2	I37560	-----	protein-tyrosine k
56	25	89.3	632	2	E88712	-----	protein C17H12.12
57	25	89.3	632	2	S88152	-----	hypothetical prote
58	25	89.3	735	2	JC5869	-----	beta-glucosidase (
59	25	89.3	840	2	B86901	-----	mismatch repair pr
60	25	89.3	927	2	T38518	-----	ribonuclease II RN
61	25	89.3	946	2	S66367	-----	H+-exporting ATPase
62	25	89.3	1012	2	A84393	-----	glycolate oxidase
63	25	89.3	1072	1	A37221	-----	neurofilament trip
64	25	89.3	1102	2	JH0717	-----	guanylate cyclase
65	25	89.3	1108	2	A55915	-----	guanylate cyclase
66	25	89.3	1110	1	S55279	-----	guanylate cyclase
67	24	85.7	16	2	PH1589	-----	Ig H chain V-B-J r
68	24	85.7	48	2	PL0090	-----	Ig heavy chain V r
69	24	85.7	97	2	PQ0068	-----	T-cell receptor be
70	24	85.7	102	2	C87226	-----	PG-family protein
71	24	85.7	116	2	S74062	-----	hypothetical prote
72	24	85.7	119	1	GIHUTE	-----	Ig heavy chain V-I
73	24	85.7	146	1	CUALBF	-----	blue copper protal
74	24	85.7	153	2	AF3598	-----	transposase BME110
75	24	85.7	154	2	S67936	-----	glycerol-3-phospha
76	24	85.7	161	2	E97102	-----	ankyrin repeats co
77	24	85.7	165	2	B98120	-----	glycerol-3-phospha
78	24	85.7	168	2	S68480	-----	succinate dehydrog
79	24	85.7	169	2	AF1039	-----	phage regulatory p
80	24	85.7	169	2	AE0925	-----	regulatory protein
81	24	85.7	169	2	JQ0857	-----	hypothetical 18.1K
82	24	85.7	171	2	E87459	-----	cytochrome c famil
83	24	85.7	172	1	WMVZTH	-----	BamHI-ORF13 protel
84	24	85.7	183	2	T49855	-----	hypothetical prote
85	24	85.7	207	2	A38143	-----	protein kinase (EC
86	24	85.7	209	2	S57156	-----	hypothetical prote
87	24	85.7	209	2	T47244	-----	b11-3 protein, blu
88	24	85.7	213	1	TVHUC4	-----	transforming prote
89	24	85.7	220	2	T12510	-----	hypothetical prote
90	24	85.7	247	2	T29733	-----	hypothetical prote
91	24	85.7	250	2	C70823	-----	hypothetical prote
92	24	85.7	272	2	AE2737	-----	hypothetical prote
93	24	85.7	279	2	D82243	-----	transcription regu
94	24	85.7	280	2	S72844	-----	beta-aspartate met
95	24	85.7	281	2	C87073	-----	conserved hypothet
96	24	85.7	282	2	T32145	-----	hypothetical prote
97	24	85.7	283	2	T01895	-----	hypothetical prote
98	24	85.7	283	2	S57134	-----	hypothetical prote
99	24	85.7	299	2	G82221	-----	transcription regu
100	24	85.7	317	2	I37371	-----	ER calcium-binding
101	24	85.7	318	2	I56519	-----	taipoxin-binding
102	24	85.7	319	2	JC5402	-----	vitamin D receptor



103	24	85.7	333	2	JE0287	chondromodulin-I p	176	24	85.7	744	2	AG1382	transport protein
104	24	85.7	335	2	JT0569	chondromodulin-I p	177	24	85.7	744	2	AH1751	transport protein
105	24	85.7	343	2	AG2770	hypothetical prote	178	24	85.7	750	2	S75636	sensory transducti
106	24	85.7	343	2	G97550	general l-amino ac	179	24	85.7	756	2	C91266	biodegradative arg
107	24	85.7	345	1	JN0465	apolipoprotein H p	180	24	85.7	756	2	H86106	biodegradative arg
108	24	85.7	351	1	OKB02C	protein kinase (EC	181	24	85.7	756	2	AH1022	arginine decarboxy
109	24	85.7	351	1	OKH02C	protein kinase (EC	182	24	85.7	756	2	S56346	arginine decarboxy
110	24	85.7	351	1	OKHYCA	protein kinase (EC	183	24	85.7	760	2	D82164	oxidoreductase, ac
111	24	85.7	351	1	OKWSCA	protein kinase (EC	184	24	85.7	771	2	A84094	virulence-associat
112	24	85.7	351	1	OKRT2C	protein kinase (EC	185	24	85.7	825	2	F95963	probable dehydroge
113	24	85.7	360	1	OKHUCG	protein kinase (EC	186	24	85.7	826	2	D86458	hypothetical prote
114	24	85.7	363	2	B83057	tRNA (uracil-5-) -m	187	24	85.7	829	2	I40014	sorbitol dehydroge
115	24	85.7	365	2	F81826	probable cytochrom	188	24	85.7	856	2	T13159	E1b-55kDa-associat
116	24	85.7	365	2	C81050	cytochrome c oxida	189	24	85.7	907	2	AB1885	hypothetical prote
117	24	85.7	367	2	AH3588	leucine- isoleuci	190	24	85.7	928	2	D72077	polymorphic outer
118	24	85.7	369	2	T33314	hypothetical prote	191	24	85.7	928	2	H86546	polymorphic outer
119	24	85.7	370	2	H84351	hypothetical prote	192	24	85.7	931	2	T32919	hypothetical prote
120	24	85.7	372	2	T21650	hypothetical prote	193	24	85.7	932	1	SWOPAI	serotype-specific
121	24	85.7	372	2	G64539	lipopolysaccharide	194	24	85.7	933	2	E64603	hypothetical prote
122	24	85.7	380	2	T25488	hypothetical prote	195	24	85.7	949	2	F81591	polymorphic membra
123	24	85.7	390	2	AC3112	hypothetical prote	196	24	85.7	1005	1	PIVXPJ	RNA 1 protein - pe
124	24	85.7	396	2	D69847	hypothetical prote	197	24	85.7	1042	2	H75112	molybdenum cofacto
125	24	85.7	402	2	B98175	hypothetical prote	198	24	85.7	1075	2	G85360	puative protein fi
126	24	85.7	403	2	H96026	hypothetical prote	199	24	85.7	1154	2	A39577	protein-tyrosine k
127	24	85.7	447	2	E95941	probable amino aci	200	24	85.7	1185	2	AH2579	ATP-dependent DNA
128	24	85.7	450	1	DCCHO	ornithine decarbox	201	24	85.7	1233	2	G97361	hypothetical prote
129	24	85.7	466	2	F84139	beta-glucosidase B	202	24	85.7	1234	2	E83415	methionine synthas
130	24	85.7	476	2	S18451	variant surface gl	203	24	85.7	1245	2	H83574	conserved hypothet
131	24	85.7	476	2	A83387	probable transport	204	24	85.7	1248	2	C89874	autoclysin limpor
132	24	85.7	483	2	A97744	isocitrate dehydro	205	24	85.7	1488	2	T02856	probable membrane
133	24	85.7	483	2	B71681	isocitrate dehydro	206	24	85.7	1613	2	A43081	vitellogenin vit-2
134	24	85.7	488	2	B75551	glutamate synthase	207	24	85.7	1613	2	F89528	protein vit-2 (imp
135	24	85.7	493	2	H69634	glutamate synthase	208	24	85.7	2285	1	G02434	DNA-directed DNA p
136	24	85.7	494	2	JX0300	ubiquinol-cytochro	209	24	85.7	2472	2	A35715	forin alpha chain
137	24	85.7	497	2	F83651	hypothetical prote	210	24	85.7	2477	1	SUCHA	spectrin alpha cha
138	24	85.7	505	2	A57156	Ca2+/calmodulin-de	211	24	85.7	4568	2	T08030	dyein beta heavy
139	24	85.7	506	2	D96672	probable Cytochrom	212	23	82.1	129	2	S03534	ig heavy chain pre
140	24	85.7	510	2	A96673	probable cytochrom	213	23	82.1	130	2	A13316	phosphohydrolase (
141	24	85.7	511	1	S31308	aldehyde dehydroge	214	23	82.1	141	2	A91249	probable transcrip
142	24	85.7	511	2	G96672	hypothetical prote	215	23	82.1	153	1	S08619	formate hydrogenly
143	24	85.7	511	2	H96672	probable cytochrom	216	23	82.1	153	2	A10846	formate hydrogenly
144	24	85.7	512	2	B84501	probable cytochrom	217	23	82.1	153	2	D85921	formate hydrogenly
145	24	85.7	512	2	G69670	glycine betaine tr	218	23	82.1	153	2	E91076	formate hydrogenly
146	24	85.7	515	2	T32217	hypothetical prote	219	23	82.1	179	1	XXECPL	ribosomal-protein-
147	24	85.7	517	2	A13201	hypothetical prote	220	23	82.1	202	2	A86850	transcription regu
148	24	85.7	521	2	T41134	aspartic acid prot	221	23	82.1	245	2	B70039	hypothetical prote
149	24	85.7	532	2	A97769	cytochrome-c oxida	222	23	82.1	252	1	REEDO	deoxyribose operon
150	24	85.7	533	2	A39410	aldehyde dehydroge	223	23	82.1	252	2	D85594	deoxyribose operon
151	24	85.7	534	2	D71698	cytochrome-c oxida	224	23	82.1	252	2	H90743	hypothetical prote
152	24	85.7	546	2	T31255	phR protein homol	225	23	82.1	256	2	D90026	formate acetyltran
153	24	85.7	548	2	C75466	phytoene dehydroge	226	23	82.1	258	2	B97900	formate acetyltran
154	24	85.7	550	1	HMIV77	hemagglutinin prec	227	23	82.1	258	2	G95028	hypothetical prote
155	24	85.7	554	2	S03809	cytochrome-c oxida	228	23	82.1	311	2	AF2064	hypothetical prote
156	24	85.7	554	2	A45818	cytolysin precurs	229	23	82.1	312	2	JC1418	replication-associ
157	24	85.7	558	2	S08270	cytochrome-c oxida	230	23	82.1	343	2	G81547	conserved hypothet
158	24	85.7	565	2	S20534	cytochrome-c oxida	231	23	82.1	343	2	D69482	hypothetical prote
159	24	85.7	569	2	C69769	hypothetical prote	232	23	82.1	344	2	AC0994	puative phosphotri
160	24	85.7	583	2	G75456	succinate dehydrog	233	23	82.1	369	1	A41147	protein-tyrosine-p
161	24	85.7	583	2	A82430	nitrate/nitrite se	234	23	82.1	391	2	T50456	etd1 protein limpo
162	24	85.7	587	2	E71020	hypothetical prote	235	23	82.1	392	2	T43652	hypothetical prote
163	24	85.7	594	2	A49804	cellular Hsp70 hom	236	23	82.1	396	2	AG0506	probable sulfatase
164	24	85.7	608	2	C95255	hypothetical prote	237	23	82.1	409	2	T45797	hypothetical prote
165	24	85.7	615	2	G84285	succinate dehydrog	238	23	82.1	482	2	E96985	altronate oxidore
166	24	85.7	619	2	I64087	translation elonga	239	23	82.1	496	2	H70668	probable polyketid
167	24	85.7	626	2	E90079	hypothetical prote	240	23	82.1	498	2	JC8008	bea3-glycosyltran
168	24	85.7	630	2	S78650	DNA endonuclease a	241	23	82.1	502	2	D86578	S/T protein kinase
169	24	85.7	632	2	AF1189	transcription anti	242	23	82.1	502	2	G72045	s/t protein kinase
170	24	85.7	632	2	AG1547	acetate-CoA ligase	243	23	82.1	512	2	C96517	hypothetical prote
171	24	85.7	670	2	A13281	conserved hypothet	244	23	82.1	528	2	T33599	hypothetical prote
172	24	85.7	670	2	C83540	probable electron	245	23	82.1	530	2	T18596	hypothetical prote
173	24	85.7	685	2	C70678	hypothetical prote	246	23	82.1	554	2	A31300	perforin precursor
174	24	85.7	730	2	T44313	hypothetical prote	247	23	82.1	570	2	A82135	2-succinyl-6-hydro
175	24	85.7	730	2	S70954	otnG protein - Vib	248	23	82.1	593	2	AI0559	probable ABC trans

249	23	82.1	593	2	A64775	ABC-type transport	322	22	78.6	261	2	D69629	glucose 1-dehydrog
250	23	82.1	593	2	G90691	ABC-type transport	323	22	78.6	261	2	J50385	glucose 1-dehydrog
251	23	82.1	593	2	C85542	ABC-type transport	324	22	78.6	261	2	I40224	glucose 1-dehydrog
252	23	82.1	609	2	A49839	odd-paired - fruit	325	22	78.6	261	2	I40225	glucose 1-dehydrog
253	23	82.1	685	2	F75370	oligopeptidase A -	326	22	78.6	261	2	I39853	glucose 1-dehydrog
254	23	82.1	704	2	T02558	hypothetical prote	327	22	78.6	261	2	AC3646	hydroxypyruvate is
255	23	82.1	736	2	B71972	DNA topoisomerase	328	22	78.6	262	2	S02299	glucose 1-dehydrog
256	23	82.1	736	2	D64534	DNA topoisomerase	329	22	78.6	263	2	S01227	glucose 1-dehydrog
257	23	82.1	789	2	FC4161	zinc finger protei	330	22	78.6	264	2	T30224	3-oxoacyl-(acyl ca
258	23	82.1	790	2	I51638	F-cadherin - Afric	331	22	78.6	265	2	A56636	retroind element PA
259	23	82.1	794	1	TLBPB7	tail tubular prote	332	22	78.6	267	2	S42241	hypothetical prote
260	23	82.1	862	2	AC1214	fibrinogen-binding	333	22	78.6	273	2	T25718	hypothetical prote
261	23	82.1	875	1	S66672	phosphatidylinosit	334	22	78.6	275	2	B70640	hypothetical prote
262	23	82.1	928	2	G85546	polymorphic outer	335	22	78.6	279	2	T18829	hypothetical prote
263	23	82.1	928	2	G81591	telomerase catalyt	336	22	78.6	281	2	T30596	hypothetical prote
264	23	82.1	989	2	T03938	hypothetical prote	337	22	78.6	282	2	A47734	F actin-capping pr
265	23	82.1	1116	2	S57382	hypothetical mbl f	338	22	78.6	282	2	T24693	hypothetical prote
266	23	82.1	1143	4	I84547	hypothetical mbl f	339	22	78.6	283	2	C71554	probable polysacch
267	23	82.1	1197	2	S26947	DNA-directed DNA p	340	22	78.6	287	2	A27082	2,4-dichlorophenox
268	23	82.1	1237	2	E86457	probable RNA helic	341	22	78.6	287	2	F96738	hypothetical prote
269	23	82.1	1682	2	A45380	sodium channel pro	342	22	78.6	289	2	F86404	unknown protein li
270	23	82.1	2103	2	G85925	probable polyketid	343	22	78.6	294	2	S68784	cathepsin L - Para
271	23	82.1	3856	2	T51174	ataxia-telangiecta	344	22	78.6	294	2	AB0115	probable carbon-ni
272	23	78.6	88	2	AH0088	probable flagellar	345	22	78.6	294	2	G90215	conserved hypothet
273	22	78.6	102	2	S51974	probable membrane	346	22	78.6	296	2	G87611	branched-chain ami
274	22	78.6	108	2	S56430	hypothetical 12.2K	347	22	78.6	297	2	F83433	DNA-3-methyladenin
275	22	78.6	110	2	S60591	lg light chain var	348	22	78.6	298	2	A12615	formamidopyrimidin
276	22	78.6	117	2	AH1658	hypothetical prote	349	22	78.6	301	2	A96990	probable membrane
277	22	78.6	129	2	C83418	hypothetical prote	350	22	78.6	302	2	T39146	hypothetical prote
278	22	78.6	131	2	E91276	hypothetical prote	351	22	78.6	302	2	AE0958	probable Ly8R-fam1
279	22	78.6	131	2	AP3338	hypothetical prote	352	22	78.6	302	2	A43708	gamma-interferon-1
280	22	78.6	134	2	D64173	hypothetical prote	353	22	78.6	303	2	B83336	hypothetical prote
281	22	78.6	146	2	F83274	conserved hypothet	354	22	78.6	304	1	S74557	acetylpolymine am
282	22	78.6	148	2	S53926	hypothetical prote	355	22	78.6	305	2	D90266	heterodisulfide re
283	22	78.6	154	2	B71149	hypothetical prote	356	22	78.6	305	2	I57039	genomic screen hom
284	22	78.6	168	2	F64689	hypothetical prote	357	22	78.6	308	2	AC3604	n-acetylglucosamin
285	22	78.6	168	2	C71828	hypothetical prote	358	22	78.6	309	2	T09166	probable peroxidase
286	22	78.6	171	2	E87417	transcription regu	359	22	78.6	312	2	C75377	probable glucosyl 6
287	22	78.6	186	2	B82649	hypothetical prote	360	22	78.6	314	1	ROSACT	repc protein - Sta
288	22	78.6	187	2	C82065	hypothetical prote	361	22	78.6	314	2	F69032	conserved hypothet
289	22	78.6	198	2	D82361	conserved hypothet	362	22	78.6	316	2	T09591	probable cdc2-like
290	22	78.6	199	2	T26329	hypothetical prote	363	22	78.6	319	2	D89778	hypothetical prote
291	22	78.6	200	1	B69854	phage-related repl	364	22	78.6	325	2	H97397	formamidopyrimidin
292	22	78.6	205	2	F69836	hypothetical prote	365	22	78.6	327	2	E71130	probable oligopept
293	22	78.6	207	2	F84563	hypothetical prote	366	22	78.6	327	2	A56553	homoeotic protein H
294	22	78.6	215	2	I51377	ependymin precurs	367	22	78.6	330	2	S53990	DNA methyltransfer
295	22	78.6	216	2	A32636	ependymin II precu	368	22	78.6	332	2	B75286	hypothetical prote
296	22	78.6	217	2	A43820	ependymin precurs	369	22	78.6	333	2	D72703	hypothetical prote
297	22	78.6	218	2	E85021	hypothetical prote	370	22	78.6	334	2	G02049	adenosine kinase (
298	22	78.6	221	2	T35551	probable phospholi	371	22	78.6	336	2	G81152	probable DNA-bind
299	22	78.6	223	2	S41286	latexin - rat	372	22	78.6	338	2	T46981	hypothetical prote
300	22	78.6	227	2	JC1248	protein-L-isoaspar	373	22	78.6	338	2	AD0241	probable dehydroge
301	22	78.6	227	2	A32449	protein-L-isoaspar	374	22	78.6	340	2	T47019	hypothetical prote
302	22	78.6	228	1	A40402	CD9 antigen (valid	375	22	78.6	340	2	AF0236	probable glutamine
303	22	78.6	239	2	C84994	hypothetical prote	376	22	78.6	340	2	T20101	hypothetical prote
304	22	78.6	240	2	H75014	3-oxoacyl-l-acyl-ca	377	22	78.6	343	2	AB1243	B. subtilis comG o
305	22	78.6	240	2	D82288	NADPH-flavin oxido	378	22	78.6	344	2	E87373	adenosine kinase (
306	22	78.6	245	2	B60944	ubiquinol-cytochro	379	22	78.6	345	2	JC5363	adenosine kinase (
307	22	78.6	247	2	D84448	probable ankryrin [	380	22	78.6	346	2	C70546	probable gale2 pro
308	22	78.6	248	2	D86012	probable membrane	381	22	78.6	349	2	S45411	methionyl aminopap
309	22	78.6	248	2	D91166	probable membrane	382	22	78.6	349	2	H85985	hypothetical prote
310	22	78.6	250	2	C60944	ubiquinol-cytochro	383	22	78.6	349	2	E91140	hypothetical prote
311	22	78.6	252	2	AB3429	O-antigen export s	384	22	78.6	351	2	JC1175	hypothetical 38.5K
312	22	78.6	253	2	F83134	probable short-cha	385	22	78.6	354	2	D83980	hypothetical prote
313	22	78.6	255	2	A60944	ubiquinol-cytochro	386	22	78.6	358	2	D84096	hypothetical prote
314	22	78.6	255	2	AF1258	hypothetical prote	387	22	78.6	361	2	JC7368	adenosine kinase (
315	22	78.6	255	2	AB1621	hypothetical prote	388	22	78.6	361	2	JC5362	adenosine kinase (
316	22	78.6	255	2	T43741	conserved hypothet	389	22	78.6	362	1	C70646	probable pflA prot
317	22	78.6	259	2	F64575	hypothetical prote	390	22	78.6	362	2	JC5364	adenosine kinase (
318	22	78.6	261	1	S00812	glucose 1-dehydrog	391	22	78.6	363	1	CBUTB	ubiquinol-cytochro
319	22	78.6	261	2	A33528	glucose 1-dehydrog	392	22	78.6	367	2	AC0907	conserved hypothet
320	22	78.6	261	2	B97589	1-2,3-butanediol d	393	22	78.6	371	1	H22848	ubiquinol-cytochro
321	22	78.6	261	2	AG2810	short chain dehydr	394	22	78.6	375	2	F65113	hypothetical 43.3K

395	22	78.6	376	2	D40511	hypothetical prote	468	22	78.6	651	2	E86242	hypothetical prote
396	22	78.6	378	2	A56653	probable UNPase -	469	22	78.6	651	2	T05869	hypothetical prote
397	22	78.6	378	2	B64553	dihydroorotase - H	470	22	78.6	656	2	A41870	dnaA protein - Str
398	22	78.6	378	2	E71356	dihydroorotase - H	471	22	78.6	662	2	T17211	hypothetical prote
399	22	78.6	379	1	B28940	cytochrome d ubiqu	472	22	78.6	688	2	D84248	hypothetical prote
400	22	78.6	379	2	A99725	cytochrome d ubiqu	473	22	78.6	689	2	G84447	hypothetical prote
401	22	78.6	379	2	B85576	cytochrome d ubiqu	474	22	78.6	690	2	T27508	hypothetical prote
402	22	78.6	388	2	D22740	hypothetical prote	475	22	78.6	693	1	E64139	DNA helicase recG
403	22	78.6	390	2	A11130	hypothetical prote	476	22	78.6	698	2	F83096	probable two-compo
404	22	78.6	391	2	A11701	hypothetical prote	477	22	78.6	700	2	T13577	hypothetical prote
405	22	78.6	398	2	D82142	hypothetical prote	478	22	78.6	713	2	I65253	disintegrin-like t
406	22	78.6	406	2	A10292	probable selenocys	479	22	78.6	716	1	A40332	macrophage-stimula
407	22	78.6	407	2	G84635	probable protein k	480	22	78.6	716	1	JC5061	macrophage-stimula
408	22	78.6	410	2	H81918	probable sodium-tr	481	22	78.6	726	2	T51519	cyclic nucleotide-
409	22	78.6	411	2	C64052	NADH2 dehydrogenas	482	22	78.6	732	2	I52361	testicular metallo
410	22	78.6	415	2	T38324	probable trna meth	483	22	78.6	754	2	T50803	hypothetical prote
411	22	78.6	421	2	H89916	diaminopimelate de	484	22	78.6	758	2	D87369	beta-D-glucosidase
412	22	78.6	423	2	AH0334	probable long-chain	485	22	78.6	759	2	AC0368	probable autotrans
413	22	78.6	425	2	A90038	hypothetical prote	486	22	78.6	762	2	E64597	DNA mismatch repai
414	22	78.6	431	2	A72037	tolB protein, prob	487	22	78.6	774	2	S55113	hypothetical prote
415	22	78.6	431	2	D86588	macromolecule tran	488	22	78.6	791	2	D81310	endopeptidase La (
416	22	78.6	434	2	D81743	virulence Appase,	489	22	78.6	794	2	G81177	phosphoenolpyruvat
417	22	78.6	434	2	D71480	probable flagellum	490	22	78.6	794	2	G81927	probable pyruvate,
418	22	78.6	443	2	T31441	probable glutamyl-	491	22	78.6	800	2	D86712	glycogen phosphory
419	22	78.6	453	2	B83242	hypothetical prote	492	22	78.6	822	2	G84552	probable retroelem
420	22	78.6	455	2	AE0181	hypothetical prote	493	22	78.6	835	2	C97322	probable alpha-ara
421	22	78.6	459	2	T19347	hypothetical prote	494	22	78.6	857	2	B69798	hypothetical prote
422	22	78.6	461	2	A96003	probable glycosyl	495	22	78.6	860	2	C82750	mannosyltransferas
423	22	78.6	462	2	B75306	probable cycloprop	496	22	78.6	872	2	H75564	probable Arp-depen
424	22	78.6	464	2	G71825	hypothetical prote	497	22	78.6	883	2	T07651	potassium channel
425	22	78.6	464	2	S71104	protein kinase JNK	498	22	78.6	920	2	T26650	hypothetical prote
426	22	78.6	466	2	B64207	heterocyst maturat	499	22	78.6	935	2	E96806	hypothetical prote
427	22	78.6	467	2	F83009	probable amino aci	500	22	78.6	983	2	T19874	hypothetical prote
428	22	78.6	471	1	PAECA	alkaline phosphata	501	22	78.6	1006	2	AD2195	hypothetical prote
429	22	78.6	471	2	I79528	alkaline phosphata	502	22	78.6	1009	2	T48727	retinoblastoma bin
430	22	78.6	473	2	D83246	probable two-compo	503	22	78.6	1020	1	QRFUH	neurofilament trip
431	22	78.6	474	2	H88473	protein C05D10.2 [	504	22	78.6	1023	2	B38932	phospholipase C (E
432	22	78.6	475	2	S55389	glutamate decarbox	505	22	78.6	1026	1	A40315	maternal effect pr
433	22	78.6	478	2	C97708	cell cycle protein	506	22	78.6	1052	2	JC7578	endo-1,4-beta-xyla
434	22	78.6	482	2	S56945	protein YJui62c -	507	22	78.6	1052	2	H33909	cell wall-associat
435	22	78.6	487	2	G75592	succinate-semialde	508	22	78.6	1060	2	S63993	acrosomal protein
436	22	78.6	488	2	E82161	hypothetical prote	509	22	78.6	1087	1	QFM5H	neurofilament trip
437	22	78.6	490	2	D90727	hypothetical prote	510	22	78.6	1091	2	F83928	hypothetical prote
438	22	78.6	494	2	A96683	alkaline phosphata	511	22	78.6	1145	2	T13810	DNA-directed DNA p
439	22	78.6	494	2	E85533	alkaline phosphata	512	22	78.6	1145	2	T13808	DNA-directed DNA p
440	22	78.6	508	2	E85578	hypothetical prote	513	22	78.6	1145	2	B75625	hypothetical prote
441	22	78.6	508	1	JC5713	25-hydroxyvitamin	514	22	78.6	1159	2	B95370	probable adenylate
442	22	78.6	514	2	B64055	periplasmic oligop	515	22	78.6	1161	2	H95903	probable chemotaxi
443	22	78.6	519	2	B87557	major facilitator	516	22	78.6	1176	1	A48047	phospholipase C (E
444	22	78.6	529	2	AC2619	virulence factor M	517	22	78.6	1205	2	T18517	procollagen N-endo
445	22	78.6	532	2	T18571	probable cycloprop	518	22	78.6	1224	2	T35770	hypothetical prote
446	22	78.6	534	2	H69056	O-sialoglycoprotei	519	22	78.6	1250	2	A39578	SSB1 protein - yea
447	22	78.6	536	2	H83776	oligopeptide ABC t	520	22	78.6	1253	2	T14349	Shyc protein - mou
448	22	78.6	536	2	F89996	hypothetical prote	521	22	78.6	1337	2	B64993	hypothetical prote
449	22	78.6	539	2	S67049	probable membrane	522	22	78.6	1442	2	S72441	protein-tyrosine-p
450	22	78.6	546	2	S48086	t-complex-type mol	523	22	78.6	1462	2	T50338	probable guanine-p
451	22	78.6	548	2	A70980	probable acd5 pro	524	22	78.6	1534	2	A85862	hypothetical prote
452	22	78.6	557	2	C97401	virulence factor m	525	22	78.6	1534	2	G31017	probable membrane
453	22	78.6	561	2	T06538	probable H+-transp	526	22	78.6	1616	2	S62504	conserved hypothet
454	22	78.6	575	2	B83586	probable permease	527	22	78.6	1647	2	T41267	hypothetical prote
455	22	78.6	576	2	S59829	hypothetical prote	528	22	78.6	1726	2	T30810	chromatin structur
456	22	78.6	581	2	B81909	exodeoxyribonuclea	529	22	78.6	1784	2	T43167	sodium channel pro
457	22	78.6	585	2	A83020	probable carbanoyl	530	22	78.6	2004	2	D88948	protein ZK1005.1 [
458	22	78.6	590	2	A26638	homeotic protein D	531	22	78.6	2326	2	T29140	hypothetical prote
459	22	78.6	601	2	B81723	conserved hypothet	532	22	78.6	2610	2	T20968	hypothetical prote
460	22	78.6	607	2	F69769	conserved hypothet	533	22	78.6	2925	2	T00133	RNA-directed RNA p
461	22	78.6	609	2	A71461	hypothetical prote	534	22	78.6	3131	2	T39553	vacuolar protein s
462	22	78.6	621	2	T15929	hypothetical prote	535	22	78.6	3175	1	RRWVEV	genome polypeptid
463	22	78.6	631	2	T13115	protein gp29 - pha	536	21	75.0	40	2	S33410	ig heavy chain v r
464	22	78.6	636	2	T33631	hypothetical prote	537	21	75.0	56	2	T35252	small hypothetical
465	22	78.6	644	2	A43370	capsid protein - N	538	21	75.0	62	2	C70057	4-oxalocrotonate t
466	22	78.6	645	2	E89883	conserved hypothet	539	21	75.0	74	2	E42506	F-ORF-F protein -
467	22	78.6	650	2	T00617	endostyle-specific	540	21	75.0	76	2	D82445	hypothetical prote

541	21	75.0	77	2	F71642	hypothetical prote	614	21	75.0	166	2	A86185	protein T7A14.4 [i
542	21	75.0	79	2	F97856	hypothetical prote	615	21	75.0	171	2	T44569	rubrerythrin [impo
543	21	75.0	84	2	S65484	cell division cont	616	21	75.0	171	2	S55668	hypothetical prote
544	21	75.0	88	2	F97888	degenerative trans	617	21	75.0	173	2	A82537	6-O-methylguanine-
545	21	75.0	91	2	D97978	alanine dehydrogen	618	21	75.0	174	2	S16528	hypothetical prote
546	21	75.0	94	2	E75556	hypothetical prote	619	21	75.0	174	2	B69257	conserved hypothet
547	21	75.0	96	2	S32165	probable secretory	620	21	75.0	175	2	C70069	NAD(P)H oxidoreduc
548	21	75.0	99	2	S24259	Ig heavy chain V r	621	21	75.0	177	2	T04397	RlcH4 protein - ba
549	21	75.0	101	2	S26460	Ig heavy chain V r	622	21	75.0	177	2	T06170	resistance protein
550	21	75.0	105	2	S38488	Ig heavy chain - h	623	21	75.0	180	2	JC4955	kappa-casein precu
551	21	75.0	106	2	S24521	Ig heavy chain V r	624	21	75.0	180	2	S70836	type 4 fibrinogen b
552	21	75.0	107	2	S41542	membrane alanyl am	625	21	75.0	180	2	G82434	hypothetical prote
553	21	75.0	108	2	PH1010	Ig heavy chain V r	626	21	75.0	181	2	C81041	pilus assembly pro
554	21	75.0	111	1	MHMS76	Ig heavy chain V-I	627	21	75.0	182	2	D83530	cytochrome b561 PA
555	21	75.0	111	1	PL0199	anti-DNA autoantib	628	21	75.0	183	2	T28926	hypothetical prote
556	21	75.0	113	1	AVMS09	Ig heavy chain V-I	629	21	75.0	184	2	D97271	rubrerythrin [impo
557	21	75.0	113	1	AVMS07	Ig heavy chain V-I	630	21	75.0	185	2	A69937	hypothetical prote
558	21	75.0	113	1	AVMS61	Ig heavy chain V-I	631	21	75.0	185	2	S21366	actin-binding prot
559	21	75.0	113	1	AVMSAB	Ig heavy chain V-I	632	21	75.0	186	2	F86830	hypothetical prote
560	21	75.0	113	1	AVMSB7	Ig heavy chain V-I	633	21	75.0	196	2	S70957	hypothetical prote
561	21	75.0	113	1	HVMSAM	Ig heavy chain V r	634	21	75.0	197	2	A82556	c-type cytochrome
562	21	75.0	113	2	T48826	hypothetical prote	635	21	75.0	197	2	B72623	hypothetical prote
563	21	75.0	114	2	A13284	hypothetical prote	636	21	75.0	198	2	B83598	conserved hypothet
564	21	75.0	115	1	AVMS06	Ig heavy chain V-I	637	21	75.0	199	2	F82836	hypothetical prote
565	21	75.0	115	1	AVMS82	Ig heavy chain V-I	638	21	75.0	202	2	B90180	ABC transporter, A
566	21	75.0	115	2	A25803	Ig heavy chain V r	639	21	75.0	202	2	T15874	hypothetical prote
567	21	75.0	115	2	S38714	Ig heavy chain V r	640	21	75.0	205	2	AC0970	probable membrane
568	21	75.0	115	2	D95035	hypothetical prote	641	21	75.0	206	2	T38251	hypothetical prote
569	21	75.0	115	2	A97911	transposase [impor	642	21	75.0	206	2	B28439	maturase-related h
570	21	75.0	115	2	B97962	transposase [impor	643	21	75.0	207	2	T20296	hypothetical prote
571	21	75.0	115	2	F97873	transposase [impor	644	21	75.0	208	1	R38T8	ribosomal protein
572	21	75.0	115	2	B98100	transposase [impor	645	21	75.0	208	2	S25022	ribosomal protein
573	21	75.0	117	2	F75288	hypothetical prote	646	21	75.0	208	2	T16343	hypothetical prote
574	21	75.0	117	2	AH0380	hypothetical prote	647	21	75.0	208	2	S42110	ribosomal protein
575	21	75.0	120	2	T1816	hypothetical prote	648	21	75.0	210	2	H87158	probable integral
576	21	75.0	120	2	G86402	hypothetical prote	649	21	75.0	210	2	H70718	hypothetical prote
577	21	75.0	121	2	F97650	hypothetical prote	650	21	75.0	212	2	F83917	hypothetical prote
578	21	75.0	122	2	F98001	transposase [impor	651	21	75.0	213	2	E85066	hypothetical prote
579	21	75.0	124	2	T15965	hypothetical prote	652	21	75.0	215	2	B86340	protein F2D10.26 l
580	21	75.0	126	2	C72603	hypothetical prote	653	21	75.0	216	2	T14844	cytochrome-c oxida
581	21	75.0	127	2	A58933	ribosomal protein	654	21	75.0	216	2	H71354	probable ribosomal
582	21	75.0	127	2	A64927	hypothetical prote	655	21	75.0	216	2	H83710	hypothetical prote
583	21	75.0	127	2	D90528	hypothetical prote	656	21	75.0	218	2	T30415	host range factor
584	21	75.0	127	2	H85776	hypothetical prote	657	21	75.0	219	2	AD1167	probable transcrip
585	21	75.0	127	2	E82950	hypothetical prote	658	21	75.0	219	2	AF1525	probable transcrip
586	21	75.0	128	2	F72661	hypothetical prote	659	21	75.0	221	1	QXAS4M	NADH2 dehydrogenas
587	21	75.0	132	1	MTON1K	melanin-concentrat	660	21	75.0	221	2	S09803	hypothetical prote
588	21	75.0	132	2	A10543	probable secreted	661	21	75.0	222	2	S26252	anther-specific pr
589	21	75.0	133	2	S57492	cytochrome-c oxida	662	21	75.0	224	2	S54218	flag protein - Yer
590	21	75.0	133	2	S57491	cytochrome-c oxida	663	21	75.0	228	1	A42929	CD9 antigen - Yee
591	21	75.0	133	2	S57493	cytochrome-c oxida	664	21	75.0	228	1	T46859	lexA repressor pro
592	21	75.0	134	2	G43868	lactate dehydrogen	665	21	75.0	228	2	T47332	hypothetical prote
593	21	75.0	135	2	I37778	Ig variable region	666	21	75.0	230	2	AE3344	integral membrane
594	21	75.0	136	2	T21590	hypothetical prote	667	21	75.0	235	2	AE3344	protein disulfide-
595	21	75.0	137	2	A69404	mutator protein Mu	668	21	75.0	236	1	E65073	protein disulfide-
596	21	75.0	137	2	T19548	hypothetical prote	669	21	75.0	236	2	E91099	protein disulfide
597	21	75.0	138	2	A90413	conserved hypothet	670	21	75.0	237	2	S27031	cytochrome-c oxida
598	21	75.0	138	2	A95133	IS630-Spn1, transp	671	21	75.0	237	2	AI0871	thiol, disulfide in
599	21	75.0	141	2	H75629	ribonucleotide red	672	21	75.0	238	2	A41568	prolactin-like pro
600	21	75.0	141	2	T25072	hypothetical prote	673	21	75.0	238	2	G82501	conserved hypothet
601	21	75.0	142	2	A07057	hypothetical prote	674	21	75.0	239	2	AE0883	probable hydrolase
602	21	75.0	148	1	MZEC6	16K mobilization p	675	21	75.0	240	2	AC2748	lexA repressor [im
603	21	75.0	149	2	S13551	stem-specific prot	676	21	75.0	240	2	B97529	lexA repressor [im
604	21	75.0	151	2	G82297	conserved hypothet	677	21	75.0	240	2	B33357	repressor LexA (BC
605	21	75.0	152	2	S72685	hypothetical prote	678	21	75.0	243	2	AP1611	3-ketoacyl-acyl ca
606	21	75.0	153	2	AB2711	30S ribosomal prot	679	21	75.0	244	2	B84957	30S ribosomal prot
607	21	75.0	157	2	F83709	hypothetical prote	680	21	75.0	245	2	T12334	L-saccharate proxi
608	21	75.0	158	2	T22829	hypothetical prote	681	21	75.0	245	2	T20171	hypothetical prote
609	21	75.0	160	2	JC5730	tumor-associated m	682	21	75.0	247	2	S75548	hypothetical prote
610	21	75.0	161	1	S43893	H+-exporting ATPas	683	21	75.0	249	2	G96952	glycerophosphoryl
611	21	75.0	162	2	C96707	hypothetical prote	684	21	75.0	249	2	B70440	conserved hypothet
612	21	75.0	163	2	A70847	hypothetical prote	685	21	75.0	249	2	T21920	hypothetical prote
613	21	75.0	166	2	C87004	conserved hypothet	686	21	75.0	249	2	F71085	hypothetical prote

687	21	75.0	250	2	C75101	transcription regu	760	21	75.0	313	2	AC1101	L-lactate dehydrog
688	21	75.0	251	2	D69848	3-oxoacyl- acyl-ca	761	21	75.0	313	2	AC1463	L-lactate dehydrog
689	21	75.0	252	2	F75067	hypothetical prote	762	21	75.0	315	2	T21141	hypothetical prote
690	21	75.0	253	2	H69263	transcription regu	763	21	75.0	316	2	E70033	transcription regu
691	21	75.0	254	2	S48497	oxidoreductase hom	764	21	75.0	317	2	T48062	hypothetical prote
692	21	75.0	255	1	E64588	glutamate racemase	765	21	75.0	317	2	T22017	hypothetical prote
693	21	75.0	255	2	AG3097	hypothetical prote	766	21	75.0	319	2	S36863	L-lactate dehydrog
694	21	75.0	255	2	B98189	hypothetical prote	767	21	75.0	319	2	B82335	hypothetical prote
695	21	75.0	259	2	A48518	probable ABC-type	768	21	75.0	320	1	DAAL2E	catechol 2,3-dioxy
696	21	75.0	260	2	A43821	homeotic protein H	769	21	75.0	321	2	S59388	probable membrane
697	21	75.0	263	2	A82069	hypothetical prote	770	21	75.0	322	2	C82293	riboflavin kinase/
698	21	75.0	264	2	T07867	MADS box protein A	771	21	75.0	322	2	D71686	hypothetical prote
699	21	75.0	266	2	G64696	tRNA delta(2)-isop	772	21	75.0	322	2	T36941	probable transcrip
700	21	75.0	267	2	D81669	tRNA pseudouridine	773	21	75.0	325	2	AC1333	conjugated bile ac
701	21	75.0	268	2	S57542	hypothetical prote	774	21	75.0	325	2	F96588	hypothetical prote
702	21	75.0	272	2	T15889	hypothetical prote	775	21	75.0	326	2	G82055	probable asparagin
703	21	75.0	277	2	AG1983	hypothetical prote	776	21	75.0	326	2	A37751	hypothetical prote
704	21	75.0	277	2	F71822	tRNA delta(2)-isop	777	21	75.0	327	2	T06602	hypothetical prote
705	21	75.0	278	2	B71730	cytochrome-c oxida	778	21	75.0	327	2	H83659	serine/threonine-p
706	21	75.0	278	2	E64937	hypothetical prote	779	21	75.0	328	2	AF0170	tetraacyldisacchar
707	21	75.0	279	2	T09620	probable lectin 2	780	21	75.0	329	2	AG0519	probable aldo/keto
708	21	75.0	279	2	G64934	hypothetical prote	781	21	75.0	329	2	H83609	sulfate transport
709	21	75.0	279	2	E85784	hypothetical prote	782	21	75.0	330	2	T27086	hypothetical prote
710	21	75.0	279	2	A90936	hypothetical prote	783	21	75.0	330	2	C90749	probable enzyme li
711	21	75.0	279	2	T02495	hypothetical prote	784	21	75.0	330	2	G85599	probable enzyme yb
712	21	75.0	280	2	AC2164	glycosyltransferas	785	21	75.0	330	2	E64826	ybX protein - Esc
713	21	75.0	280	2	G82510	hypothetical prote	786	21	75.0	332	2	D90405	geranylgeranyl hyd
714	21	75.0	282	2	T25071	hypothetical prote	787	21	75.0	333	1	SKPSXX	secretion protein
715	21	75.0	283	2	F91285	hypothetical prote	788	21	75.0	333	2	T05121	hypothetical prote
716	21	75.0	284	2	F81729	signal recognition	789	21	75.0	334	2	T11633	hypothetical prote
717	21	75.0	286	2	A25242	tropomyosin, exon	790	21	75.0	334	2	AH0300	conserved hypothet
718	21	75.0	286	2	T21545	hypothetical prote	791	21	75.0	335	1	S35126	antranilate phosp
719	21	75.0	287	2	T40403	hypothetical prote	792	21	75.0	335	2	AE0165	conserved hypothet
720	21	75.0	288	2	B89930	hypothetical prote	793	21	75.0	335	2	T23544	hypothetical prote
721	21	75.0	289	2	D69152	hypothetical prote	794	21	75.0	336	2	C82146	probable tetraacyl
722	21	75.0	290	2	D81938	probable RNA polym	795	21	75.0	338	2	AF1822	ATP-binding protei
723	21	75.0	290	2	G81166	RNA polymerase sig	796	21	75.0	338	2	T22016	hypothetical prote
724	21	75.0	290	2	H82870	fructose-bisphosph	797	21	75.0	339	2	AG1278	antranilate phosp
725	21	75.0	290	2	T17597	transcription init	798	21	75.0	339	2	AG1641	antranilate phosp
726	21	75.0	291	1	F36516	3-methylcatechol 2	799	21	75.0	340	2	F75007	suas related prote
727	21	75.0	292	2	F83827	hypothetical prote	800	21	75.0	341	2	D37082	branched-chain-am
728	21	75.0	294	2	B86127	hypothetical prote	801	21	75.0	341	2	G90112	N-myristoyltransfe
729	21	75.0	295	2	AD3577	sugar transport sy	802	21	75.0	341	2	AD2987	hypothetical prote
730	21	75.0	295	2	T06355	hypothetical prote	803	21	75.0	341	2	D98296	sulfate ABC transp
731	21	75.0	296	2	AE3263	short-chain dehydr	804	21	75.0	342	2	D86808	hypothetical prote
732	21	75.0	296	2	T27269	hypothetical prote	805	21	75.0	344	1	GVCS7	sulfate transport
733	21	75.0	299	1	WMNV35	early 35K protein,	806	21	75.0	344	2	C81933	probable tetraacyl
734	21	75.0	299	2	B83888	transcription regu	807	21	75.0	344	2	F81170	tetraacyldisacchar
735	21	75.0	299	2	S61248	hypothetical prote	808	21	75.0	345	2	T25408	hypothetical prote
736	21	75.0	299	2	A45720	p35 orf135 - Bomby	809	21	75.0	347	2	A95403	probable sulfate/t
737	21	75.0	299	2	C75384	conserved hypothet	810	21	75.0	348	2	H82694	sulfate ABC transp
738	21	75.0	299	2	F95294	probable LysR-type	811	21	75.0	349	2	T25348	hypothetical prote
739	21	75.0	303	2	T15694	hypothetical prote	812	21	75.0	351	2	E71372	probable translati
740	21	75.0	305	2	G83628	probable transcrip	813	21	75.0	351	2	AG2677	hypothetical prote
741	21	75.0	305	2	S64612	hypothetical prote	814	21	75.0	351	2	E97459	sulfate ABC transp
742	21	75.0	306	2	AE1911	hypothetical prote	815	21	75.0	352	2	D84329	heme biosynthesis
743	21	75.0	306	2	A85015	hypothetical prote	816	21	75.0	354	2	G96795	hypothetical prote
744	21	75.0	306	2	D82126	histone deacetylase	817	21	75.0	354	2	S71925	angel protein - fr
745	21	75.0	308	2	H97729	cytochrome-c oxida	818	21	75.0	355	2	D71429	hypothetical prote
746	21	75.0	308	2	B64202	prolyl aminopeptid	819	21	75.0	355	2	S76743	hypothetical trans
747	21	75.0	309	2	E70319	phosphoribosylanth	820	21	75.0	356	2	T46182	hypothetical prote
748	21	75.0	309	2	AC1351	ferrochelatase hom	821	21	75.0	356	2	AC2319	hypothetical prote
749	21	75.0	309	2	AF1721	probable transcrip	822	21	75.0	357	2	S49443	cinnamyl-alcohol d
750	21	75.0	309	2	G83547	hypothetical prote	823	21	75.0	357	2	S49444	cinnamyl-alcohol d
751	21	75.0	309	2	B38545	proteinase specifi	824	21	75.0	357	2	F81875	sulfate ABC transp
752	21	75.0	310	2	B84044	1-phosphofructokin	825	21	75.0	357	2	B81147	sulfate ABC transp
753	21	75.0	310	2	AD1707	1-phosphofructokin	826	21	75.0	357	2	B84041	flagellar biosynth
754	21	75.0	310	2	AG1336	methionyl-tRNA for	827	21	75.0	358	2	S35250	flagellar biosynth
755	21	75.0	311	2	B95202	methionyl-tRNA for	828	21	75.0	358	2	F71897	flagellar biosynth
756	21	75.0	311	2	B98069	D-serine deaminase	829	21	75.0	358	2	B64616	probable cathepsin
757	21	75.0	312	2	A65010	methionyl-tRNA for	830	21	75.0	359	2	T02011	flagellar biosynth
758	21	75.0	312	2	AG1302	methionyl-tRNA for	831	21	75.0	360	2	D69623	conserved hypothet
759	21	75.0	312	2	AG1674	methionyl-tRNA for	832	21	75.0	361	2	A95089	

833	21	75.0	361	2	D97956	conserved hypother	906	21	75.0	409	2	T43703	respiratory protei
834	21	75.0	361	2	A87383	flagellar biosynth	907	21	75.0	409	2	JC7293	activated T cell c
835	21	75.0	362	2	C81453	flagellar biosynth	908	21	75.0	412	2	G64685	hypothetical prote
836	21	75.0	363	2	AD0366	sulfate transport	909	21	75.0	412	2	B71831	hypothetical prote
837	21	75.0	363	2	G83954	flagella-associate	910	21	75.0	413	2	A11349	3-oxoacyl-acyl-car
838	21	75.0	364	2	AF0811	sulfate transport	911	21	75.0	413	2	AD1720	conserved hypother
839	21	75.0	365	1	QRECSA	sulfate transport	912	21	75.0	413	2	C95886	probable beta-keto
840	21	75.0	365	2	H85884	hypothetical prote	913	21	75.0	414	1	JN0826	multidrug resistan
841	21	75.0	365	2	E91040	hypothetical prote	914	21	75.0	414	2	D82487	6-phospho-beta-glu
842	21	75.0	367	2	T23387	hypothetical prote	915	21	75.0	415	2	E72273	hypothetical prote
843	21	75.0	367	2	E95930	probable sulfate u	916	21	75.0	416	2	T45669	DNA-directed RNA p
844	21	75.0	370	1	BVLVMX	mbpX protein - liv	917	21	75.0	417	2	S00933	hypothetical prote
845	21	75.0	370	2	AC1272	alanine dehydrogen	918	21	75.0	418	2	G70558	creatine kinase IE
846	21	75.0	370	2	AE1634	alanine dehydrogen	919	21	75.0	418	2	A35756	competence-damage
847	21	75.0	370	2	A83621	probable ATP-bind	920	21	75.0	420	2	A83948	middle T antigen -
848	21	75.0	371	2	AD1206	pyruvate dehydroge	921	21	75.0	421	1	TVVPMP	middle T antigen -
849	21	75.0	371	2	AC1563	pyruvate dehydroge	922	21	75.0	421	2	S22561	levanucrase - Zym
850	21	75.0	371	2	D84047	alanine dehydrogen	923	21	75.0	423	2	S33771	levanucrase (EC 2
851	21	75.0	371	2	T16391	hypothetical prote	924	21	75.0	423	2	JC2519	probable beta-keto
852	21	75.0	371	2	F90581	hypothetical prote	925	21	75.0	424	1	S11975	3-phosphoshikimate
853	21	75.0	371	2	A55302	probable transcrip	926	21	75.0	424	2	S76359	hypothetical prote
854	21	75.0	371	2	S55588	D-nopaline dehydro	927	21	75.0	425	1	S48469	probable membrane
855	21	75.0	371	2	H97452	cytochrome c oxida	928	21	75.0	426	2	A82660	glucose/galactose
856	21	75.0	372	2	A89955	alanine dehydrogen	929	21	75.0	426	2	A10287	conserved hypother
857	21	75.0	372	2	A34261	alanine dehydrogen	930	21	75.0	426	2	T47931	hypothetical prote
858	21	75.0	372	2	B34261	alanine dehydrogen	931	21	75.0	427	2	S13266	hypothetical prote
859	21	75.0	377	2	S21302	succinate dehydrog	932	21	75.0	427	2	AF0839	4-aminobutyrate tr
860	21	75.0	377	2	JB0388	lipopolysaccharide	933	21	75.0	429	2	AC0801	probable amino aci
861	21	75.0	377	2	G69937	alanine dehydrogen	934	21	75.0	429	2	T29711	hypothetical prote
862	21	75.0	378	2	A49337	alanine dehydrogen	935	21	75.0	429	2	AG3150	hypothetical prote
863	21	75.0	378	2	A83941	alanine dehydrogen	936	21	75.0	433	2	S55968	probable membrane
864	21	75.0	380	2	A73500	aminopeptidase - D	937	21	75.0	434	2	D85531	probable permease,
865	21	75.0	380	2	T04284	hypothetical prote	938	21	75.0	435	2	H90680	probable regulator
866	21	75.0	381	1	KIRBCM	creatine kinase IS	939	21	75.0	435	2	H30522	gtp-binding protei
867	21	75.0	381	2	JC4647	kw8 protein - rat	940	21	75.0	436	2	F82422	anaerobic glycerol
868	21	75.0	381	2	G02668	neurogenic basic-h	941	21	75.0	436	2	D70693	probable ugpB lipo
869	21	75.0	382	2	S63638	ubiquinol-cytochro	942	21	75.0	436	2	T36320	hypothetical prote
870	21	75.0	383	2	S54213	flagellar biosynth	943	21	75.0	436	2	AG0272	probable integral
871	21	75.0	383	2	JC4688	neuro D-related fa	944	21	75.0	436	2	T44439	indole-3-acetyl-L-
872	21	75.0	386	2	AD0218	flagellar biosynth	945	21	75.0	436	2	G85749	aminoacylase (EC 3
873	21	75.0	387	2	T38046	hypothetical prote	946	21	75.0	437	2	S73284	hypothetical prote
874	21	75.0	387	2	A82750	hypothetical prote	947	21	75.0	437	2	AF0667	probable phosphor
875	21	75.0	387	2	D97531	hypothetical prote	948	21	75.0	437	2	S56529	middle T antigen -
876	21	75.0	389	2	B64935	hypothetical prote	949	21	75.0	440	1	TVVPMP	UDP-N-acetylmuram
877	21	75.0	389	2	D90936	hypothetical prote	950	21	75.0	440	2	F86667	probable amidohydr
878	21	75.0	389	2	H85784	hypothetical prote	951	21	75.0	441	2	B64883	probable aminohydr
879	21	75.0	391	2	G71285	conserved hypother	952	21	75.0	441	2	B08869	hypothetical prote
880	21	75.0	392	2	E91290	probable transport	953	21	75.0	441	2	T20840	probable oxidoredu
881	21	75.0	392	2	H86131	hypothetical prote	954	21	75.0	442	2	E82980	hypothetical prote
882	21	75.0	393	2	C71254	conserved hypother	955	21	75.0	445	1	F71033	epithelial zinc-fi
883	21	75.0	394	2	H75372	hypothetical prote	956	21	75.0	445	2	T49556	cytochrome-c oxida
884	21	75.0	394	2	C83840	hypothetical prote	957	21	75.0	446	2	T10103	interphase linporce
885	21	75.0	396	2	S22909	interleukin-3 rece	958	21	75.0	446	2	AC0617	alpha-1,3-mannosyl
886	21	75.0	398	2	D85080	KNAT1 homeobox-lik	959	21	75.0	447	1	A42500	transcription fact
887	21	75.0	399	2	D95279	probable alcohol l	960	21	75.0	448	1	B42022	hypothetical prote
888	21	75.0	400	1	B65075	probable monooxyge	961	21	75.0	448	2	G89933	hypothetical prote
889	21	75.0	400	2	AF0873	probable monooxyge	962	21	75.0	448	2	A27631	cellulase (EC 3.2.
890	21	75.0	400	2	E85946	hypothetical prote	963	21	75.0	448	2	T31586	hypothetical prote
891	21	75.0	400	2	A98101	hypothetical prote	964	21	75.0	451	2	S56717	calcium-dependent
892	21	75.0	400	2	T35334	probable membrane	965	21	75.0	451	2	G70241	hypothetical prote
893	21	75.0	402	2	A82394	hypothetical prote	966	21	75.0	452	2	T41108	transcription init
894	21	75.0	403	2	C75405	streptomycin biosy	967	21	75.0	453	2	AD1556	conserved hypother
895	21	75.0	404	2	AH3481	sulfate transport	968	21	75.0	453	2	AF1198	hypothetical prote
896	21	75.0	406	2	G96497	hypothetical prote	969	21	75.0	454	2	D87424	hypothetical prote
897	21	75.0	407	2	D87010	probable membrane	970	21	75.0	454	2	B82412	probable magnesium
898	21	75.0	407	2	E70595	hypothetical prote	971	21	75.0	455	1	JC4338	cryptophan dimethy
899	21	75.0	407	2	D82377	Para family protei	972	21	75.0	457	2	H86193	hypothetical prote
900	21	75.0	409	1	G69000	polyubiquitin cofac	973	21	75.0	458	2	S57914	probable sakacin P
901	21	75.0	409	2	S00662	cyclin - sea urchi	974	21	75.0	459	2	B89927	hypothetical prote
902	21	75.0	409	2	AE0320	probable N-acetylgl	975	21	75.0	461	1	GORTT1	tumor necrosis fac
903	21	75.0	409	2	T31910	hypothetical prote	976	21	75.0	467	2	AG0771	probable two-compo
904	21	75.0	409	2	A43256	mobilization prote	977	21	75.0	468	2	G98041	H+-transporting tw
905	21	75.0	409	2	T50311	oxalasp2 protein [i	978	21	75.0	468	2	F95175	ATP synthase F1, b

979 21 75.0 468 2 B72351 clostripain-relate  
980 21 75.0 468 2 A97626 hypothetical prote  
981 21 75.0 469 2 T51882 hypothetical prote  
982 21 75.0 470 2 E75085 transmembrane tran  
983 21 75.0 470 2 H70795 hypothetical prote  
984 21 75.0 471 2 T43803 cytochrome-c oxida  
985 21 75.0 471 2 T43827 cytochrome-c oxida  
986 21 75.0 471 2 T43830 cytochrome-c oxida  
987 21 75.0 472 1 PWSBM H+-transporting tw  
988 21 75.0 472 2 I57445 alkaline phosphata  
989 21 75.0 472 2 T05852 hypothetical prote  
990 21 75.0 473 2 AI1390 H+-transporting At  
991 21 75.0 473 2 I40368 H+-transporting tw  
992 21 75.0 474 2 A71533 probable phospholi  
993 21 75.0 474 2 H81688 phospholipase D fa  
994 21 75.0 480 2 AE2971 amidohydrolase [im  
995 21 75.0 481 2 AC0280 alkaline phosphata  
996 21 75.0 481 2 D64883 Aminobenzoyl-gluta  
997 21 75.0 481 2 A90869 hypothetical prote  
998 21 75.0 481 2 H85749 hypothetical prote  
999 21 75.0 482 2 T43885 cytochrome-c oxida  
1000 21 75.0 482 2 T43872 cytochrome-c oxida

## ALIGNMENTS

RESULT 1  
E89999  
holo-ACP synthase [imported] - Staphylococcus aureus (strain N315)  
C:Species: Staphylococcus aureus  
C:Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 09-Jul-2004  
C:Accession: E89999  
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguchi, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.  
Lancet 357, 1225-1240, 2001  
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.  
A:Reference number: A89758; MUID:21311952; PMID:11418146  
A:Accession: E89999  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-119 <KUR>  
A:Cross-references: UNIPROT:Q99S14; UNIPARC:UPI0000125346; GB:BA000018; PID:gl3701866; E89999  
A:Experimental source: strain N315  
C:Genetics:  
A:Gene: dpj  
C:Superfamily: holo-ACP synthase

Query Match 100.0%; Score 28; DB 2; Length 119;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5  
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DB 106 HYAMS 110

RESULT 2  
A71051  
hypothetical protein PH1104 - Pyrococcus horikoshii  
C:Species: Pyrococcus horikoshii  
C:Date: 14-Aug-1998 #sequence\_revision 14-Aug-1998 #text\_change 12-Jul-2004  
C:Accession: A71051  
R:Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekin, M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi, DNA Res. 5, 55-76, 1998  
A:Title: Complete sequence and gene organization of the genome of a hyper-thermophilic archaeon.  
A:Reference number: A71000; MUID:98344137; PMID:9679194  
A:Accession: A71051  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-143 <KAW>

A:Cross-references: UNIPROT:O58831; UNIPARC:UPI0000062FB4; GB:AP000005; NID:G3236132; PI  
A:Experimental source: strain OT3  
A:Note: This accession replaces an interim accession for a sequence replaced by GenBank  
C:Genetics:  
A:Gene: PH1104

Query Match 100.0%; Score 28; DB 2; Length 143;  
Best Local Similarity 100.0%; Pred. No. 17;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5  
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DB 128 HYAMS 132

RESULT 3  
AD3630  
pseudocourin [imported] - Brucella melitensis (strain 16M)  
C:Species: Brucella melitensis  
C:Date: 01-Feb-2002 #sequence\_revision 01-Feb-2002 #text\_change 05-Oct-2004  
C:Accession: AD3630  
R:DeIvecchio, V.G.; Kapatal, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, .; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess, Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002  
A:Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis  
A:Reference number: AD3252; PMID:11756688  
A:Accession: AD3630  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-146 <KUR>  
A:Cross-references: UNIPROT:Q8YBD5; UNIPARC:UPI00000586B2; GB:AE008918; PIDN:AAL54207.1;  
A:Experimental source: strain 16M  
C:Genetics:  
A:Gene: BME110965  
A:Map position: II  
C:Superfamily: plastocyanin/Azurin

Query Match 100.0%; Score 28; DB 2; Length 146;  
Best Local Similarity 100.0%; Pred. No. 18;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5  
|||||  
DB 104 HYAMS 108

RESULT 4  
T37007  
probable aminoglycoside nucleotidyltransferase - Streptomyces coelicolor  
C:Species: Streptomyces coelicolor  
C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004  
C:Accession: T37007  
R:Oliver, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrrell, B.G.; Rajandream, M.A. submitted to the EMBL Data Library, August 1999  
A:Reference number: Z21618  
A:Accession: T37007  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-185 <OLI>  
A:Cross-references: UNIPROT:Q9RI70; UNIPARC:UPI00000DB34B; EMBL:AL109949; PIDN:CA852921.1;  
A:Experimental source: strain A3(2)  
C:Genetics:  
A:Gene: SCOEDB:SCJ11.36C

Query Match 100.0%; Score 28; DB 2; Length 185;  
Best Local Similarity 100.0%; Pred. No. 23;  
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QY 1 HYAMS 5  
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DB 14 HYAMS 18



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RESULT 5
E75216
hypothetical protein PAB2437 - Pyrococcus abyssi (strain Orsay)
C:Species: Pyrococcus abyssi
C>Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C:Accession: E75216
R:anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A:Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stru
A:Reference number: A75001
A:Accession: E75216
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-280 <KAW>
A:Cross-references: UNIPROT:Q9V218; UNIPARC:UPI000003471E; GB:AJ248283; GB:AL096836; NID
A:Experimental source: strain Orsay
C:Genetics:
A:Gene: PAB2437
C:Superfamily: Aeropyrum pernix hypothetical protein APE2212

Query Match 100.0%; Score 28; DB 2; Length 280;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HVAMS 5
Db 126 HYAMS 130

RESULT 6
C71453
hypothetical protein PH0282 - Pyrococcus horikoshii
C:Species: Pyrococcus horikoshii
C>Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 05-Oct-2004
C:Accession: C71453
R:Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Seki
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi
DNA Res. 5, 55-76, 1998
A>Title: Complete sequence and gene organization of the genome of a hyper-thermophilic e
A:Reference number: A71000; MUID:98344137; PMID:9679194
A:Accession: C71453
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-280 <KAW>
A:Cross-references: UNIPROT:O58020; UNIPARC:UPI0000062D82; GB:AP0000001; NID:g33236128; PI
A:Experimental source: strain OT3
A>Note: this accession replaces an interim accession for a sequence replaced by GenBank
C:Genetics:
A:Gene: PH0282
C:Superfamily: Aeropyrum pernix hypothetical protein APE2212

Query Match 100.0%; Score 28; DB 2; Length 280;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HVAMS 5
Db 126 HYAMS 130

RESULT 7
C72320
conserved hypothetical protein - Thermotoga maritima (strain MSB8)
C:Species: Thermotoga maritima
C>Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
A:Accession: C72320
R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
C.M.
Nature 399, 323-329, 1999
A>Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
A:Reference number: A72200; MUID:99287316; PMID:10360571
A:Accession: C72320

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A>Status: preliminary
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A:Residues: 1-284 <ARN>
A:Cross-references: UNIPROT:Q9X018; UNIPARC:UPI00000C135E; GB:AE001755; GB:AE000512; NI
A:Experimental source: strain MSB8
C:Genetics:
A:Gene: TM0916
C:Superfamily: Aeropyrum pernix hypothetical protein APE2212

Query Match 100.0%; Score 28; DB 2; Length 284;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HVAMS 5
Db 125 HYAMS 129

RESULT 8
A64317
hypothetical protein M30137 - Methanococcus jannaschii
C:Species: Methanococcus jannaschii
C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C:Accession: A64317
R:Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake,
Reich, C.I.; Overbeek, R.; Kirkness, E.P.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.;
erson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese,
A>Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
A:Reference number: A64300; MUID:96337999; PMID:8688087
A:Accession: A64317
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-286 <BUL>
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C:Genetics:
A:Map position: REV134976-134116
C:Superfamily: Aeropyrum pernix hypothetical protein APE2212

Query Match 100.0%; Score 28; DB 2; Length 286;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HVAMS 5
Db 131 HYAMS 135

RESULT 9
A70371
conserved hypothetical protein aq_814 - Aquifex aeolicus
C:Species: Aquifex aeolicus
C>Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
C:Accession: A70371
R:Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; O
V.
Nature 392, 353-358, 1998
A>Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A:Reference number: A70300; MUID:98196566; PMID:9537320
A:Accession: A70371
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-288 <AQF>
A:Cross-references: UNIPROT:O66996; UNIPARC:UPI000005645F; GB:AE000708; NID:g2983356; PI
A:Experimental source: strain VFS
C:Genetics:
A:Gene: aq_814
C:Superfamily: Aeropyrum pernix hypothetical protein APE2212

Query Match 100.0%; Score 28; DB 2; Length 288;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```



QY	1 HVAMS 5 	C:Accession: H72529 R:Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takahawa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K DNA Res. 6, 83-101, 1999 A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyrum
Db	128 HVAMS 132	A:Reference number: A72450; MUID:99310339; PMID:10382966 A:Accession: H72529 A:Status: preliminary A:Molecule type: DNA A:Residues: 1-295 <KAW> A:Cross-references: UNIPROT:Q9Y9S6; UNIPARC:UPI000005E264; DDBJ:AP000063; NID:q5105654; A:Experimental source: strain K1 C:Genetics: A:Gene: APE2212 C:Superfamily: Aeropyrum pernix hypothetical protein APE2212
RESULT 10		
H69356		Query Match 100.0%; Score 28; DB 2; Length 295; Best Local Similarity 100.0%; Pred. No. 37; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
C:Species: Archaeoglobus fulgidus		
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004		
C:Accession: H69356		
R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson		
.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.		
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.		
Nature 350, 364-370, 1997		
A:Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.		
Smith, H.O.; Woese, C.R.; Venter, J.C.		
A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaea		
A:Reference number: A69250; MUID:98049343; PMID:9389475		
A:Accession: H69356		
A:Status: preliminary; nucleic acid sequence not shown; translation not shown		
A:Molecule type: DNA		
A:Residues: 1-291 <KLE>		
A:Cross-references: UNIPROT:Q29403; UNIPARC:UPI0000056F58; GB:AE001045; GB:AE000782; NID		
C:Superfamily: Aeropyrum pernix hypothetical protein APE2212		
Query Match 100.0%; Score 28; DB 2; Length 291;		
Best Local Similarity 100.0%; Pred. No. 37;		
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 HVAMS 5 	
Db	134 HVAMS 138	
RESULT 11		
F64486		hypothetical protein MJ1495 - Methanococcus jannaschii
C:Species: Methanococcus jannaschii		
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004		
C:Accession: F64486		
R:Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake,		
; Reich, C.I.; Overbeek, R.; Kirkness, B.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.		
ron, J.D.; Sadov, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.		
Science 273, 1058-1073, 1996		
A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C		
A:Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii		
A:Reference number: A64300; MUID:96337999; PMID:8688087		
A:Accession: F64486		
A:Status: preliminary; nucleic acid sequence not shown; translation not shown		
A:Molecule type: DNA		
A:Residues: 1-292 <BUL>		
A:Cross-references: UNIPROT:Q58890; UNIPARC:UPI000013AB7D; GB:U67590; GB:L77117; NID:g15		
C:Genetics:		
A:Map position: FOR1468504-1469382		
A:Start codon: GTG		
C:Superfamily: Aeropyrum pernix hypothetical protein APE2212		
Query Match 100.0%; Score 28; DB 2; Length 292;		
Best Local Similarity 100.0%; Pred. No. 37;		
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 HVAMS 5 	
Db	135 HVAMS 139	
RESULT 12		
H72529		hypothetical protein APE2212 - Aeropyrum pernix (strain K1)
C:Species: Aeropyrum pernix		
C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004		

, C:Date: 20-Aug-1999 #sequence\_revision 20-Aug-1999 #text\_change 09-Jul-2004

A:Cross-references: UNIPROT:Q82871; UNIPARC:UPI00000D4259; GB:AE004806; GB:AE004091; NID:

A;Experimental source: strain PA01

C;Genetics:

A;Gene: nhap; PA3887

C;Superfamily: hypothetical protein MJ0057

Query Match 100.0%; Score 28; DB 2; Length 424;

Best Local Similarity 100.0%; Pred. No. 54;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5

|||||

Db 272 HYAMS 276

RESULT 15

S62963

hypothetical protein YNL041c - yeast (Saccharomyces cerevisiae)

N;Alternate names: hypothetical protein N2675

C;Species: Saccharomyces cerevisiae

C;Date: 27-Apr-1996 #sequence\_revision 03-May-1996 #text\_change 09-Jul-2004

C;Accession: S62963

R;Duesterhoeft, A.; Floeth, M.; Fritz, C.; Heuss-Neitzel, D.; Hilbert, H.; Moestl, D.

submitted to the Protein Sequence Database, April 1996

A;Reference number: S62944

A;Accession: S62963

A;Molecule type: DNA

A;Residues: 1-839 <DUE>

A;Cross-references: UNIPROT:P53959; UNIPARC:UPI0000127B13; EMBL:Z71317; NID:g1301893; PI

A;Experimental source: strain S288C

C;Genetics:

A;Gene: SGD:TF12; MIPS:YNL041C

A;Cross-references: SGD:S0004986

A;Map position: 14L

Query Match

Best Local Similarity 100.0%; Score 28; DB 2; Length 839;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5

|||||

Db 78 HYAMS 82

RESULT 16

F82072

holo- (acyl-carrier-protein) synthase VC2457 [imported] - Vibrio cholerae (strain N16961

C;Species: Vibrio cholerae

C;Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 09-Jul-2004

C;Accession: F82072

R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;

chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, H.

l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.

Nature 406, 477-483, 2000

A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.

A;Reference number: A82035; MUID:20406833; PMID:10952301

A;Accession: F82072

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-126 <HEI>

A;Cross-references: UNIPROT:Q9KPB6; UNIPARC:UPI000012534D; GB:AE004316; GB:AE003852; NID

A;Experimental source: serogroup O1; strain N16961; biotype El Tor

C;Genetics:

A;Gene: VC2457

A;Map position: 1

C;Superfamily: holo-ACP synthase

Query Match

Best Local Similarity 89.3%; Score 25; DB 2; Length 126;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5

|||||

Db 115 HYAMA 119

RESULT 17

JL0090

ependymin precursor - goldfish

N;Alternate names: preproependymin

C;Species: Carassius auratus (Goldfish)

C;Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 09-Jul-2004

C;Accession: JL0090; E80306; I51378

R;Koenigsforfer, A.; Sterrer, S.; Eckerskorn, C.; Lottspeich, F.; Schmidt, R.; Hoffmann, J.

A;Title: Molecular characterization of an ependymin precursor from goldfish brain.

A;Reference number: JL0090; MUID:89068004; PMID:2908890

A;Accession: JL0090

A;Molecule type: mRNA

A;Residues: 1-216 <KOE>

A;Cross-references: UNIPROT:P13506; UNIPARC:UPI00001711C3; GB:X14134; NID:g62577; PIDN:

A;Experimental source: brain

A;Accession: PS0306

A;Molecule type: protein

A;Residues: 22-27, X'29-45;110-123 <K02>

A;Cross-references: UNIPARC:UPI00001788FD; UNIPARC:UPI00001788FE

A;Note: ependymins beta and gamma have the same amino-terminal sequence

A;Note: 24-Asp, 29-Glu, and 34-Ile were also found

R;Adams, D.S.; Shashoua, V.E.

Gene 141, 237-241, 1994

A;Title: Cloning and sequencing the genes encoding goldfish and carp ependymin.

A;Reference number: I51377; MUID:94215910; PMID:8163195

A;Accession: I51378

A;Status: preliminary; translated from GB/EMBL/DBDJ

A;Molecule type: DNA

A;Residues: 2-216 <ADA>

A;Cross-references: UNIPARC:UPI000012A091; EMBL:U00433; NID:g997657; PIDN:AAA19566.1; P

C;Comment: Ependymins beta and gamma are nervous-system specific glycoproteins localize

C;Comment: These proteins are reported as brain proteins that display enhanced turnover

C;Comment: Ependymin forms dimer with intermolecular disulfide bonds.

C;Genetics:

A;Gene: epn

A;introns: 29/1; 40/3; 85/3; 148/1; 176/2

C;Superfamily: ependymin

C;Keywords: calcium binding; cell adhesion; glycoprotein

F;1-21/Domain: signal sequence #status predicted <SIG>

F;22-216/Product: ependymin #status experimental <MAT>

F;72,95/Binding site: carbohydrate (Asn) (covalent) #status predicted

F;181,185,186/Binding site: calcium (Glu, Glu, Asp, Asp) #status predicted

F;202,203,206,207/Binding site: calcium (Glu, Glu, Asp, Asp) #status predicted

Query Match

Best Local Similarity 89.3%; Score 25; DB 2; Length 216;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5

|||||

Db 149 HYSMS 153

RESULT 18

S69682

hypothetical protein YDR399w - yeast (Saccharomyces cerevisiae)

C;Species: Saccharomyces cerevisiae

C;Date: 22-Aug-1996 #sequence\_revision 06-Sep-1996 #text\_change 09-Jul-2004

C;Accession: S69682

R;Dietrich, F.S.

submitted to the EMBL Data Library, July 1995

A;Description: The sequence of S. cerevisiae cosmids 9481, 9509, 9926, 9461, and lambda

A;Reference number: S69685

A;Accession: S69682

A;Molecule type: DNA

A;Residues: 1-221 <DIS>

A;Cross-references: UNIPROT:Q04178; UNIPARC:UPI000004F900; EMBL:U32274; NID:g927313; PID

C;Genetics:

A;Gene: SGD:HPT1; MIPS:YDR399w

A;Cross-references: SGD:S0002807

A:Map position: 4R  
C:Superfamily: Schizosaccharomyces pombe hypothetical protein SPAC23C11.13c

Query Match 89.3%; Score 25; DB 2; Length 221;  
Best Local Similarity 80.0%; Pred. No. 1.4e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5  
|||:|  
Db 120 HYALS 124

RESULT 19  
C82182  
hypothetical protein VC1577 [imported] - Vibrio cholerae (strain N16961 serogroup O1)  
C:Species: Vibrio cholerae  
C>Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 05-Oct-2004  
C:Accession: C82182  
R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;  
chardon, D.; Emolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, B.  
l. R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.  
Nature 406, 477-483, 2000  
A:Title: DNA sequence of both chromosomes of the cholera pathogen Vibrio cholerae.  
A:Reference number: A82035; MUID:20406833; PMID:10952301  
A:Accession: C82182  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-273 <HEI>  
A:Cross-references: UNIPROT:Q9K0R9; UNIPARC:UPI00000C3029; GB:AE004235; GB:AE003852; NID  
A:Experimental source: serogroup O1; strain N16961; biotype El Tor  
C:Genetics:  
A:Gene: VC1577  
A:Map position: 1  
C:Superfamily: lipid A biosynthesis (KDO)2-(lauroyl)-lipid IVA acyltransferase

Query Match 89.3%; Score 25; DB 2; Length 273;  
Best Local Similarity 80.0%; Pred. No. 1.7e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5  
|||:|  
Db 215 HYALS 219

RESULT 20  
T15932  
hypothetical protein EGAP2.1 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C>Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 09-Jul-2004  
C:Accession: T15932  
R:Bentley, D.  
submitted to the EMBL Data Library, December 1995  
A:Description: The sequence of C. elegans cosmid EGAP2.  
A:Reference number: Z18430  
A:Accession: T15932  
A:Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 1-283 <BEN>  
A:Cross-references: UNIPROT:Q19075; UNIPARC:UPI000016409F; EMBL:U42842; NID:g1125787; PI  
C:Genetics:  
A:Gene: CESP:EGAP2.1  
A:Introns: 97/2; 164/1; 214/2

Query Match 89.3%; Score 25; DB 2; Length 283;  
Best Local Similarity 80.0%; Pred. No. 1.8e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5  
|||:|  
Db 16 HYALS 20

RESULT 21

T22325  
hypothetical protein F46G10.3 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C:Accession: T22325  
R:Coles, L.  
submitted to the EMBL Data Library, July 1995  
A:Reference number: Z19548  
A:Accession: T22325  
A:Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 1-287 <WIL>  
A:Cross-references: UNIPROT:Q20481; UNIPARC:UPI00000785B0; EMBL:Z50177; PIDN:CAA90547.1;  
A:Experimental source: clone F46G10  
C:Genetics:  
A:Gene: CESP:F46G10.3  
A:Map position: X  
A:Introns: 43/1; 77/2; 124/2; 151/2; 189/3; 250/3  
C:Superfamily: conserved hypothetical protein bil20

Query Match 89.3%; Score 25; DB 2; Length 287;  
Best Local Similarity 80.0%; Pred. No. 1.8e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5  
|||:|  
Db 98 HYALS 102

RESULT 22  
T22324  
hypothetical protein F46G10.7 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C:Accession: T22324  
R:Coles, L.  
submitted to the EMBL Data Library, July 1995  
A:Reference number: Z19548  
A:Accession: T22324  
A:Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 1-287 <WIL>  
A:Cross-references: UNIPROT:Q20480; UNIPARC:UPI000007C46B; EMBL:Z50177; PIDN:CAA90546.1;  
A:Experimental source: clone F46G10  
C:Genetics:  
A:Gene: CESP:F46G10.7  
A:Map position: X  
A:Introns: 43/1; 77/2; 124/2; 151/2; 189/3; 250/3  
C:Superfamily: conserved hypothetical protein bil20

Query Match 89.3%; Score 25; DB 2; Length 287;  
Best Local Similarity 80.0%; Pred. No. 1.8e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5  
|||:|  
Db 98 HYALS 102

RESULT 23  
T43158  
probable GTP-binding protein beta chain - fission yeast (Schizosaccharomyces pombe) (fra  
C:Species: Schizosaccharomyces pombe  
C>Date: 11-Jan-2000 #sequence\_revision 11-Jan-2000 #text\_change 05-Oct-2004  
C:Accession: T43158  
R:Yoshioka, S.; Kato, K.; Nakai, K.; Okayama, H.; Nojima, H.  
DNA Res. 4, 363-369, 1997  
A:Title: Identification of open reading frames in Schizosaccharomyces pombe cDNAs.  
A:Reference number: Z17323; MUID:98162722; PMID:9501991  
A:Accession: T43158  
A:Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: mRNA  
A:Residues: 1-310 <YOS>

A:Cross-references: UNIPARC:UPI000016911E; EMBL:D89247; NID:gl749701; PIDN:BAAL13908.1; H  
A:Experimental source: strain PR745  
C:Keywords: GTP binding

Query Match 89.3%; Score 25; DB 2; Length 310;  
Best Local Similarity 80.0%; Pred. No. 2e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5  
|||:|  
DB 72 HYALS 76

RESULT 24  
H89884  
hypothetical protein SA0987 [imported] - Staphylococcus aureus (strain N315)  
C:Species: Staphylococcus aureus  
C:Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 09-Jul-2004  
C:Accession: H89884  
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc  
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;  
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayaishi, H.; Hiramatsu, K.  
Lancet 357, 1225-1240, 2001  
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.  
A:Reference number: A89758; MUID:21311952; PMID:11418146  
A:Accession: H89884  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-312 <KUR>  
A:Cross-references: UNIPROT:Q99UW5; UNIPARC:UPI00000CAA86; GB:BA000018; PID:gl3700940; H  
A:Experimental source: strain N315  
C:Genetics:  
A:Gene: SA0987

Query Match 89.3%; Score 25; DB 2; Length 312;  
Best Local Similarity 80.0%; Pred. No. 2e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5  
|||:|  
DB 216 HYALS 220

RESULT 25  
T23675  
hypothetical protein M02B1.4 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C:Accession: T23675  
R:Lightning, J.  
submitted to the EMBL Data Library, October 1996  
A:Reference number: Z19780  
A:Accession: T23675  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-313 <WIL>  
A:Cross-references: UNIPROT:Q93893; UNIPARC:UPI0000079493; EMBL:Z81102; PIDN:CAB03203.1;  
A:Experimental source: clone M02B1  
C:Genetics:  
A:Gene: CESP:M02B1.4  
A:Map position: 4  
A:Introns: 31/2; 195/3; 228/1

Query Match 89.3%; Score 25; DB 2; Length 313;  
Best Local Similarity 80.0%; Pred. No. 2e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5  
|||:|  
DB 173 HYALS 177

RESULT 26

T43299  
probable GTP-binding regulatory protein beta chain - fission yeast (Schizosaccharomyces  
N:Alternate names: guanine nucleotide regulatory protein  
C:Species: Schizosaccharomyces pombe  
C:Date: 11-Jan-2000 #sequence\_revision 11-Jan-2000 #text\_change 05-Oct-2004  
C:Accession: T43299; T39022  
R:Park, S.K.; Yoo, H.S.  
unpublished results 1994, cited by EMBL  
A:Reference number: Z22403  
A:Accession: T43299  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-314 <PAR>  
A:Cross-references: UNIPROT:Q10281; UNIPARC:UPI000012B255; EMBL:L37895; PIDN:AAAS6865.1  
A:Experimental source: isolate ED616  
R:Gentles, S.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, V.  
submitted to the EMBL Data Library, August 1995  
A:Reference number: Z21815  
A:Accession: T39022  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-314 <GEN>  
A:Cross-references: UNIPARC:UPI000012B255; EMBL:Z98531; PIDN:CAB11079.1; GSPDB:GN000066;  
A:Experimental source: strain 972h-; cosmid c6B12  
C:Genetics:  
A:Gene: SPAC6B12.15  
A:Map position: 1  
A:Introns: 42/3; 175/3  
C:Keywords: GTP binding

Query Match 89.3%; Score 25; DB 2; Length 314;  
Best Local Similarity 80.0%; Pred. No. 2e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5  
|||:|  
DB 76 HYALS 80

RESULT 27  
T50249  
conserved hypothetical protein SPAC694.04c [imported] - fission yeast (Schizosaccharomyces  
C:Species: Schizosaccharomyces pombe  
C:Date: 09-Jun-2000 #sequence\_revision 09-Jun-2000 #text\_change 09-Jul-2004  
C:Accession: T50249  
R:Aert, R.; Voickaert, G.; McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.  
submitted to the EMBL Data Library, February 2000  
A:Reference number: Z25049  
A:Accession: T50249  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-324 <AER>  
A:Cross-references: UNIPROT:Q9PT76; UNIPARC:UPI000013B48B; EMBL:AL138666; PIDN:CAB71842  
A:Experimental source: strain 972h(-); cosmid c694  
C:Genetics:  
A:Gene: SPAC:SPAC694.04c  
A:Map position: 1  
A:Introns: 19/1  
C:Superfamily: Arabidopsis thaliana hypothetical protein F3K15.180

Query Match 89.3%; Score 25; DB 2; Length 324;  
Best Local Similarity 80.0%; Pred. No. 2.1e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5  
|||:|  
DB 193 HYALS 197

RESULT 28  
A86202  
hypothetical protein [imported] - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004  
 C;Accession: A86202  
 R;Theologos, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, C.; Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Hansen, N.F.; Hughes, B.; Huizar, L.  
 Nature 408, 816-820, 2000  
 A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
 A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
 A;Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.  
 A;Reference number: A86141; MUID:21016719; PMID:11130712  
 C;Accession: A86202  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-335 <STO>  
 A;Cross-references: UNIPROT:Q9M9Y1; UNIPARC:UPI00000AA7A9; GB:AE005172; NID:g7523706; PID:11130712  
 C;Genetics:  
 A;Map position: 1

Query Match 89.3%; Score 25; DB 2; Length 325;  
 Best Local Similarity 80.0%; Pred. No. 2.1e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5  
 DB 16 HYALS 20

RESULT 29  
 S15238  
 O-antigen acetylase (EC 2.3.1.-) - enterobacterial phase SF6  
 N;Alternate names: acetyl transferase  
 C;Species: enterobacterial phase SF6  
 C;Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 15-Oct-1999  
 C;Accession: S15238; J50588; S24220  
 R;Verma, N.K.; Brandt, J.M.; Verma, D.J.; Lindberg, A.A.  
 Mol. Microbiol. 5, 71-75, 1991  
 A;Title: Molecular characterization of the O-acetyl transferase gene of converting bacterium  
 A;Reference number: S15238; MUID:91194560; PMID:2014005  
 A;Accession: S15238  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-333 <VER>  
 A;Cross-references: UNIPARC:UPI0000130B51; EMBL:X56800; NID:g14867; PIDN:CAA40136.1; PID:11130712  
 R;Clark, C.A.; Beltrame, J.; Manning, P.A.  
 Gene 107, 43-52, 1991  
 A;Title: The oac gene encoding a lipopolysaccharide O-antigen acetylase maps adjacent to the oac gene  
 A;Reference number: J50587; MUID:92077435; PMID:1720755  
 A;Accession: J50588  
 A;Molecule type: DNA  
 A;Residues: 1-157, 'L', 159-168, 'Q', 170-333 <CLA>  
 A;Cross-references: UNIPARC:UPI000016D841; EMBL:X59553; NID:g15748; PID:g15750  
 C;Comment: This enzyme catalyzes O-acetylation of the O-antigen of the lipopolysaccharide  
 C;Genetics:  
 A;Gene: oac  
 C;Keywords: acyltransferase

Query Match 89.3%; Score 25; DB 2; Length 333;  
 Best Local Similarity 80.0%; Pred. No. 2.1e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5  
 DB 23 HYALS 27

RESULT 30  
 E75301  
 conserved hypothetical protein - *Deinococcus radiodurans* (strain R1)  
 C;Species: *Deinococcus radiodurans*  
 C;Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 03-Nov-2003

C;Accession: E75301  
 R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodsodn, R.J.; M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Smith, H.O.; Venter, J.C.; Fraser, C.M.  
 Science 286, 1571-1577, 1999  
 A;Title: Genome sequence of the radioresistant bacterium *Deinococcus radiodurans* R1.  
 A;Reference number: A75250; MUID:20036896; PMID:10567266  
 C;Accession: E75301  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-338 <WHI>  
 A;Cross-references: UNIPARC:UPI00000C1A9F; GB:AE002054; GB:AE000513; NID:g6460010; PIDN:10567266  
 A;Experimental source: strain R1  
 C;Genetics:  
 A;Gene: DR2213  
 A;Map position: 1  
 C;Superfamily: uncharacterized conserved protein

Query Match 89.3%; Score 25; DB 2; Length 338;  
 Best Local Similarity 80.0%; Pred. No. 2.2e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5  
 DB 260 HYALS 264

RESULT 31  
 BVECHD  
 molybdenum transport protein modC - *Escherichia coli* (strain K-12)  
 N;Alternate names: molybdenum transport protein chld  
 C;Species: *Escherichia coli*  
 C;Date: 31-Dec-1990 #sequence\_revision 31-Oct-1997 #text\_change 09-Jul-2004  
 C;Accession: E64812; B26871  
 R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; A.; Rose, D.J.; Mau, B.; Shao, Y.  
 Science 277, 1453-1462, 1997  
 A;Title: The complete genome sequence of *Escherichia coli* K-12.  
 A;Reference number: A64720; MUID:97426617; PMID:9278503  
 A;Accession: E64812  
 A;Status: nucleic acid sequence not shown; translation not shown  
 A;Molecule type: DNA  
 A;Residues: 1-352 <BLAT>  
 A;Cross-references: UNIPROT:P09833; UNIPARC:UPI000016804B; GB:AE000179; GB:U00096; NID:g14867  
 A;Experimental source: strain K-12, substrain MG1655  
 R;Johann, S.; Hinton, S.M.  
 J. Bacteriol. 169, 1911-1916, 1987  
 A;Title: Cloning and nucleotide sequence of the chld locus.  
 A;Reference number: A26871; MUID:87194564; PMID:3553151  
 A;Accession: B26871  
 A;Molecule type: DNA  
 A;Residues: 1-243, 'SALRDDR', 251-268, 'LRYYPHSGPCFSWFVNRSKP', 269, 'FVT', 273, 'AGKSC' <JOH>  
 A;Cross-references: UNIPARC:UPI000016E85C; EMBL:X07875  
 A;Experimental source: strain K12  
 A;Note: the authors translated the codon GAA for residue 74 as Gly  
 C;Genetics:  
 A;Gene: modC; chld  
 A;Map position: 17 min  
 C;Function:  
 A;Description: nucleotide-binding protein component of the binding protein-dependent transport system  
 C;Superfamily: molybdenum transport protein modC; ATP-binding cassette homology  
 C;Keywords: ATP; inner membrane; molybdenum transport; nucleotide binding; P-loop  
 F;14-205/Domain: ATP-binding cassette homology <ABC>  
 F;31-38/Region: nucleotide-binding motif A (P-loop)  
 F;149-153/Region: nucleotide-binding motif B

Query Match 89.3%; Score 25; DB 1; Length 352;  
 Best Local Similarity 80.0%; Pred. No. 2.3e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5  
 DB 245 HYAMT 249

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RESULT 32
AE0595
molybdenum transport ATP-binding protein ModC STY0816 [imported] - Salmonella enterica
C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C;Accession: AE0595
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Accession: AE0595
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-352 <PAR>
A;Cross-references: UNIPARC:UPI000005A0FF; GB:AL513382; PIDN:CAD05231.1; PID:g16502001;
C;Genetics:
C;Superfamily: molybdenum transport protein modC; ATP-binding cassette homology
A;Gene: STY0816
Query Match 89.3%; Score 25; DB 2; Length 352;
Best Local Similarity 80.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 HYAMS 5
Db 245 HYAMT 249
|||||
RESULT 33
B85579
ATP-binding component of molybdate transport [imported] - Escherichia coli (strain O157:
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Accession: B85579
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: B85579
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-352 <STO>
A;Cross-references: UNIPROT:Q8X4V7; UNIPARC:UPI00000D0D69; GB:AE005174; NID:g12513697; E
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: modC
C;Superfamily: molybdenum transport protein modC; ATP-binding cassette homology
Query Match 89.3%; Score 25; DB 2; Length 352;
Best Local Similarity 80.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 HYAMS 5
Db 245 HYAMT 249
|||||
RESULT 34
A90728
ATP-binding component of molybdate transport [imported] - Escherichia coli (strain O157:
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C;Accession: A90728
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Iehii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shingagawa, H.
DNA Res. 8, 11-22, 2001

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A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gen
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: A90728
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-352 <HAY>
A;Cross-references: UNIPROT:Q8X4V7; UNIPARC:UPI00000D0D69; GB:BA000007; PIDN:BA834216.1;
A;Experimental source: strain O157:H7, substrain RMD 0509952
C;Genetics:
A;Gene: Ecs0793
C;Superfamily: molybdenum transport protein modC; ATP-binding cassette homology
Query Match 89.3%; Score 25; DB 2; Length 352;
Best Local Similarity 80.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 HYAMS 5
Db 245 HYAMT 249
|||||
RESULT 35
AB0844
membrane-bound lytic transglycosylase B precursor (EC 3.2.1.-) [imported] - Salmonella
C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 05-Oct-2004
C;Accession: AB0844
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Accession: AB0844
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-359 <PAR>
A;Cross-references: UNIPARC:UPI000005A336; GB:AL513382; PIDN:CAD05937.1; PID:g16503908;
C;Genetics:
A;Gene: STY2952
C;Superfamily: membrane-bound lytic murein transglycosylase B precursor
C;Keywords: glycosidase; hydrolase
Query Match 89.3%; Score 25; DB 2; Length 359;
Best Local Similarity 80.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 HYAMS 5
Db 341 HYAMA 345
|||||
RESULT 36
B85918
membrane-bound lytic murein transglycosylase B [imported] - Escherichia coli (strain O15
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 05-Oct-2004
C;Accession: B85918
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: B85918
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-361 <STO>
A;Cross-references: UNIPROT:Q8X872; UNIPARC:UPI00000D0D98A; GB:AE005174; NID:g12517141; I
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: mtb

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C:Superfamily: membrane-bound lytic murein transglycosylase B precursor

Query Match 89.3%; Score 25; DB 2; Length 361;  
Best Local Similarity 80.0%; Pred. No. 2.3e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5  
|||||  
Db 343 HYAMA 347

## RESULT 37

A65050 membrane-bound lytic transglycosylase (EC 3.2.1.1.-) B precursor - Escherichia coli (strain

N:Alternate names: mltB protein  
C:Species: Escherichia coli

C:Date: 12-Sep-1997 #sequence\_revision 17-Sep-1997 #text\_change 05-Oct-2004

C:Accession: A65050; S65868; S77642

R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co

A.; Rose, D.J.; Mau, B.; Shao, Y.

Science 277, 1453-1462, 1997

A:Title: The complete genome sequence of Escherichia coli K-12.

A:Reference number: A64720; MUID:97426617; PMID:9278503

A:Accession: A65050

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-361 <BLAT>

A:Cross-references: UNIPROT:P41052; UNIPARC:UPI000012F231; GB:AE0000354; GB:U000996; NID:9

A:Experimental source: strain K-12, substrain MGL655

R:DiJkstra, A.J.; Hermann, F.; Keck, W.

FEBS Lett. 366, 115-118, 1995

A:Title: Cloning and controlled overexpression of the gene encoding the 35 kDa soluble l

A:Reference number: S65868; MUID:95309413; PMID:7789526

A:Accession: S65868

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 1-34, 'A', '36-361 <DIJ>

A:Cross-references: UNIPARC:UPI0000179B3D

R:Ehlert, K.; Hoeltje, J.V.; Templin, M.F.

Mol. Microbiol. 16, 761-768, 1995

A:Title: Cloning and expression of a murein hydrolase lipoprotein from Escherichia coli.

A:Reference number: S77642; MUID:96065704; PMID:7476170

A:Accession: S77642

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-361 <EHL>

A:Cross-references: UNIPARC:UPI000012F231; EMBL:U18785; NID:G642537; PIDN:AA60060.1; PI

A>Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1994

C:Genetics:

A:Gene: mltB

C:Superfamily: membrane-bound lytic murein transglycosylase B precursor

C:Keywords: glycosidase; hydrolase

F:1-18/Domain: signal sequence #status predicted <SIG>

F:19-361/Product: mltB protein #status predicted <MAT>

Query Match 89.3%; Score 25; DB 2; Length 361;

Best Local Similarity 80.0%; Pred. No. 2.3e+02;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5

|||||

Db 343 HYAMA 347

## RESULT 38

F91073 membrane-bound lytic murein transglycosylase B ECs3558 [imported] - Escherichia coli (eb

C:Species: Escherichia coli

C:Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 05-Oct-2004

C:Accession: F91073

R:Hayaashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.

Gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.

DNA Res. 8, 11-22, 2001

A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and geno

A:Reference number: A99629; MUID:21156231; PMID:11258796

A:Accession: F91073

A:Status: Preliminary

A:Molecule type: DNA

A:Residues: 1-361 <HAY>

A:Cross-references: UNIPROT:Q8X872; UNIPARC:UPI00000D098A; GB:BA000007; PIDN:BA836981.1;

A:Experimental source: strain O157:H7, substrain RIMD 0509952

C:Genetics:

A:Gene: ECs3558

C:Superfamily: membrane-bound lytic murein transglycosylase B precursor

Query Match 89.3%; Score 25; DB 2; Length 361;

Best Local Similarity 80.0%; Pred. No. 2.3e+02;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5

|||||

Db 343 HYAMA 347

## RESULT 39

H83088 membrane-bound lytic transglycosylase PA4444 [imported] - Pseudomonas aeruginosa (strain

C:Species: Pseudomonas aeruginosa

C:Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 05-Oct-2004

C:Accession: H83088

R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Br

adman, S.; Yuan, Y.; Brody, L.L.; Coulter, K.R.; Kas, A.; Larbig, K.; Lim,

; Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho

A:Reference number: A82950; MUID:20437337; PMID:10984043

A:Accession: H83088

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-367 <STO>

A:Cross-references: UNIPROT:Q9HVX3; UNIPARC:UPI00000C5D14; GB:AE004859; GB:AE004091; NID

A:Experimental source: strain PA01

C:Genetics:

A:Gene: mltB1; PA4444

C:Superfamily: membrane-bound lytic murein transglycosylase B precursor

Query Match 89.3%; Score 25; DB 2; Length 367;

Best Local Similarity 80.0%; Pred. No. 2.4e+02;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5

|||||

Db 343 HYAMA 347

## RESULT 40

AB1068 probable membrane protein STY4872 [imported] - Salmonella enterica subsp. enterica serov

C:Species: Salmonella enterica subsp. enterica serovar Typhi

A>Note: this species has also been called Salmonella typhi

C:Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 18-Nov-2002

C:Accession: AB1068

R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,

th, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,

; S.; Moule, S.; O'Gaora, P.

Nature 413, 848-852, 2001

A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;

A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov

A:Reference number: AB0502; MUID:21534947; PMID:11677608

A:Accession: AB1068

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-394 <PAR>

A:Cross-references: UNIPARC:UPI000005A98A; GB:AL513382; PIDN:CAD03361.1; PID:91650563;

C:Genetics:

A:Gene: STY4872



Query Match 89.3%; Score 25; DB 2; Length 394;  
 Best Local Similarity 80.0%; Pred. No. 2.5e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HVAMS 5  
 |||||  
 Db 163 HYALS 167

RESULT 41  
 F87356  
 hypothetical protein CC0865 [imported] - Caulobacter crescentus  
 C:Species: Caulobacter crescentus  
 C:Date: 20-Apr-2001 #sequence\_revision 20-Apr-2001 #text\_change 05-Oct-2004  
 C:Accession: F87356  
 R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.  
 B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon  
 n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.  
 Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001  
 A:Title: Complete Genome Sequence of Caulobacter crescentus.  
 A:Reference number: A87249; MUID:21173698; PMID:11259647  
 A:Accession: F87356  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-399 <STO>  
 A:Cross-references: UNIPROT:Q9A9U6; UNIPARC:UPI000000C71CA; GB:AE005673; NID:g13422124; F  
 C:Genetics:  
 A:Gene: CC0865  
 C:Superfamily: 3-oxoacyl-[acyl-carrier-protein] synthase III

Query Match 89.3%; Score 25; DB 2; Length 399;  
 Best Local Similarity 80.0%; Pred. No. 2.6e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HVAMS 5  
 |||||  
 Db 74 HYALS 78

RESULT 42  
 G85775  
 selenocysteine lyase [similarity] - Escherichia coli (strain O157:H7, substrain EDL933)  
 C:Species: Escherichia coli  
 C:Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 09-Jul-2004  
 C:Accession: G85775  
 R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew  
 Miller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,  
 Nature 409, 529-533, 2001  
 A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.  
 A:Reference number: A85480; MUID:21074935; PMID:11206551  
 A:Accession: G85775  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-406 <STO>  
 A:Cross-references: UNIPROT:Q8X602; UNIPARC:UPI000000D0C1F; GB:AE005174; NID:g12515682; F  
 A:Experimental source: strain O157:H7, substrain EDL933  
 C:Genetics:  
 A:Gene: 22708  
 C:Superfamily: nifs protein

Query Match 89.3%; Score 25; DB 2; Length 406;  
 Best Local Similarity 80.0%; Pred. No. 2.6e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HVAMS 5  
 |||||  
 Db 311 HYALS 315

RESULT 43  
 C90927  
 selenocysteine lyase [imported] - Escherichia coli (strain O157:H7, substrain RMD 05099

C:Species: Escherichia coli  
 C:Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 09-Jul-2004  
 C:Accession: C90927  
 R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.  
 gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shingawa, H.  
 DNA Res. 8, 11-22, 2001  
 A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gene  
 A:Reference number: A99629; MUID:21156231; PMID:11258796  
 A:Accession: C90927  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-406 <HAV>  
 A:Cross-references: UNIPROT:Q8X602; UNIPARC:UPI000000D0C1F; GB:BA000007; PIDN:BA835810.1,  
 A:Experimental source: strain O157:H7, substrain RMD 0509952  
 C:Genetics:  
 A:Gene: EC82387  
 C:Superfamily: nifs protein

Query Match 89.3%; Score 25; DB 2; Length 406;  
 Best Local Similarity 80.0%; Pred. No. 2.6e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HVAMS 5  
 |||||  
 Db 311 HYALS 315

RESULT 44  
 H64925  
 aminotransferase nifs homolog b1680, pyridoxal phosphate-dependent - Escherichia coli (E  
 C:Species: Escherichia coli  
 C:Date: 12-Sep-1997 #sequence\_revision 17-Sep-1997 #text\_change 09-Jul-2004  
 C:Accession: H64925  
 R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co  
 .A.; Rose, D.J.; Mau, B.; Shao, Y.  
 Science 277, 1453-1462, 1997  
 A:Title: The complete genome sequence of Escherichia coli K-12.  
 A:Reference number: A64720; MUID:97426617; PMID:9278503  
 A:Accession: H64925  
 A:Status: nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-406 <BLAT>  
 A:Cross-references: UNIPROT:P77444; UNIPARC:UPI0000000A41; GB:AE000263; GB:U00096; NID:Y  
 A:Experimental source: strain K-12, substrain MG1655  
 C:Superfamily: nifs protein  
 C:Keywords: pyridoxal phosphate

Query Match 89.3%; Score 25; DB 2; Length 406;  
 Best Local Similarity 80.0%; Pred. No. 2.6e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HVAMS 5  
 |||||  
 Db 311 HYALS 315

RESULT 45  
 B87201  
 hypothetical protein [imported] - Mycobacterium leprae  
 C:Species: Mycobacterium leprae  
 C:Date: 20-Apr-2001 #sequence\_revision 20-Apr-2001 #text\_change 09-Jul-2004  
 C:Accession: B87201  
 R:Coile, S.T.; Siglmeyer, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; H  
 R.; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd,  
 eam, M.A.; Rutherford, K.M.  
 Nature 409, 1007-1011, 2001  
 A:Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squires, R.; S  
 A:Title: Massive gene decay in the leprosy bacillus.  
 A:Reference number: A86909; MUID:21128732; PMID:11234002  
 A:Accession: B87201  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-420 <STO>



A;Cross-references: UNIPROT:Q9CB74; UNIPARC:UPI00000C6E74; GB:AL450380; NID:gl3093950; F  
 C;Genetics:  
 A;Gene: ML2334  
 C;Superfamily: cyclopropane-fatty-acyl-phospholipid synthase; MCM homology

Query Match 89.3%; Score 25; DB 2; Length 420;  
 Best Local Similarity 80.0%; Pred. No. 2.7e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5  
 |||||:  
 Db 347 HYAMT 351

RESULT 46  
 A70796  
 probable cyclopropane-fatty-acyl-phospholipid synthase (EC 2.1.1.79) RV3720 [similarity]  
 C;Species: Mycobacterium tuberculosis  
 C;Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 09-Jul-2004  
 C;Accession: A70796  
 R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.  
 ; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.  
 Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.  
 Nature 393, 537-544, 1998  
 A;Authors: Sgares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.  
 A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome  
 A;Reference number: A70500; MUID:98295987; PMID:9634230  
 A;Accession: A70796  
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A;Molecule type: DNA  
 A;Residues: 1-420 <COL>  
 A;Cross-references: UNIPROT:O69687; UNIPARC:UPI0000165379; GB:AL022121; GB:AL123456; NID  
 A;Experimental source: strain H37RV  
 C;Genetics:  
 A;Gene: RV3720

Query Match 89.3%; Score 25; DB 2; Length 420;  
 Best Local Similarity 80.0%; Pred. No. 2.7e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5  
 |||||:  
 Db 347 HYAMT 351

RESULT 47  
 B81418  
 adenylosuccinate lyase (EC 4.3.2.2) Cj0023 [imported] - Campylobacter jejuni (strain NCTC  
 C;Species: Campylobacter jejuni  
 C;Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 09-Jul-2004  
 C;Accession: B81418  
 R;Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chilling  
 C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrell  
 Nature 403, 665-668, 2000  
 A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp  
 A;Reference number: B81250; MUID:20150912; PMID:10698204  
 A;Accession: B81418  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-442 <PAR>  
 A;Cross-references: UNIPROT:Q9PJ88; UNIPARC:UPI00000C2003; GB:AL139074; GB:AL1111168; NID  
 A;Experimental source: serotype O2, strain NCTC 11168  
 C;Genetics:  
 A;Gene: purB; Cj0023  
 C;Superfamily: fumarate hydratase  
 C;Keywords: amidine-lyase; carbon-nitrogen lyase

Query Match 89.3%; Score 25; DB 2; Length 442;  
 Best Local Similarity 80.0%; Pred. No. 2.9e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5  
 |||||:  
 Db 89 HYAMT 93

RESULT 48  
 A55476  
 protein kinase (EC 2.7.1.37) gskA - slime mold (Dictyostelium discoideum)  
 N;Alternate names: glycogen synthase kinase 3  
 C;Species: Dictyostelium discoideum  
 C;Date: 10-Feb-1995 #sequence\_revision 10-Feb-1995 #text\_change 09-Jul-2004  
 C;Accession: A55476  
 R;Harwood, A.J.; Plyte, S.E.; Woodgett, J.; Strutt, H.; Kay, R.R.  
 Cell 80, 139-148, 1995  
 A;Title: Glycogen synthase kinase 3 regulates cell fate in Dictyostelium.  
 A;Reference number: A55476; MUID:95112340; PMID:7813009  
 A;Accession: A55476  
 A;Status: preliminary  
 A;Molecule type: mRNA  
 A;Residues: 1-468 <HAR>  
 A;Cross-references: UNIPROT:P51136; UNIPARC:UPI000012DDC1; GB:L34674; NID:9511848; PIDN:  
 A;Note: authors translated the codon AAT for residue 20 as Asp, and CTC for residue 414  
 C;Genetics:  
 A;Gene: gskA  
 C;Superfamily: kinase-related transforming protein; protein kinase homology  
 C;Keywords: ATP; phosphotransferase  
 F;55-115/Domain: protein kinase homology <KIN>  
 F;63-71/Region: protein kinase ATP-binding motif  
 F;86/Active site: Lys #status predicted

Query Match 89.3%; Score 25; DB 2; Length 468;  
 Best Local Similarity 80.0%; Pred. No. 3.1e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5  
 |||||:  
 Db 144 HYSMS 148

RESULT 49  
 H82756  
 conserved hypothetical protein XF0843 [imported] - Xylella fastidiosa (strain 985c)  
 C;Species: Xylella fastidiosa  
 C;Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 09-Dec-2002  
 C;Accession: H82756  
 R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen  
 Nature 406, 151-157, 2000  
 A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.  
 A;Reference number: A82515; MUID:20365717; PMID:10910347  
 A;Note: for a complete list of authors see reference number A59328 below  
 A;Accession: H82756  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-516 <SIM>  
 A;Cross-references: UNIPARC:UPI00000C253D; GB:AE003923; GB:AE003849; NID:99105736; PIDN:  
 A;Experimental source: strain 985c  
 R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A  
 Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H  
 as-Neco, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S.  
 submitted to GenBank, June 2000  
 A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm  
 J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.B.; Laigr  
 chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.P.; Marino, C.L.; Marques, M.V.; Martins, E  
 A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.  
 , F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmeri, D.A  
 Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.B.; de Sa, R.G.; Sancelli, R.V.; Sawaas  
 A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir  
 M.; Tshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z  
 A;Reference number: A59328  
 A;Contents: annotation  
 C;Genetics:  
 A;Gene: XF0843  
 C;Superfamily: uncharacterized conserved protein

Query Match 89.3%; Score 25; DB 2; Length 516;  
Best Local Similarity 80.0%; Pred. No. 3.4e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HVAMS 5  
|||:  
Db 438 HYALS 442

RESULT 50  
AC2392  
hypothetical protein alr4691 [imported] - Nostoc sp. (strain PCC 7120)  
C:Species: Nostoc sp. PCC 7120  
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120  
C:Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 09-Jul-2004  
C:Accession: AC2392  
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,  
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.  
DNA Res. 8, 205-213, 2001  
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana  
A:Reference number: AB1807; MUID:21595285; PMID:11759840  
A:Accession: AC2392  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-541 <KUR>  
A:Cross-references: UNIPROT:Q8YV79; UNIPARC:UPI000000CEBFE; GB:BA0000019; PIDN:BA076390.1;  
A:Experimental source: strain PCC 7120  
C:Genetics:  
A:Gene: alr4691

Query Match 89.3%; Score 25; DB 2; Length 541;  
Best Local Similarity 80.0%; Pred. No. 3.6e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HVAMS 5  
|||:  
Db 323 HYALS 327

Search completed: April 6, 2006, 08:58:14  
Job time : 17 secs

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GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: April 6, 2006, 08:55:21 ; Search time 33.2203 Seconds  
(without alignments)  
106.189 Million cell updates/sec

Title: US-10-089-500-3

Perfect score: 28

Sequence: 1 HYAMS 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Uniprot\_05.80:\*

1: uniprot\_sprot:\*

2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	28	100.0	95	2 Q4S1G2	TETNG
2	28	100.0	119	1 ACPS_STAAC	
3	28	100.0	119	1 ACPS_STAAM	
4	28	100.0	119	1 ACPS_STAAH	
5	28	100.0	119	1 ACPS_STAAR	
6	28	100.0	119	1 ACPS_STAAS	
7	28	100.0	119	1 ACPS_STAAU	
8	28	100.0	119	1 ACPS_STAAW	
9	28	100.0	119	2 Q4L7V6	STAHJ
10	28	100.0	138	2 Q4WBD6	ASPFU
11	28	100.0	143	2 O58831	PYRHO
12	28	100.0	146	2 Q8YBD5	BRUME
13	28	100.0	185	2 Q9R170	STRCO
14	28	100.0	274	2 Q6M194	METNP
15	28	100.0	275	2 Q5S199	THET8
16	28	100.0	275	2 Q721M1	THET2
17	28	100.0	280	2 Q5JFF4	PYRKO
18	28	100.0	280	2 Q8U454	PYRFU
19	28	100.0	280	2 Q9V218	PYRAB
20	28	100.0	280	2 Q58020	PYRHO
21	28	100.0	284	2 Q9X018	THEMA
22	28	100.0	286	1 Y137	METJA
23	28	100.0	288	2 Q66956	AQUAE
24	28	100.0	291	2 Q29403	ARCFU
25	28	100.0	291	2 Q4LSG1	9BURK
26	28	100.0	292	1 Y1495	METJA
27	28	100.0	292	2 Q4UVS4	XANCP
28	28	100.0	292	2 Q8PB83	XANCP
29	28	100.0	295	2 Q9Y866	AERPE
30	28	100.0	297	2 Q8YQJ8	ANASP
31	28	100.0	337	2 Q5NNN3	ZYMO

32	28	100.0	345	1 HEMH_FORGI	
33	28	100.0	424	2 Q82871	PSEAE
34	28	100.0	448	2 Q8A516	BACTN
35	28	100.0	453	2 Q6N245	RHOPA
36	28	100.0	456	2 Q5K2P1	PROAT
37	28	100.0	464	1 Q89UC7	BRAJA
38	28	100.0	473	1 DNAA_LEIXX	
39	28	100.0	545	2 Q5FS80	GLUOX
40	28	100.0	555	1 NUSM_CANPA	
41	28	100.0	566	2 Q5N753	ORYSA
42	28	100.0	699	2 Q4RKT5	TEFNG
43	28	100.0	839	1 COG6	YEAST
44	28	100.0	1012	2 Q6CHS4	YARLI
45	28	100.0	1268	1 SC24B	HUMAN
46	28	100.0	1675	2 Q9VLT1	DROME
47	25	89.3	19	2 Q86DB6	HALRO
48	25	89.3	56	2 Q6TFAB	AERHY
49	25	89.3	60	2 Q8GWL8	ARATH
50	25	89.3	88	2 Q4TDA6	TEFNG
51	25	89.3	98	2 Q8HM19	9TELE
52	25	89.3	106	2 Q5AC38	CANAL
53	25	89.3	107	2 Q656P6	ORYSA
54	25	89.3	116	2 Q8RBB0	THETN
55	25	89.3	119	2 Q6Q7C4	9BACT
56	25	89.3	120	2 Q711E4	LACDL
57	25	89.3	126	1 ACPS_VTBCH	
58	25	89.3	126	2 Q5C7Y4	SCHJA
59	25	89.3	133	2 Q5SMY7	ORYSA
60	25	89.3	141	2 Q4QJ62	LEIMA
61	25	89.3	147	2 Q6N4G2	RHOPA
62	25	89.3	154	2 Q7XHN0	ORYSA
63	25	89.3	160	2 Q5IZL0	9HELI
64	25	89.3	160	2 Q5IZM1	9HELI
65	25	89.3	160	2 Q5IZL9	9HELI
66	25	89.3	163	2 Q5G819	9UCUC
67	25	89.3	169	2 Q7WP98	BORBR
68	25	89.3	184	2 Q6VEY0	SULTO
69	25	89.3	189	2 Q5NFE9	FRATT
70	25	89.3	192	2 Q5QMN8	ORYSA
71	25	89.3	193	2 Q98KW6	RHILO
72	25	89.3	200	2 Q9AER3	SERMA
73	25	89.3	202	2 Q9FIJ8	ARATH
74	25	89.3	203	2 Q8FC26	ECOL6
75	25	89.3	204	2 Q9WX65	ACEXY
76	25	89.3	205	2 Q5KJ93	CRYNE
77	25	89.3	212	2 Q4Z6S9	PLABE
78	25	89.3	215	1 EPD1	CARAU
79	25	89.3	221	2 Q04178	YEAST
80	25	89.3	225	2 Q5ST48	CRYNE
81	25	89.3	229	2 Q9X738	9HELI
82	25	89.3	230	2 Q7S631	NEUCR
83	25	89.3	243	2 Q8PT40	METMA
84	25	89.3	243	2 Q9RG88	9HELI
85	25	89.3	243	2 Q9RG88	9HELI
86	25	89.3	243	2 Q9RG88	9HELI
87	25	89.3	247	2 Q8TVK3	METKA
88	25	89.3	248	2 Q4KRD8	LACJO
89	25	89.3	250	2 Q8DLDO	SYNEL
90	25	89.3	255	2 Q4WK17	ASPFU
91	25	89.3	259	2 Q6ICB4	HUMAN
92	25	89.3	259	2 Q8BUL8	MOUSE
93	25	89.3	261	2 Q5NPD9	ZYMO
94	25	89.3	262	2 Q7UGW4	RHOBA
95	25	89.3	262	2 Q7UTV9	RHOBA
96	25	89.3	265	2 Q5SP07	CRYNE
97	25	89.3	272	2 Q70SV1	BEMTA
98	25	89.3	272	2 Q82XL0	NITEU
99	25	89.3	273	2 Q9KRQ9	VTBCH
100	25	89.3	282	2 Q5GZ49	XANOR
101	25	89.3	287	2 Q7NCE7	GLOVI
102	25	89.3	283	2 Q6FCT6	ACINOBACT
103	25	89.3	284	2 Q61G31	CAEBR
104	25	89.3	285	2 Q6FDDL2	ACIAD

Q7mxp4	porphyromon
Q82871	peudomonas
Q8A516	bacteroides
Q6N245	rhodopeudo
Q5K2P1	protococcus
Q89UC7	bradyrhizob
Q6AHN6	leifsonia x
Q5FS80	gluconobact
P48919	candida par
Q5N753	oryza sativ
Q4RKT5	tetradon n
P53959	saccharomyc
Q6CHS4	yarrowia li
Q95487	homo sapien
Q9VLT1	drosofila
Q86DB6	halocynthia
Q6TFAB	aeromonas h
Q8GWL8	arabidopsis
Q4TDA6	tetradon n
Q8HM19	caulophryne
Q5AC38	candida alb
Q656P6	oryza sativ
Q8RBB0	thermoanaer
Q6Q7C4	uncultured
Q711E4	lactobacill
Q9KPB6	vibrio chol
Q5C7Y4	schistoosoma
Q5SMY7	oryza sativ
Q4QJ62	leishmania
Q6N4G2	rhodopeudo
Q7XHN0	oryza sativ
Q5IZL0	helicobacte
Q5IZM1	helicobacte
Q5IZL9	helicobacte
Q5G819	coenopoeus
Q7WP98	borderella
Q96VE0	sulfolobus
Q5NFE9	francisella
Q5QMN8	oryza sativ
Q98KW6	rhizobium l
Q9AER3	serratia ma
Q9FIJ8	arabidopsis
Q8FC26	escherichia
Q9WX65	acetobacter
Q5KJ93	cryptococcu
Q4Z6S9	plasmococcu
P13506	carassius a
Q04178	saccharomyc
Q55E48	cryptococcu
Q9X738	flexispira
Q7S631	neurospora
Q8PT40	methanosaer
Q9RG88	flexispira
Q9RG88	flexispira
Q9RG88	flexispira
Q8TVK3	methanopyru
Q4KRD8	lactobacill
Q8DLDO	synechococc
Q4WK17	aspergillus
Q6ICB4	homo sapien
Q8BUL8	mus musculu
Q5NPD9	zymomonas m
Q7UGW4	rhodopirell
Q7UTV9	rhodopirell
Q5SP07	cryptococcu
Q70SV1	bemisia tab
Q82XL0	nitrosomona
Q9KRQ9	vibrio chol
Q5GZ49	xanthomonas
Q7NCE7	gloeobacter
Q6FCT6	acinetobact
Q61G31	caenorhabdi
Q6FDDL2	acinetobact

105	25	89.3	287	2	Q20480_CABEL	Q20480 caenorhabdi	178	25	89.3	386	2	Q43916_AC1AD	Q43916 acinetobact
106	25	89.3	287	2	Q20481_CABEL	Q20481 caenorhabdi	179	25	89.3	394	2	Q408U5_LEIMA	Q408U5 leishmania
107	25	89.3	289	2	Q7JMD3_CABEL	Q7JMD3 caenorhabdi	180	25	89.3	394	2	Q57G86_SALCH	Q57G86 salmonella
108	25	89.3	290	2	Q8PH30_XANAC	Q8PH30 xanthomonas	181	25	89.3	394	2	Q5PIF9_SALPA	Q5PIF9 salmonella
109	25	89.3	291	2	Q8MS21_DROME	Q8MS21 drosophila	182	25	89.3	394	2	Q820X3_SALTI	Q820X3 salmonella
110	25	89.3	294	2	Q8JRN7_ACTAC	Q8JRN7 actinobacil	183	25	89.3	394	2	Q8ZJZ6_SALTY	Q8ZJZ6 salmonella
111	25	89.3	296	2	Q53MB9_ORYSA	Q53MB9 oryza sativ	184	25	89.3	396	2	Q8CVS7_ECOL6	Q8CVS7 escherichia
112	25	89.3	305	2	Q61JT2_CAEBR	Q61JT2 caenorhabdi	185	25	89.3	396	2	Q8RI68_FUSNN	Q8RI68 fusobacteri
113	25	89.3	305	2	Q43917_ACTAD	Q43917 acinetobact	186	25	89.3	397	2	Q4LMV3_BURCK	Q4LMV3 burkholderi
114	25	89.3	306	2	Q5AI90_CANAL	Q5AI90 candida alb	187	25	89.3	399	2	Q9A9U6_CAUCR	Q9A9U6 caulobacter
115	25	89.3	308	1	RNH3_STAEP	Q8CPL8 staphylococ	188	25	89.3	400	2	Q63T55_BURPS	Q63T55 burkholderi
116	25	89.3	308	1	RNH3_STAEP	Q8CPL8 staphylococ	188	25	89.3	400	2	Q63T55_BURPS	Q63T55 burkholderi
117	25	89.3	309	1	RNH3_STAEP	Q8CPL8 staphylococ	189	25	89.3	402	2	Q8XR85_RALSO	Q8XR85 raistonia s
118	25	89.3	311	2	Q9N2U8_CABEL	Q9N2U8 caenorhabdi	190	25	89.3	406	1	SUFS_ECOL6	Q7ADI4 escherichia
119	25	89.3	312	1	Q9U1Z9_CABEL	Q9U1Z9 caenorhabdi	191	25	89.3	406	1	SUFS_ECOL6	Q8TH54 escherichia
120	25	89.3	312	1	RNH3_STAAC	Q5HQU4 staphylococ	192	25	89.3	406	1	SUFS_SHIFL	P77444 escherichia
121	25	89.3	312	1	RNH3_STAAM	Q99UW5 staphylococ	193	25	89.3	406	1	SUFS_SHIFL	Q7UAH4 shigella fl
122	25	89.3	312	1	RNH3_STAAN	Q6A47 staphylococ	194	25	89.3	408	2	Q7X692_ORYSA	Q7X692 oryza sativ
123	25	89.3	312	1	RNH3_STAAR	Q6GHN5 staphylococ	195	25	89.3	409	2	Q8XYX5_8ASCI	Q8XYX5 herdmania c
124	25	89.3	312	1	RNH3_STAAS	Q6GHN5 staphylococ	196	25	89.3	416	2	Q86913_9SPHN	Q86913 spingomona
125	25	89.3	312	2	Q7MZP8_PHOLL	Q6GHN5 staphylococ	197	25	89.3	418	2	Q51XH7_MAGGR	Q51XH7 magnaporthe
126	25	89.3	313	2	Q91893_CABEL	Q8NX59 staphylococ	198	25	89.3	419	2	Q8RI67_FUSNN	Q8RI67 fusobacteri
127	25	89.3	313	2	Q5UEY1_9PROT	Q7MSP8 photorhabdi	199	25	89.3	420	2	Q7QR99_GIALA	Q7QR99 giardia lam
128	25	89.3	314	1	Q6FJZ6_CANGA	Q93893 caenorhabdi	200	25	89.3	420	2	Q9CB74_MYCLE	Q9CB74 mycobacteri
129	25	89.3	317	2	Q6FJZ6_CANGA	Q5UEY1 uncultured	201	25	89.3	420	2	Q86987_MYCTU	Q86987 mycobacteri
130	25	89.3	319	2	Q4SNY0_TETNG	Q10281 schizosacch	202	25	89.3	420	2	Q7TVU8_MYCBO	Q7TVU8 mycobacteri
131	25	89.3	323	1	FABH1_LACPL	Q6FJF6 candida gla	203	25	89.3	421	2	Q46033_HALRO	Q46033 halocynthia
132	25	89.3	324	1	YIM4_SCHPO	Q88VZ4 lactobacill	204	25	89.3	422	2	Q95YL3_CIOSA	Q95YL3 ciona savig
133	25	89.3	325	2	Q9M9Y1_ARATH	Q9P7C6 schizosacch	205	25	89.3	425	2	Q9BMT6_CIOIN	Q9BMT6 ciona intes
134	25	89.3	333	1	OAC_BPSF6	Q9M9Y1 arabidopsis	206	25	89.3	425	2	Q4H303_CIOIN	Q4H303 ciona intes
135	25	89.3	333	1	LECT1_MOUSE	P23214 bacterioph	207	25	89.3	427	2	Q7DS02_MYCTU	Q7DS02 mycobacteri
136	25	89.3	334	1	Q80UX1_MOUSE	Q921F6 bacterioph	208	25	89.3	429	2	Q5CQZ2_CRYPU	Q5CQZ2 cryptospori
137	25	89.3	334	2	Q5P976_AZOSE	Q921F6 mus musculu	209	25	89.3	429	2	Q83BZ2_COXBU	Q83BZ2 coxiella bu
138	25	89.3	335	2	Q4UX58_CORJK	Q80UX1 mus musculu	210	25	89.3	433	2	Q4HEG0_CAMCA	Q4HEG0 campylobact
139	25	89.3	336	2	Q4UX58_CORJK	Q5P976 azoarcus sp	211	25	89.3	433	2	Q4HJ58_CAMLA	Q4HJ58 campylobact
140	25	89.3	337	2	Q4F1X2_USTMA	Q4JX58 corynebacte	212	25	89.3	436	2	Q744M0_MYCPA	Q744M0 mycobacteri
141	25	89.3	337	2	Q6J502_BURARE	Q4PIX2 ustilago ma	213	25	89.3	437	2	Q7NID8_GLOVI	Q7NID8 gloebacter
142	25	89.3	338	2	Q9RSB2_DEIRA	Q6J502 brachydanio	214	25	89.3	439	2	Q69515_MYCLE	Q69515 mycobacteri
143	25	89.3	340	2	Q41VE2_AZOVI	Q9RSB2 deinococcus	215	25	89.3	442	2	Q4HQU4_CAMJR	Q4HQU4 campylobact
144	25	89.3	341	2	Q13075_CABEL	Q41VE2 azotobacter	216	25	89.3	442	2	Q5HXD5_CAMJR	Q5HXD5 campylobact
145	25	89.3	341	2	Q82V21_NITEUC	Q13075 caenorhabdi	217	25	89.3	446	2	Q9PJ88_CAMJE	Q9PJ88 campylobact
146	25	89.3	348	2	Q6FJRV_XANAC	Q82V21 nitrosomona	218	25	89.3	446	2	Q7MMH1_VIBVY	Q7MMH1 vibrio vuln
147	25	89.3	349	2	Q6ZA74_ORYSA	Q8PJRV xanthomonas	219	25	89.3	446	2	Q8DG23_VIBVU	Q8DG23 vibrio vuln
148	25	89.3	350	2	Q9XH36_ORYSA	Q9XHB36 oryza sativ	220	25	89.3	447	2	Q59LF9_CANAL	Q59LF9 candida alb
149	25	89.3	352	1	MODC_EGO57	Q8X4V7 escherichia	221	25	89.3	450	2	Q6KIB6_MYCMO	Q6KIB6 mycoplasma
150	25	89.3	352	1	MODC_ECOL6	Q8X4V7 escherichia	222	25	89.3	459	2	Q5FRF9_GLUOX	Q5FRF9 gluconobact
151	25	89.3	352	1	MODC_ECOL6	Q8FJ44 escherichia	223	25	89.3	467	1	GSKH3_DICDI	P51136 dictyosteli
152	25	89.3	352	1	MODC_ERWCT	P09833 escherichia	224	25	89.3	467	2	Q55A28_DICDI	Q55A28 dictyosteli
153	25	89.3	352	1	MODC_ERWCT	Q6D7D0 erwinia car	225	25	89.3	467	2	Q7WPM2_BORBR	Q7WPM2 bordetella
154	25	89.3	352	1	MODC_SALTY	Q8Z8A4 salmonella	226	25	89.3	467	2	Q4PNY4_CRIGR	Q4PNY4 cricetulus
155	25	89.3	352	1	MODC_SALTY	Q8Z8A4 salmonella	227	25	89.3	469	2	Q7S8B7_NBUCR	Q7S8B7 neurospora
156	25	89.3	352	2	Q5TRH4_SALCH	P59738 shigella fl	228	25	89.3	473	2	Q74FQ3_GEOSL	Q74FQ3 geobacter s
157	25	89.3	352	2	Q5PG54_SALPA	Q57RH4 salmonella	229	25	89.3	478	2	Q9RKH0_STRCO	Q9RKH0 streptomyce
158	25	89.3	355	2	Q4IHT8_GIBZE	Q5PG54 salmonella	230	25	89.3	482	2	Q4IG85_GIBZE	Q4IG85 gibberella
159	25	89.3	356	2	Q6DB91_ERWCT	Q4IHT8 gibberella	231	25	89.3	485	2	Q9NDK9_DUGJA	Q9NDK9 dugesia jap
160	25	89.3	359	2	Q5P288_SALPA	Q6DB91 erwinia car	232	25	89.3	487	2	Q7R7C7_PLAYO	Q7R7C7 plasmodium
161	25	89.3	359	2	Q7CPY6_SALTY	Q5P288 salmonella	233	25	89.3	488	2	Q9ASV2_ARATH	Q9ASV2 arabidopsis
162	25	89.3	359	2	Q8XG33_SALTI	Q7CPY6 salmonella	234	25	89.3	490	2	Q6FWQ0_ORYSA	Q6FWQ0 oryza sativ
163	25	89.3	360	2	Q6LRC9_PHOPR	Q8XG33 salmonella	235	25	89.3	492	2	Q6C512_YARLI	Q6C512 yarrowia li
164	25	89.3	361	1	MLTB_ECOLI	Q6LRC9 photobacter	236	25	89.3	492	2	Q4Q3X7_LEIMA	Q4Q3X7 leishmania
165	25	89.3	361	2	Q830G2_SHIFL	P41052 escherichia	237	25	89.3	492	2	Q5X8K3_LBGP	Q5X8K3 legionella
166	25	89.3	361	2	Q8X872_ECO57	Q830G2 shigella fl	238	25	89.3	494	2	Q5G9G6_BACLD	Q5G9G6 bacillus li
167	25	89.3	363	2	Q5TPM6_ANOGA	Q8X872 escherichia	239	25	89.3	497	2	Q5WZY4_LBGPL	Q5WZY4 legionella
168	25	89.3	364	2	Q668Q6_YERPS	Q5TPM6 anophelis g	240	25	89.3	498	2	Q5Z228_LBGPL	Q5Z228 legionella
169	25	89.3	365	2	Q5W92_9TRYP	Q668Q6 yersinia ps	241	25	89.3	504	2	Q51JC5_MAGGR	Q51JC5 magnaporthe
170	25	89.3	367	2	Q9HVX3_PSEAE	Q5W92 trypanosoma	242	25	89.3	506	2	Q18683_DROME	Q18683 drosophila
171	25	89.3	368	2	Q8TU31_METAC	Q9HVX3 pseudomonas	243	25	89.3	510	2	Q505H8_XENTR	Q505H8 xenopus tro
172	25	89.3	368	2	Q702G8_ANOGA	Q8TU31 methanosarc	244	25	89.3	513	2	Q81NX2_DROME	Q81NX2 drosophila
173	25	89.3	371	2	Q7XND4_ORYSA	Q7Q2G8 anophelis g	245	25	89.3	513	2	Q8INY3_DROME	Q8INY3 drosophila
174	25	89.3	375	2	Q57KU2_SALCH	Q7XND4 oryza sativ	246	25	89.3	514	2	Q4YV50_PLABE	Q4YV50 plasmidium
175	25	89.3	376	2	Q8PMQ3_METMA	Q57KU2 salmonella	247	25	89.3	516	2	Q9PP35_XYLPA	Q9PP35 xyella fas
176	25	89.3	381	2	Q5ETX2_ESCHE	Q8PMQ3 methanosarc	248	25	89.3	523	2	Q6SL04_9CRUS	Q6SL04 hutchinsoni
177	25	89.3	384	2	Q6D3V1_ERWCT	Q5ETX2 escherichia	249	25	89.3	532	2	Q5E5Y0_VIBFI	Q5E5Y0 vibrio fies
						Q6D3V1 erwinia car	250	25	89.3	534	2	Q7P242_CHRVO	Q7P242 chromobacte

251	25	89.3	541	2	Q8YN79_ANASP	Q8VN79_anabaena sp	324	25	89.3	1030	2	Q8GM72_PSEFL	Q8gm72_pseudomonas
252	25	89.3	549	1	TAGH_BACC2	Q63Y93 bacillus ce	325	25	89.3	1030	2	Q8L1B1_PSEFL	Q8l1b1_pseudomonas
253	25	89.3	551	2	Q6AJ32_DESPS	Q6aj32 desulfotale	326	25	89.3	1030	2	Q8RLS8_PSEFL	Q8rls8_pseudomonas
254	25	89.3	552	2	Q9B8C9_CANAL	Q9b8c9 candida alb	327	25	89.3	1032	2	Q9W0T7_DROME	Q9w0t7_drosophila
255	25	89.3	554	2	Q5E680_9ASCO	Q5e680 candida ort	328	25	89.3	1044	2	Q8IRJ7_DROME	Q8irj7_drosophila
256	25	89.3	559	2	Q5L1U9_MAGGR	Q5l1u9 magnaporthe	329	25	89.3	1044	2	Q6AWL1_DROME	Q6awl1_drosophila
257	25	89.3	559	2	Q8VRR7_ANASP	Q8vrr7 anabaena ep	330	25	89.3	1047	2	Q5SLV0_CRYNE	Q5slv0_cryptococcus
258	25	89.3	580	2	Q4W9U3_ASPFU	Q4w9u3 aspergillus	331	25	89.3	1060	2	Q5SLC4_CRYNE	Q5slc4_cryptococcus
259	25	89.3	594	1	RYK_MOUSE	Q01887 mus musculus	332	25	89.3	1060	2	Q5KA62_CRYNE	Q5ka62_cryptococcus
260	25	89.3	594	2	Q6BC88_RAT	Q6bc88 rattus norv	333	25	89.3	1067	2	Q6Z6A3_CRYSA	Q6z6a3_cryza sativ
261	25	89.3	596	2	Q6BHU1_DEBHA	Q6bhu1 debaryomyce	334	25	89.3	1072	2	Q35482_RAT	Q35482 rattus norv
262	25	89.3	598	2	Q4V865_XENLA	Q4v865 xenopus lae	335	25	89.3	1079	2	Q52FS3_MAGGR	Q52fs3 magnaporthe
263	25	89.3	599	2	Q6GLP3_XENLA	Q6glp3 xenopus lae	336	25	89.3	1080	2	Q7XZE4_AGSTA	Q7xze4_aegilops ta
264	25	89.3	600	2	Q7ZZ90_BRARE	Q7zz90 brachydanio	337	25	89.3	1103	1	GUC2D_HUMAN	Q02846 homo sapien
265	25	89.3	604	1	RYK_HUMAN	P34295 homo sapien	338	25	89.3	1108	1	GUC2E_MOUSE	P52785 mus musculus
266	25	89.3	607	2	Q4Y193_PLACH	Q4y193 plasmodium	339	25	89.3	1108	1	GUC2E_RAT	P51840 rattus norv
267	25	89.3	614	2	Q7VH61_HELHP	Q7vh61 helicobacte	340	25	89.3	1108	2	Q5NCF5_MOUSE	Q5ncf5 mus musculus
268	25	89.3	615	2	Q7V1P9_HELHP	Q7v1p9 helicobacte	341	25	89.3	1109	1	GUC2D_CANFA	Q19179 canis famli
269	25	89.3	629	2	Q6CT75_KLULA	Q6ct75 kluyveromyc	342	25	89.3	1110	1	GUC2D_BOVIN	P55203 bos taurus
270	25	89.3	631	2	Q5QN02_ORYSA	Q5qn02 oryza sativ	343	25	89.3	1122	2	Q7T947_ADE35	Q7t947 human adeno
271	25	89.3	632	1	YA28_SCHPO	Q09699 schizosacch	344	25	89.3	1122	2	Q5UW17_9ADEN	Q5uw17 human adeno
272	25	89.3	632	2	Q45084_CAEEL	Q45084 caenorhabdi	345	25	89.3	1122	2	Q8B8U2_9ADEN	Q8b8u2 human adeno
273	25	89.3	635	2	Q9VUK7_DROSOPH	Q9vuk7 drosophila	346	25	89.3	1129	2	Q4ML69_BACCE	Q4ml69 bacillus ce
274	25	89.3	648	2	Q4JVE8_CORJK	Q4jve8 corynebacte	347	25	89.3	1161	2	Q736A2_BACCI	Q736a2 bacillus ce
275	25	89.3	649	2	Q7T007_BRARE	Q7t007 brachydanio	348	25	89.3	1170	2	Q4PP90_USTMA	Q4pf90 usilago ma
276	25	89.3	652	2	Q9S195_CAEEL	Q9s195 caenorhabdi	349	25	89.3	1185	2	Q4P121_USTMA	Q4p121 usilago ma
277	25	89.3	658	2	Q61XJ9_CAEER	Q61xj9 caenorhabdi	350	25	89.3	1240	2	Q418S9_GIBZE	Q418s9 gibberella
278	25	89.3	663	2	Q8FUH2_COREF	Q8fuh2 corynebacte	351	25	89.3	1251	2	Q9ZBD1_9PSEU	Q9zbd1 saccharopol
279	25	89.3	671	2	Q98DL4_RHILO	Q98dl4 rhizobium l	352	25	89.3	1270	2	Q4QEV8_LEIMA	Q4qev8 leishmania
280	25	89.3	679	1	ATG322_MAGGR	Q5l1z9 magnaporthe	353	25	89.3	1341	1	RSGPR_DROME	Q9vkb9 drosophila
281	25	89.3	686	2	Q6Q1Q5_CHICK	Q6qlq9 gallus gall	354	25	89.3	1465	2	Q5KBV3_CRYNE	Q5kby3_cryptococcus
282	25	89.3	687	2	Q74ZA2_ASHGO	Q74za2 ashyba gos	355	25	89.3	1484	2	Q4GYD0_9TRYP	Q4gyd0 trypanosoma
283	25	89.3	687	2	Q9VCK7_DROME	Q9vcvk7 drosophila	356	25	89.3	1528	2	Q5SNJ7_CRYNE	Q5snj7_cryptococcus
284	25	89.3	693	2	Q5P9K1_ANAMM	Q5p9k1 anaplasma m	357	25	89.3	1709	2	Q4SDC9_TETNG	Q4sdc9 tetraodon n
285	25	89.3	698	2	Q8D8C4_VIBVU	Q8dc84 vibrio vuln	358	25	89.3	2163	2	Q4IMG9_GIBZE	Q4img9 gibberella
286	25	89.3	700	2	Q7NM42_VIBVU	Q7nm42 vibrio vuln	359	25	89.3	2211	2	Q9NKQ7_LEIMA	Q9nkq7 leishmania
287	25	89.3	704	2	Q7M9H6_WOLSU	Q7m9h6 wolinnella s	360	25	89.3	2747	2	Q6LFB6_PLAF7	Q6lfb6 plasmodium
288	25	89.3	713	2	Q6MMZ5_BDEBA	Q6mmz5 bdellovibri	361	25	89.3	2804	2	Q7RID0_PLAYO	Q7rid0 plasmodium
289	25	89.3	715	2	Q3O965_RHILE	Q3o965 rhizobium l	362	25	89.3	2874	2	Q4QE22_LEIMA	Q4qe22 leishmania
290	25	89.3	725	2	Q781W7_NEUCR	Q781w7 neurospora	363	25	89.3	3044	2	Q7QYR7_GIOLA	Q7qyr7 giardia lam
291	25	89.3	731	2	Q4RVV0_TETNG	Q4rvv0 tetraodon n	364	25	89.3	3393	2	Q7QAL3_XANO	Q7qal3 anopheles g
292	25	89.3	735	2	Q24749_ACEXY	Q24749 acetobacter	365	25	89.3	6420	2	Q7QUZ9_GIALA	Q7quz9 giardia lam
293	25	89.3	750	2	Q6FTV8_CANGA	Q6ftv8 candida gla	366	25	89.3	9579	2	Q4HWW4_GIBZE	Q4hww4 gibberella
294	25	89.3	756	2	Q5SKA9_CRYNE	Q5ska9 cryptococcus	367	25	89.3	52	2	Q5GV02_XANOR	Q5gv02 xanthomonas
295	25	89.3	766	2	Q7N7B7_PHOLL	Q7n7b7 photorhabdu	368	25	89.3	52	2	Q44286_HPV04	Q44286 human papil
296	25	89.3	768	2	Q8C8X5_MOUSE	Q8c8x5 mus musculus	369	25	89.3	52	2	Q4WMC9_ASPFU	Q4wmc9 aspergillus
297	25	89.3	794	2	Q7Q1I6_ANOGA	Q7qi16 anopheles g	370	25	89.3	65	2	Q6GB00_STAAS	Q6gb00 staphylococ
298	25	89.3	795	2	Q8LLA2_AEGTA	Q8lla2 aegilops ta	371	25	89.3	65	2	Q6GJ82_STAAR	Q6gj82 staphylococ
299	25	89.3	797	2	Q6BYB2_DEBHA	Q6byb2 debaryomyce	372	25	89.3	75	2	Q6XQGI_9CAUD	Q6xqgi enterobacte
300	25	89.3	798	2	Q4H7E1_9DEIO	Q4h7e1 deinococcus	373	25	89.3	86	2	Q94AT2_ARATH	Q94at2 arabidopsis
301	25	89.3	801	2	Q9FZT0_9VIRU	Q9fzt0 pseudomonas	374	25	89.3	89	2	Q6F2G2_ORYSA	Q6f2g2 oryza sativ
302	25	89.3	807	2	Q6CFE5_YARLI	Q6cfe5 yarowia li	375	25	89.3	95	2	Q4QID6_LEIMA	Q4qid6 leishmania
303	25	89.3	807	2	Q5H3J9_XANOR	Q5h3j9 xanthomonas	376	25	89.3	97	2	Q87XV9_PSESM	Q87xv9 pseudomonas
304	25	89.3	831	2	Q6FWQ5_CANGA	Q6fwq5 candida gla	377	25	89.3	99	2	Q7QVX7_GIALA	Q7qv7 giardia lam
305	25	89.3	841	1	MUTS_LACLA	Q93r04 lactococcus	378	25	89.3	99	2	Q8ENJ5_OCEIH	Q8enj5 oceanobacil
306	25	89.3	841	2	Q3R0R4_9LACT	Q93r04 lactococcus	379	25	89.3	102	2	Q6KGV5_BRUAB	Q6kgv5 bruceella ab
307	25	89.3	847	2	Q6BSV6_DEBHA	Q6bsv6 debaryomyce	380	25	89.3	102	2	Q9CDJ1_MYCLE	Q9cdj1 mycobacteri
308	25	89.3	866	2	Q580M0_9TRYP	Q580m0 trypanosoma	381	25	89.3	103	2	Q86DDB_TYCR	Q86ddb trypanosoma
309	25	89.3	882	2	Q6PAW8_XENLA	Q6paw8 xenopus lae	382	25	89.3	104	2	Q8SX82_DROME	Q8sx82 drosophila
310	25	89.3	893	2	Q82RG8_STRAW	Q82rg8 streptomyce	383	25	89.3	107	2	Q5M8Q4_MOUSE	Q5m8q4 mus musculus
311	25	89.3	897	2	Q5ARCO_EMENI	Q5arco aspergillus	384	25	89.3	107	2	Q6D1O8_BRARE	Q6d1o8 brachydanio
312	25	89.3	925	2	Q5ATY5_EMENI	Q5aty5 aspergillus	385	25	89.3	114	2	Q7UEG6_RHOBA	Q7ueg6 rhodopirell
313	25	89.3	927	2	O14040_SCHPO	O14040 schizosacch	386	25	89.3	116	2	P95929_SULSO	P95929 sulfolobus
314	25	89.3	927	2	Q6GM27_XENLA	Q6gm27 xenopus lae	387	25	89.3	117	2	Q5VZ18_NOCFA	Q5vzi8 nocardia fa
315	25	89.3	934	2	Q7UZE0_RHOBA	Q7ure0 rhodopirell	388	25	89.3	118	2	Q5BZF3_SCHJA	Q5bzfi schistosoma
316	25	89.3	947	1	PMAL0_ARATH	Q43128 arabidopsis	389	25	89.3	118	2	Q8SCN1_9CAUD	Q8scn1 pseudomonas
317	25	89.3	970	2	Q5X8X0_CRYNE	Q5x8x0 cryptococcus	390	25	89.3	119	1	HV3P_HUMAN	P01777 homo saplen
318	25	89.3	979	2	Q9VEN2_DROME	Q9ven2 drosophila	391	25	89.3	123	2	Q55QB4_CRYNE	Q55qb4 cryptococcus
319	25	89.3	1012	2	Q9HMR2_HALSA	Q9hmr2 halobacteri	392	25	89.3	125	2	Q8XRI3_RALSO	Q8xri3 ralestonia a
320	25	89.3	1014	2	Q5V671_HALMA	Q5v671 haloarcula	393	25	89.3	133	2	Q8U120_PYRFU	Q8u120 pyrococcus
321	25	89.3	1014	2	Q5SJ19_ORYSA	Q5sj19 oryza sativ	394	25	89.3	133	2	Q6ZV09_HUMAN	Q6zv09 homo saplen
322	25	89.3	1019	2	Q7N3T7_PHOLL	Q7n3t7 photorhabdu	395	25	89.3	135	2	Q6UJZ0_HUMAN	Q6ujz0 homo saplen
323	25	89.3	1021	2	Q4H9S3_9DEIO	Q4h9s3 deinococcus	396	25	89.3	137	2	Q8NDU5_HUMAN	Q8ndu5 homo saplen

397	24	85.7	144	2	Q974A5_SULTO	Q974A5 sulfolobus	470	24	85.7	214	2	Q7T1C4_CHICK	Q7T1C4 gallus gall
398	24	85.7	145	1	CASK_HIPCAP	P08441 hippopotamu	471	24	85.7	216	1	Y1382_RHIME	Q5q8 rhizobium m
399	24	85.7	146	1	AZUP_ALCPFA	P04377 alcaligenes	472	24	85.7	216	2	Q65GS0_BACLD	Q65ge0 bacillus li
400	24	85.7	146	2	Q719I0_HUMAN	Q719i0 homo sapien	473	24	85.7	220	2	Q9Y4M6_HUMAN	Q9Y4m6 homo sapien
401	24	85.7	146	2	Q576Z9_BRUAB	Q576z9 brucella ab	474	24	85.7	220	2	Q6FD80_ACIAD	Q6fd80 acinetobact
402	24	85.7	146	2	Q77TH4_BORDE	Q77th4 bordetella	475	24	85.7	223	2	Q4UX80_XANCP	Q4ux80 xanthomonas
403	24	85.7	146	2	Q60CV7_BRUSU	Q60cv7 brucella su	476	24	85.7	223	2	Q8P6X9_XANCP	Q8p6x9 xanthomonas
404	24	85.7	148	2	Q6ABA7_PROAC	Q6aba7 propionibac	477	24	85.7	223	2	Q8P193_XANCP	Q8p193 xanthomonas
405	24	85.7	148	2	Q6F8K5_ACIAD	Q6f8k5 acinetobact	478	24	85.7	224	2	Q4UXK8_XANCP	Q4uxk8 xanthomonas
406	24	85.7	153	2	Q888I7_PSESM	Q888i7 pseudomonas	479	24	85.7	224	2	Q8P6F6_XANCP	Q8p6f6 xanthomonas
407	24	85.7	153	2	Q8YC22_BRUME	Q8yc22 brucella me	480	24	85.7	226	2	Q4R434_MACFA	Q4r434 macaca fasc
408	24	85.7	154	2	Q33695_STRPN	Q33695 streptococc	481	24	85.7	232	2	Q7N7S2_PHOLI	Q7n7s2 photorhabdu
409	24	85.7	155	2	Q4JLG6_LACRE	Q4jlg6 lactobacill	482	24	85.7	233	2	Q9CMM4_PASMU	Q9cmw4 pasteurella
410	24	85.7	155	2	Q577V8_BRUAB	Q577v8 brucella ab	483	24	85.7	236	2	Q4RN58_TETNG	Q4rn58 tetraodon n
411	24	85.7	155	2	Q8FWA1_BRUSU	Q8fwa1 brucella su	484	24	85.7	243	2	Q5TAN5_HUMAN	Q5tan5 homo sapien
412	24	85.7	159	2	Q6STG0_ORISA	Q6stg0 oryza sativ	485	24	85.7	243	2	Q5H3G8_XANOR	Q5h3g8 xanthomonas
413	24	85.7	159	2	Q572F1_PHYIN	Q572f1 phytophthor	486	24	85.7	246	1	CAH_KLEPN	Q52535 klebsiella
414	24	85.7	159	2	Q7VY38_BORPE	Q7vy38 bordetella	487	24	85.7	250	2	Q53799_MYCBO	Q53799 mycobacteri
415	24	85.7	159	2	Q7WB12_BORPA	Q7wb12 bordetella	488	24	85.7	250	2	Q7D9D3_MYCTU	Q7d9d3 mycobacteri
416	24	85.7	159	2	Q7WMH7_BORBR	Q7wmh7 bordetella	489	24	85.7	252	2	Q4QDE3_LEIMA	Q4qde3 leishmania
417	24	85.7	160	2	Q5G7P1_9CAUD	Q5g7p1 listonella	490	24	85.7	255	2	Q74YS5_YERPE	Q74ys5 yersinia pe
418	24	85.7	161	2	Q97I39_CLOAB	Q97i39 clostridium	491	24	85.7	255	2	Q4SY65_TETNG	Q4sy65 tetraodon n
419	24	85.7	163	2	Q4FV19_9GAMM	Q4fv19 psychrobact	492	24	85.7	256	2	Q4MKG4_BACCE	Q4mkg4 bacillus ce
420	24	85.7	163	2	Q9NGV1_9NEOB	Q9ngv1 litoria fal	493	24	85.7	256	2	Q63A10_BACCH	Q63a10 bacillus th
421	24	85.7	165	2	Q8DN08_STRR6	Q8dn08 streptococc	494	24	85.7	256	2	Q81PN7_BACAN	Q81pn7 bacillus an
422	24	85.7	167	2	Q5M8N9_MOUSE	Q5m8n9 mus musculu	495	24	85.7	256	2	Q82L48_STRAW	Q82l48 streptomyc
423	24	85.7	168	2	Q06Z36_YEAST	Q06z36 saccharomyc	496	24	85.7	259	2	Q93JW4_PSEPU	Q93jw4 pseudomonas
424	24	85.7	169	1	YR7B_ECOLI	P21316 escherichia	497	24	85.7	264	2	Q82P97_STRAW	Q82p97 streptomyc
425	24	85.7	169	2	Q5J517_9HYME	Q5j517 euglossa mi	498	24	85.7	266	2	Q96383_HYPCU	Q96383 hypanthria
426	24	85.7	169	2	Q5PET4_SALPA	Q5pet4 salmonella	499	24	85.7	266	2	Q6LU65_PROPR	Q6lu65 photobacter
427	24	85.7	169	2	Q821D4_SALTI	Q821d4 salmonella	500	24	85.7	266	2	Q5N8V7_ORYSA	Q5n8v7 oryza sativ
428	24	85.7	169	2	Q8ZMR7_SALTY	Q8zmr7 salmonella	501	24	85.7	268	2	Q5N8V7_ORYSA	Q5n8v7 oryza sativ
429	24	85.7	169	2	Q8Z371_SALTI	Q8z371 salmonella	502	24	85.7	269	1	TRUA_METAC	Q6fnf2 candida gla
430	24	85.7	171	2	Q9AYM5_CAUCR	Q9aym5 caulobacter	503	24	85.7	269	2	Q6FNE2_CANGA	Q6fne2 candida gla
431	24	85.7	172	2	Q5J516_9HYME	Q5j516 euglossa mi	504	24	85.7	270	2	Q9RGM6_ACICA	Q9rgm6 acinetobact
432	24	85.7	172	2	Q6SCS5_BACLD	Q6scs5 bacillus li	505	24	85.7	272	2	Q8UFT8_AGRTS	Q8uft8 agrobacteri
433	24	85.7	173	2	Q62NA3_BACLD	Q62na3 bacillus li	506	24	85.7	273	2	Q5WES3_BACSK	Q5wes3 bacillus cl
434	24	85.7	174	2	Q75V96_BACSU	Q75v96 bacillus su	507	24	85.7	275	2	Q84QU7_ORYSA	Q84qu7 oryza sativ
435	24	85.7	174	2	Q9CKY8_PASMU	Q9cky8 pasteurella	508	24	85.7	277	2	Q6M8S1_CORGL	Q6m8s1 corynebacte
436	24	85.7	174	2	Q6SEJ8_BACLD	Q6sej8 bacillus li	509	24	85.7	277	2	Q4RZ94_TETNG	Q4rz94 tetraodon n
437	24	85.7	178	2	Q4XNX0_PLACH	Q4xnx0 plasmodium	510	24	85.7	279	2	Q7NJC9_GLOVI	Q7njc9 gloebacter
438	24	85.7	178	2	Q84K40_ARATH	Q84k40 arabidopsis	511	24	85.7	279	2	Q9KT29_VIBCH	Q9kt29 vibrio chol
439	24	85.7	178	2	Q8LES8_ARATH	Q8les8 arabidopsis	512	24	85.7	280	2	Q49777_MYCLE	Q49777 mycobacteri
440	24	85.7	178	2	Q8GEH2_ERWYP	Q8geh2 erwinia pyr	513	24	85.7	281	2	Q8FUC4_COREF	Q8fuc4 corynebacte
441	24	85.7	178	2	Q6F8M9_ACIAD	Q6f8m9 acinetobact	514	24	85.7	281	2	Q9S376_MYCLE	Q9s376 mycobacteri
442	24	85.7	181	2	Q9DAR4_MOUSE	Q9dar4 mus musculu	515	24	85.7	282	2	Q16874_CABEL	Q16874 caenorhabdi
443	24	85.7	181	2	Q6P8W9_MOUSE	Q6p8w9 mus musculu	516	24	85.7	283	1	YU81_YEAST	P47148 saccharomyc
444	24	85.7	183	2	Q7RU29_NEUCR	Q7ru29 neurospora	517	24	85.7	283	2	Q5TY25_ANOGA	Q5ty25 anopheles g
445	24	85.7	185	2	Q5WKZ7_LEGPL	Q5wkz7 legionella	518	24	85.7	283	2	Q81632_ARATH	Q81632 arabidopsis
446	24	85.7	185	2	Q5XKJ3_LEGPA	Q5xkj3 legionella	519	24	85.7	288	2	Q9VT16_DROME	Q9vt16 drosophila
447	24	85.7	185	2	Q5XKJ3_LEGPA	Q5xkj3 legionella	520	24	85.7	290	2	Q4QBG1_LEIMA	Q4qbg1 leishmania
448	24	85.7	185	2	Q5XKJ3_LEGPH	Q5xkj3 legionella	521	24	85.7	290	2	Q63LS1_BURPS	Q63ls1 burkholderi
449	24	85.7	187	2	Q68JM4_9SAUR	Q68jm4 sternoheru	522	24	85.7	291	2	Q62BL7_BURDI	Q62bl7 burkholderi
450	24	85.7	187	2	Q8FJU5_ECOL6	Q8fju5 escherichia	523	24	85.7	292	2	Q5SE99_DICDI	Q5se99 dictyosteli
451	24	85.7	191	2	Q8R8X8_THRTN	Q8r8x8 thermoanaer	524	24	85.7	293	2	Q4TNV5_98PHN	Q4tnv5 erythrobact
452	24	85.7	192	2	Q51675_PARDE	Q51675 paracoccoc	525	24	85.7	295	2	Q5ELJ7_VIBF1	Q5elj7 vibrio fi
453	24	85.7	198	2	Q7U5Y2_SYNPX	Q7u5y2 synechococc	526	24	85.7	297	1	Y2046_METAC	P58850 methanosarc
454	24	85.7	201	2	Q5DGB7_SCHUA	Q5dgb7 schistosoma	527	24	85.7	297	1	Y3190_METNA	Q8p992 methanosarc
455	24	85.7	205	1	RHOQ_HUMAN	P17081 homo sapien	528	24	85.7	297	2	Q7W4D8_BORPA	Q7w4d8 bordetella
456	24	85.7	205	1	RHOQ_MOUSE	Q8j527 mus musculu	529	24	85.7	297	2	Q7W4D8_BORPA	Q7w4d8 bordetella
457	24	85.7	205	1	RHOQ_RAT	Q8j514 rattus norv	530	24	85.7	298	2	Q6TQD1_ECHGR	Q6tqd1 echinococcu
458	24	85.7	205	2	Q52LS8_HUMAN	Q52ls8 homo sapien	531	24	85.7	298	2	Q6TWD1_ECHGR	Q6twd1 echinococcu
459	24	85.7	205	2	Q7PK24_ANOGA	Q7pk24 anopheles g	532	24	85.7	298	2	Q6TWD2_ECHGR	Q6twd2 echinococcu
460	24	85.7	205	2	Q7ZV13_BRARE	Q7zv13 brachydanio	533	24	85.7	298	2	Q6TWD2_ECHGR	Q6twd2 echinococcu
461	24	85.7	207	1	Q15136_HUMAN	Q15136 homo sapien	534	24	85.7	298	2	Q6TWD2_ECHGR	Q6twd2 echinococcu
462	24	85.7	208	2	KAPCC_MACMU	Q62846 macaca mula	535	24	85.7	299	2	Q4MXW6_BACCE	Q4mxw6 bacillus ce
463	24	85.7	209	1	BLI3_NEUCR	Q01358 neurospora	536	24	85.7	299	2	Q7U920_SYNPX	Q7u920 synechococ
464	24	85.7	209	1	XP11_YEAST	P47165 saccharomyc	537	24	85.7	299	2	Q9KSJ6_VIBCH	Q9ksj6 vibrio chol
465	24	85.7	209	2	Q6BUA3_DEBHA	Q6bja3 debaryomyc	538	24	85.7	300	2	Q4HCJ6_9PEIO	Q4hcj6 deinococcu
466	24	85.7	209	2	Q8D6D2_VIBVU	Q8d6d2 vibrio vuln	539	24	85.7	303	2	Q57G97_SALCH	Q57g97 salmonella
467	24	85.7	209	2	Q7MD83_VIBVY	Q7md83 vibrio vuln	540	24	85.7	303	2	Q5PID9_SALPA	Q5pid9 salmonella
468	24	85.7	211	2	Q6CSM6_YARLI	Q6csm6 yarrowia li	541	24	85.7	303	2	Q82K04_SALTY	Q82k04 salmonella
469	24	85.7	213	2	Q5A0H9_CANAL	Q5a0h9 candida alb	542	24	85.7	305	2	Q7PMZ6_ANOGA	Q7pmz6 anopheles g

543	24	85.7	305	2	Q88Q99_PSEPK	Q88g99 pseudomonas	616	24	85.7	351	2	Q95J97_RABIT	Q95j97 oryctolagus
544	24	85.7	306	2	Q8W770_YEAST	Q8w770 saccharomyc	617	24	85.7	351	2	Q9Z4P1_SHEEP	Q9z4p1 shewanella
545	24	85.7	307	2	Q8NU61_CORGL	Q8nu61 corynebacte	618	24	85.7	351	2	Q5EST2_GLUOX	Q5est2 gluconobact
546	24	85.7	308	2	Q72D56_DESVH	Q72d56 desulfovibr	619	24	85.7	351	2	Q65SX1_MANSM	Q65sx1 mannelmia
547	24	85.7	309	2	Q5FUN9_LACAC	Q5fun9 lactobacilli	620	24	85.7	351	2	Q6MHQ2_DBEBB	Q6mhq2 dbellovibri
548	24	85.7	310	1	QXAA2_STRMU	Q8d9p8 streptococc	621	24	85.7	351	2	Q6DBV8_BRARE	Q6dbv8 brachydanio
549	24	85.7	310	2	Q4NUG2_9DELT	Q4nug2 anaeromycob	622	24	85.7	352	2	Q757D8_ASHGO	Q757d8 ashbya goss
550	24	85.7	311	2	Q54MF9_DICDI	Q54mf9 dictyosteli	623	24	85.7	352	2	Q7P123_CHEVO	Q7p123 chromobacte
551	24	85.7	315	2	Q5KGE6_CRYNE	Q5kge6 cryptococcu	624	24	85.7	354	2	Q7V896_PROMM	Q7v896 prochloroco
552	24	85.7	316	2	Q8CGR1_MOUSE	Q8cgr1 mus musculu	625	24	85.7	355	2	Q5LN13_SILPO	Q5ln13 silicibacte
553	24	85.7	316	2	Q9D3V4_MOUSE	Q9d3v4 mus musculu	626	24	85.7	356	2	Q7UY62_RHOBA	Q7uy62 rhodopirell
554	24	85.7	316	2	Q6RWN6_9ZZZZ	Q6rwn6 uncultured	627	24	85.7	357	2	Q5WXB2_LEGPL	Q5wxb2 legionella
555	24	85.7	317	1	RCN2_HUMAN	Q14257 homo sapien	628	24	85.7	357	2	Q5X520_LEGPA	Q5x520 legionella
556	24	85.7	317	2	Q53XN8_HUMAN	Q53xn8 homo sapien	629	24	85.7	357	2	Q5ZWA8_LEGPH	Q5zwa8 legionella
557	24	85.7	318	2	Q5LF79_BACFN	Q5lf79 bacteroides	630	24	85.7	358	2	Q60TK1_CAEBR	Q60tk1 caenorhabdi
558	24	85.7	320	1	RCN2_MOUSE	Q8bp92 mus musculu	631	24	85.7	359	2	Q4KSP2_PSEPF5	Q4ksp2 pseudomonas
559	24	85.7	320	1	RCN2_RAT	Q62703 rattus norv	632	24	85.7	359	1	TRMA_PSEPK	Q88g14 pseudomonas
560	24	85.7	320	2	Q75N78_ENTFC	Q75n78 enterococcu	633	24	85.7	361	1	V227_FOWPV	Q9j508 fowlpox vir
561	24	85.7	320	2	Q83YR4_STRGN	Q83yr4 streptococc	634	24	85.7	361	2	Q9C5B8_ARATH	Q9c5b8 arabidopola
562	24	85.7	321	2	Q6L5S5_STROR	Q6l5s5 streptococc	635	24	85.7	361	2	Q4IWC3_AZOVI	Q4iwc3 azotobacter
563	24	85.7	322	2	Q6LSQ4_STRMT	Q6lsq4 streptococc	636	24	85.7	361	2	Q7OGT5_FOWPV	Q7ogt5 fowlpox vir
564	24	85.7	322	2	Q4TNP5_9SPHN	Q4tnp5 erythrobact	637	24	85.7	361	2	Q4SLS4_TETNG	Q4sls4 tetraodon n
565	24	85.7	322	2	Q4JZJ4_STRFN	Q4jzj4 streptococc	638	24	85.7	362	2	Q7Q1F2_ANOGA	Q7q1f2 anopheles g
566	24	85.7	324	2	Q83YZ2_ENTFC	Q83yz2 enterococcu	639	24	85.7	363	1	TRMA_PSEAE	Q9hv78 pseudomonas
567	24	85.7	325	2	Q5FKM3_LACAC	Q5fkm3 lactobacilli	640	24	85.7	363	1	TRMA_PSEFL	Q9rha9 pseudomonas
568	24	85.7	325	2	Q9AHJ7_9LACO	Q9ahj7 lactobacilli	641	24	85.7	365	2	Q5DTE7_CABEL	Q5dte7 caenorhabdi
569	24	85.7	325	2	Q74JG0_LACAO	Q74jg0 lactobacilli	642	24	85.7	365	2	Q9JUT4_NEIMA	Q9jut4 neisseria m
570	24	85.7	325	2	Q9YJG0_RAT	Q9y3g0 rattus norv	643	24	85.7	365	2	Q9JY60_NEIMB	Q9jy60 neisseria m
571	24	85.7	327	2	Q97529_RABIT	Q97529 oryctolagus	644	24	85.7	367	2	Q5XOL7_LEGPL	Q5xol7 legionella
572	24	85.7	327	2	Q8F4N0_LEPIN	Q8f4n0 leptospira	645	24	85.7	367	2	Q5X989_LEGPA	Q5x989 legionella
573	24	85.7	327	2	Q72R51_LEPIC	Q72r51 leptospira	646	24	85.7	367	2	Q5ZK7_LEGPH	Q5zk7 legionella
574	24	85.7	331	2	Q7VV74_BORPE	Q7vv74 bordetella	647	24	85.7	367	2	Q8YC99_BRUCHE	Q8yc99 brucella me
575	24	85.7	333	1	LECT1_RABIT	Q77v70 oryctolagus	648	24	85.7	368	2	Q32860_MYCFO	Q32860 mycobacteri
576	24	85.7	333	2	Q8TAY6_HUMAN	Q8tay6 homo sapien	649	24	85.7	369	2	Q6OSV6_CAEBR	Q6osv6 caenorhabdi
577	24	85.7	334	1	LECT1_HUMAN	Q75829 homo sapien	650	24	85.7	369	2	Q76443_CABEL	Q76443 caenorhabdi
578	24	85.7	334	1	LECT1_RAT	Q70367 rattus norv	651	24	85.7	369	2	Q87RU5_VIBPA	Q87ru5 vibrio para
579	24	85.7	334	2	Q5SRZ4_CRYNE	Q5srz4 cryptococcu	652	24	85.7	370	2	Q9HNP0_HALSA	Q9hnp0 halobacteri
580	24	85.7	334	2	Q5TAM4_HUMAN	Q5tab4 homo sapien	653	24	85.7	370	2	Q9H736_HUMAN	Q9h736 homo sapien
581	24	85.7	334	2	Q7QAE6_GIALA	Q7qae6 giardia lam	654	24	85.7	370	2	Q8WU23_HUMAN	Q8wu23 homo sapien
582	24	85.7	334	2	Q5L9R2_BACFN	Q5l9r2 bacteroides	655	24	85.7	372	2	Q19960_CABEL	Q19960 caenorhabdi
583	24	85.7	334	2	Q64O09_BACFR	Q64o09 bacteroides	656	24	85.7	372	2	Q24967_HELPY	Q24967 helicobacte
584	24	85.7	334	2	Q920W9_MUSSI	Q920w9 mus spicile	657	24	85.7	373	2	Q813B7_BACCR	Q813b7 bacillus ce
585	24	85.7	335	1	LECT1_BOVIN	P17404 bos taurus	658	24	85.7	376	2	Q4MXS0_BACCE	Q4mxs0 bacillus ce
586	24	85.7	335	2	Q57UB4_9TRYP	Q57ub4 trypanosoma	659	24	85.7	376	2	Q6HG58_BACHK	Q6hg58 bacillus th
587	24	85.7	335	2	Q4LET1_SODGL	Q4let1 sodalis glo	660	24	85.7	376	2	Q734M4_BACCI	Q734m4 bacillus ce
588	24	85.7	335	2	Q9CNW6_PASMU	Q9cnw6 pasteurella	661	24	85.7	376	2	Q81N09_BACAN	Q81n09 bacillus an
589	24	85.7	335	2	Q6AZQ7_XENLA	Q6azq7 xenopus lae	662	24	85.7	376	2	Q638M5_BACCC	Q638m5 bacillus ce
590	24	85.7	336	2	Q7MZP4_PHOLL	Q7mpz4 photorhabdu	663	24	85.7	376	2	Q8EQD5_OCEIH	Q8eqd5 oceanobacil
591	24	85.7	336	2	Q7QH7_VIBPA	Q7qh7 vibrio para	664	24	85.7	377	2	Q9VSF0_DROME	Q9vsf0 drosophila
592	24	85.7	337	2	Q9CUC5_MOUSE	Q9cuc5 m mus muscu	665	24	85.7	378	2	Q9W124_DROME	Q9w124 drosophila
593	24	85.7	338	2	Q5B868_EMENI	Q5b868 aspergillus	666	24	85.7	379	2	Q8ZV38_PYRAE	Q8zv38 pyrobaculum
594	24	85.7	338	2	Q8CFX4_MOUSE	Q8cfx4 mus musculu	667	24	85.7	379	2	Q7VA67_PROMA	Q7va67 prochloroco
595	24	85.7	338	2	Q7ZY92_XENLA	Q7zy92 xenopus lae	668	24	85.7	380	2	O01448_CABEL	O01448 caenorhabdi
596	24	85.7	340	2	Q81V82_HUMAN	Q81v82 homo sapien	669	24	85.7	380	2	Q7XAB5_BRARP	Q7xab5 brasica ra
597	24	85.7	342	2	Q5QBE8_9CAUD	Q5qbe8 enterobacte	670	24	85.7	381	2	Q65RK5_MANSM	Q65rk5 mannelmia
598	24	85.7	342	2	Q5SRV3_MOUSE	Q5srv3 mus musculu	671	24	85.7	382	2	Q8U337_PYRFU	Q8u337 pyrococcus
599	24	85.7	343	2	Q7NG64_GLOVI	Q7ng64 gloeobacteri	672	24	85.7	382	2	Q89MQ7_BRAJA	Q89mq7 bradyrhizob
600	24	85.7	343	2	Q8UF23_AGRIT5	Q8uf23 agrobacteri	673	24	85.7	384	2	Q4NJA7_9MICC	Q4nja7 arthrobacte
601	24	85.7	345	1	APOH_CANFA	P33703 canis famil	674	24	85.7	384	2	Q7VNU0_HAEDU	Q7vnu0 haemophilus
602	24	85.7	346	1	ACSF_GLOVI	Q7nra1 gloeobacter	675	24	85.7	385	2	Q82Y21_NITRO	Q82y21 nitrosomona
603	24	85.7	346	2	Q721P2_THET2	Q721p2 thermus the	676	24	85.7	386	2	Q7QKB3_ANOGA	Q7qkb3 anopheles g
604	24	85.7	347	1	LECT1_CHICK	Q9puu8 gallus gall	677	24	85.7	386	2	Q701Y3_STRTN	Q701y3 streptomyce
605	24	85.7	347	2	Q5M913_XENTR	Q5m913 xenopus tro	678	24	85.7	390	2	Q582G4_TRYTP	Q582g4 trypanosoma
606	24	85.7	350	1	KAPCA_BOVIN	P0517 bos taurus	679	24	85.7	390	2	Q578E0_BRUAB	Q578e0 brucella ab
607	24	85.7	350	1	KAPCA_CRIGR	P25321 cricetus	680	24	85.7	390	2	Q6NB45_RUOPA	Q6nb45 rhodopseudo
608	24	85.7	350	1	KAPCA_HUMAN	P17612 homo sapien	681	24	85.7	390	2	Q8U7D0_AGRIT5	Q8u7d0 agrobacteri
609	24	85.7	350	1	KAPCA_MOUSE	P05132 mus musculu	682	24	85.7	390	2	Q8FW17_BRUSU	Q8fw17 brucella su
610	24	85.7	350	1	KAPCA_RAT	P27791 rattus norv	683	24	85.7	391	2	Q4FVQ5_9GAMM	Q4fvq5 psychrobact
611	24	85.7	350	1	KAPCA_SHEEP	Q9mad9 ovis aries	684	24	85.7	392	2	Q6NSD4_RHOPA	Q6nsd4 rhodopseudo
612	24	85.7	350	1	KAPCG_HUMAN	P22612 homo sapien	685	24	85.7	395	2	Q9FIH4_ARATH	Q9fih4 arabidopsia
613	24	85.7	351	2	Q6CWM5_KUJULA	Q6cwm5 kluyveromyc	686	24	85.7	396	2	Q31634_BACSU	Q31634 bacillus su
614	24	85.7	351	2	Q6P669_HUMAN	Q6p669 homo sapien	687	24	85.7	396	2	Q8A2S1_BACTN	Q8a2s1 bacteroides
615	24	85.7	351	2	Q5V202_HUMAN	Q5v202 homo sapien	688	24	85.7	397	2	Q5TW82_ANOGA	Q5tw82 anopheles g



689	24	85.7	400	1	TRPB_CHLTE	Q8kf11 chlorobium	762	24	85.7	472	2	Q4SLA7_TETNG	Q4sla7 tetraodon n
690	24	85.7	400	2	Q769CB_9GAM1	Q9l5c8 psychrobact	763	24	85.7	473	2	Q8X1B5_PICAN	Q8xie5 pichia angu
691	24	85.7	400	2	Q9L514_PSYG1	Q9l514 psychrobact	764	24	85.7	474	2	Q51RB2_MAGNAR	Q51rb2 magnaporthe
692	24	85.7	400	2	Q5YXH6_NOCFA	Q5yxh6 nocardia fa	765	24	85.7	474	2	Q51E61_ENTHI	Q51e61 entamoeba h
693	24	85.7	402	2	Q7CV59_AGR15	Q7cv59 agrobacteri	766	24	85.7	476	1	VSM2_TRYBB	P26132 trypanosoma
694	24	85.7	402	2	Q4HWC0_CAMLA	Q4hwc0 campylobact	767	24	85.7	476	2	Q8N1H6_HUMAN	Q8nlh6 homo sapien
695	24	85.7	403	2	Q5LWC9_SILPO	Q5lwc9 silicibacte	768	24	85.7	476	2	Q9I242_PSEAE	Q9i242 pseudomonas
696	24	85.7	403	2	Q92TN0_RHIME	Q92tn0 rhizobium m	769	24	85.7	476	2	Q6A8M2_PROAC	Q6a8m2 propionibac
697	24	85.7	406	2	Q7PWZ2_ANOGA	Q7pwz2 anopheles g	770	24	85.7	477	2	Q6M8Q7_CORG1	Q6m8q7 corynebacte
698	24	85.7	408	2	Q9CL28_PASMU	Q9cl28 pasteurella	771	24	85.7	477	2	Q9ILY2_BTML	Q9ily2 beet mosaic
699	24	85.7	409	2	Q82VG2_NITEU	Q82vg2 nitrosomona	772	24	85.7	478	1	FUMC2_BRAJA	Q89xm2 bradyrhizob
700	24	85.7	410	2	Q7Y4J0_9CAUD	Q7y4j0 streptococc	773	24	85.7	478	2	Q88D86_PSEPK	Q88d86 pseudomonas
701	24	85.7	410	2	Q7Y4CR7_GEOSL	Q7y4cr7 geobacter s	774	24	85.7	478	2	Q9DB72_MOUSE	Q9db72 m mus muscu
702	24	85.7	411	2	Q7XTD4_ORYSA	Q7xtd4 oryza sativ	775	24	85.7	481	2	Q6T415_LEPMC	Q6t415 leptosphaer
703	24	85.7	411	2	Q8RBZ2_THETN	Q8rbz2 thermoanaer	776	24	85.7	481	2	Q53P80_ORYSA	Q53p80 oryza sativ
704	24	85.7	415	2	Q6C3D6_YARLI	Q6c3d6 yarrowia li	777	24	85.7	481	2	Q7UUY2_RHOBA	Q7uuy2 rhodospirell
705	24	85.7	415	2	Q7P4Z5_FUSNV	Q7p4z5 fusobacteri	778	24	85.7	482	2	Q4XWC9_PLACH	Q4xwc9 plasmodium
706	24	85.7	416	2	Q92WV9_9VIRU	Q92wv9 corynebacte	779	24	85.7	483	1	IDH_RICCN	Q9air7 rickettsia
707	24	85.7	416	2	Q5P2A8_AZOSE	Q5p2a8 azoarcus sp	780	24	85.7	483	1	IDH_RICPR	Q6xdr0 rickettsia
708	24	85.7	419	2	Q62B72_BURMA	Q62b72 burkholderi	781	24	85.7	483	1	IDH_RICTY	Q6xas5 rickettsia
709	24	85.7	419	2	Q63NJ6_BURPS	Q63nj6 burkholderi	782	24	85.7	483	2	Q7PB86_RICSI	Q7pb86 rickettsia
710	24	85.7	421	2	Q70PR7_RAUSE	Q70pr7 raoultella s	783	24	85.7	483	2	Q89CQ2_BRAJA	Q89cq2 bradyrhizob
711	24	85.7	424	1	CRIC3_ARATH	O04153 arabidopsis	784	24	85.7	485	2	Q9D5K0_MOUSE	Q9d5k0 m mus muscu
712	24	85.7	424	2	Q5J991_HALDI	Q5j991 haliotis di	785	24	85.7	487	2	Q4QON9_BTMA	Q4qon9 leishmania
713	24	85.7	424	2	Q5J993_HALDI	Q5j993 haliotis di	786	24	85.7	487	2	Q9LS94_BTMA	Q9ls94 beet mosaic
714	24	85.7	424	2	Q5J996_HALDV	Q5j996 haliotis di	787	24	85.7	488	2	Q9RXX3_DIRA	Q9rxx3 deinococcus
715	24	85.7	424	2	Q5J997_HALDV	Q5j997 haliotis di	788	24	85.7	489	2	Q5SRW5_CRYNE	Q5srw5 cryptococcu
716	24	85.7	424	2	Q8GU11_ARATH	Q8gu11 arabidopsis	789	24	85.7	489	2	Q5KGB8_CRYNE	Q5kgb8 cryptococcu
717	24	85.7	424	2	Q93ZR4_ARATH	Q93zr4 arabidopsis	790	24	85.7	490	2	Q7TOV0_XENLA	Q7tov0 xenopus lae
718	24	85.7	424	2	Q5ZKW0_CHICK	Q5zkw0 gallus gall	791	24	85.7	491	2	Q4UKR1_RICFE	Q4ukr1 rickettsia
719	24	85.7	426	2	Q4MYR3_BACEE	Q4myr3 bacillus ce	792	24	85.7	491	2	Q4VBR9_BRARE	Q4vbr9 brachydanio
720	24	85.7	426	2	Q6HDE4_BACHK	Q6hde4 bacillus th	793	24	85.7	493	1	GLTB_BACSU	Q34399 bacillus su
721	24	85.7	426	2	Q730F3_BACCL	Q730f3 bacillus ce	794	24	85.7	493	2	Q4PIJ1_USGTA	Q4pij1 ustilago ma
722	24	85.7	426	2	Q817Z4_BACCR	Q817z4 bacillus ce	795	24	85.7	493	2	Q4IDQ8_GIBZE	Q4idq8 gibberella
723	24	85.7	426	2	Q634G3_BACCC	Q634g3 bacillus ce	796	24	85.7	493	2	Q5SJM5_THET8	Q5sjm5 thermus the
724	24	85.7	426	2	Q81LK7_BACAN	Q81lk7 bacillus an	797	24	85.7	493	2	Q7ZJZ9_THET8	Q7zjz9 thermus the
725	24	85.7	428	1	V234_FOWPV	P14368 fowlpox vir	798	24	85.7	493	2	Q9ROR6_CRIGR	Q9ror6 cricerculus
726	24	85.7	428	2	Q89PW4_BRAJA	Q89pw4 bradyrhizob	799	24	85.7	494	1	UQCR1_EUGRK	Q9r0r6 cricerculus
727	24	85.7	428	2	Q70GS8_FOWPV	Q70gs8 fowlpox vir	800	24	85.7	494	2	Q4LSG0_9BURK	P43264 euglena gra
728	24	85.7	430	2	Q4PCCS_USGTA	Q4pccs ustilago ma	801	24	85.7	494	2	Q5WGD6_BACSK	Q4lsq0 burkholderi
729	24	85.7	430	2	Q7FAM0_ORYSA	Q7fam0 oryza sativ	802	24	85.7	494	2	Q7TV65_PROMM	Q5wgd6 bacillus cl
730	24	85.7	435	2	Q4IXU9_AZOVI	Q4ixu9 azotobacter	803	24	85.7	497	2	Q9KGP3_BACHD	Q7tv65 prochloroco
731	24	85.7	438	2	Q7QJ62_ANOGA	Q7qj62 anopheles g	804	24	85.7	500	2	Q54D28_DICDI	Q9kqp3 bacillus ha
732	24	85.7	438	2	Q4QIZ0_LEIMA	Q4qiz0 leishmania	805	24	85.7	500	2	Q6VZ44_CNPV	Q54d28 dictyostei
733	24	85.7	439	2	Q7QEZ2_ANOGA	Q7qez2 anopheles g	806	24	85.7	501	2	Q4IJC8_GIBZE	Q6vz44 canarypox v
734	24	85.7	439	2	Q5F718_NEIG1	Q5f718 neisseria g	807	24	85.7	502	2	Q9WC75_9BROM	Q4ijc8 gibberella
735	24	85.7	440	2	Q6VHK2_BDEBA	Q6vhk2 belliovibri	808	24	85.7	503	2	Q8BG07_MOUSE	Q9wc75 peanut stun
736	24	85.7	440	2	Q9RL73_STAAU	Q9rl73 staphylococ	809	24	85.7	503	2	Q8BGO7_MOUSE	Q8bg07 m mus muscu
737	24	85.7	441	2	Q6AJK5_DEGFS	Q6ajk5 desulfotale	810	24	85.7	505	1	KKCC1_HUMAN	Q8bgo7 homo sapien
738	24	85.7	443	2	Q6A569_9BRAD	Q6a569 bradyrhizob	811	24	85.7	505	1	KKCC1_MOUSE	Q8vby2 mus musculu
739	24	85.7	443	2	Q89FY2_BRAJA	Q89fy2 bradyrhizob	812	24	85.7	505	1	KKCC1_RAT	P97756 r calcium/c
740	24	85.7	445	2	Q4WJE8_ASPFU	Q4wj8 aspergillus	813	24	85.7	505	2	Q5SRU3_MOUSE	Q5aru3 mus musculu
741	24	85.7	447	2	Q92VB1_RHIME	Q92vb1 rhizobium m	814	24	85.7	506	2	C89A2_ARATH	Q42602 arabidopsis
742	24	85.7	450	1	DCOR_CHICK	P27118 gallus gall	815	24	85.7	507	2	Q4LRB2_9BURK	Q4lr2 burkholderi
743	24	85.7	451	2	Q9HCVJ7_HUMAN	Q9hcvj7 homo sapien	816	24	85.7	508	2	Q63TZ1_BURPS	Q63tz1 burkholderi
744	24	85.7	451	2	Q7QCV5_ANOGA	Q7qcv5 anopheles g	817	24	85.7	510	2	Q8SRR6_ENCCU	Q8srr6 encephalito
745	24	85.7	452	2	Q4I7N4_GIBZE	Q4i7n4 gibberella	818	24	85.7	510	2	Q94OJ8_ARATH	Q94ou8 arabidopsis
746	24	85.7	453	2	Q9Z9T3_BACHD	Q9z9t3 bacillus ha	819	24	85.7	510	2	Q9XIQ1_ARATH	Q9xiq1 arabidopsis
747	24	85.7	454	2	Q5CVB3_CRYPV	Q5cvb3 cryptospori	820	24	85.7	510	2	Q6ZRF3_BACLD	Q6zrf3 bacillus li
748	24	85.7	454	2	Q5CIF5_CRYHO	Q5cif5 cryptospori	821	24	85.7	511	1	ALDHY_YEAST	P34872 saccharomyc
749	24	85.7	454	2	Q4V4Z0_DROME	Q4v4z0 drosophila	822	24	85.7	511	2	Q9XIQ2_ARATH	Q9xiq2 arabidopsis
750	24	85.7	454	2	Q95LM2_MACFA	Q95lm2 macaca faec	823	24	85.7	511	2	Q9XIQ3_ARATH	Q9xiq3 arabidopsis
751	24	85.7	456	1	DCOR2_XENLA	Q91884 xenopus lae	824	24	85.7	512	1	Q9PSX7_ARATH	Q4pex7 arabidopsis
752	24	85.7	456	2	Q5BCA0_EMENT	Q5bca0 aspergillus	825	24	85.7	512	1	OPUD_BACSU	P54417 bacillus su
753	24	85.7	456	2	Q80IS1_XENLA	Q80is1 xenopus lae	826	24	85.7	512	1	V233_FOWPV	Q91502 fowlpox vir
754	24	85.7	461	2	Q8VU93_LACCA	Q8vu93 lactobacill	827	24	85.7	512	2	Q9ZUQ6_ARATH	Q9zuq6 arabidopsis
755	24	85.7	464	2	Q4ION3_GIBZE	Q4ion3 gibberella	828	24	85.7	512	2	Q65FZ6_BACLD	Q65fz6 bacillus li
756	24	85.7	466	2	Q4QAX5_LEIMA	Q4qax5 leishmania	829	24	85.7	512	2	Q7QGS9_FOWPV	Q7qgs9 fowlpox vir
757	24	85.7	466	2	Q9KG15_BACHD	Q9kg15 bacillus ha	830	24	85.7	513	1	KRHB2_HUMAN	Q9nsb4 homo sapien
758	24	85.7	472	2	Q8ZY23_PYRAE	Q8zy23 pyrobaculum	831	24	85.7	513	2	Q7O1L7_HUMAN	Q7o1l7 homo sapien
759	24	85.7	472	2	Q56OU3_CRYNE	Q56ou3 cryptococcu	832	24	85.7	513	2	Q6PPD3_9VEST	Q6ppd3 haliotis ru
760	24	85.7	472	2	Q5KPU3_CRYNE	Q5kpu3 cryptococcu	833	24	85.7	514	2	Q8KZ28_9PROT	Q8kz28 uncultured
761	24	85.7	472	2	Q8NU52_CRYNL	Q8nu52 corynebacte	834	24	85.7	514	2	Q6VZ29_CNPV	Q6vz29 canarypox v

835	24	85.7	515	2	016988_CABEL	016988_caenorhabdi	908	24	85.7	554	2	05FV55_RAT	05FV55_rattus norv
836	24	85.7	515	2	Q747A6_GEOL	Q747A6_wolbacter s	909	24	85.7	555	2	Q8B625_VIBVU	Q8B625_vibrio vuln
837	24	85.7	516	2	Q5G5X8_WOLTR	Q5G5X8_wolbacteria s	910	24	85.7	556	2	Q6VZK3_CNPV	Q6VZK3_canarypox v
838	24	85.7	517	2	Q73176_WOLPM	Q73176_hymenolepis p	911	24	85.7	558	1	COX1B_PARDE	P98002_paracoccu
839	24	85.7	517	2	Q958J3_HYMDI	Q958J3_hymenolepis	912	24	85.7	558	2	Q7QP88_GIALA	Q7QP88_giardia lam
840	24	85.7	517	2	Q8UUY1_AGRG'S	Q8UUY1_agrobacteri r	913	24	85.7	559	2	Q4W999_ASPFU	Q4W999_aspergillus
841	24	85.7	518	2	Q5FGC4_EHRRW	Q5FGC4_ehrlichia r	914	24	85.7	559	2	Q4SF68_TETNG	Q4SF68_tetradodon n
842	24	85.7	518	2	Q5HAA7_EHRRW	Q5HAA7_ehrlichia r	915	24	85.7	560	2	Q5B523_EMENI	Q5B523_aspergillus
843	24	85.7	521	2	Q59774_SCHPO	Q59774_schizosacch	916	24	85.7	560	2	Q4WB04_ASPFU	Q4WB04_aspergillus
844	24	85.7	521	2	Q413V7_GIBZE	Q413V7_gibberella	917	24	85.7	565	2	Q4WIE5_ASPFU	Q4WIE5_aspergillus
845	24	85.7	521	2	Q78728_9CEST	Q78728_spirogameta p	918	24	85.7	566	1	COX1_RHOS	P33517_rhodobacter
846	24	85.7	521	2	Q78729_9CEST	Q78729_spirogameta p	919	24	85.7	566	2	Q523D4_MAGGR	P33517_rhodobacter
847	24	85.7	521	2	Q78730_9CEST	Q78730_diphylobot	920	24	85.7	568	2	Q8NKG3_SACKL	Q8NKG3_saccharomyce
848	24	85.7	521	2	Q5P9Y9_ANAMR	Q5P9Y9_anaplagma m	921	24	85.7	568	2	Q89FH7_BRAJA	Q89FH7_brachyrihizob
849	24	85.7	528	2	Q502F8_BRARE	Q502F8_brachydanlio	922	24	85.7	569	2	Q31487_BACSU	Q31487_bacillus s
850	24	85.7	530	2	Q953M3_ECHGR	Q953M3_echinococcu	923	24	85.7	570	2	Q4P8J7_USTMA	Q4P8J7_ustilago ma
851	24	85.7	531	2	Q7SXE6_BRARE	Q7SXE6_brachydanlio	924	24	85.7	571	2	Q9HKD1_THEAC	Q9HKD1_thermoplaem
852	24	85.7	532	1	COX1_RICCN	Q72167_rickettsia	925	24	85.7	571	2	Q857A5_CLOTE	Q857A5_clostridium
853	24	85.7	532	2	Q7PB85_RICSI	Q7PB85_rickettsia	926	24	85.7	571	2	Q7MD48_VIBVU	Q7MD48_vibrio vuln
854	24	85.7	532	2	Q4ULU5_RICFE	Q4ULU5_rickettsia	927	24	85.7	572	2	Q4V4D9_DROME	Q4V4D9_drosophila
855	24	85.7	532	2	Q83AE9_COXBU	Q83AE9_coxiella bu	928	24	85.7	572	2	Q6CMK7_KLULA	Q6CMK7_kluyveromyc
856	24	85.7	532	2	Q8CI74_MOUSE	Q8CI74_mus musculu	929	24	85.7	573	2	Q8NKG8_KLULA	Q8NKG8_kluyveromyc
857	24	85.7	533	1	ALDHX_YEAST	P22281_saccharomyc	930	24	85.7	574	2	Q4HYW3_GIBZE	Q4HYW3_gibberella
858	24	85.7	533	2	Q7PX65_ANOGA	Q7PX65_anopheles g	931	24	85.7	575	1	CCNB3_DROME	Q91710_drosophila
859	24	85.7	534	2	Q4GYQ1_9TRYP	Q4GYQ1_trypanosoma	932	24	85.7	576	2	P96586_BACSU	P96586_bacillus au
860	24	85.7	534	1	COX1_RICPR	Q54069_rickettsia	933	24	85.7	577	2	Q976K9_SULTO	Q976K9_sulfolobus
861	24	85.7	535	2	Q6C544_YARLI	Q6C544_yarrowia li	934	24	85.7	577	2	Q5SIC0_THET8	Q5SIC0_thermus the
862	24	85.7	535	2	Q58A06_9CEST	Q58A06_echinococcu	935	24	85.7	581	2	Q5A632_CANAL	Q5A632_candida alb
863	24	85.7	535	2	Q958U2_ECHGR	Q958U2_echinococcu	936	24	85.7	581	2	Q96K43_HUMAN	Q96K43_homo sapien
864	24	85.7	535	2	Q9TE74_ECHMU	Q9TE74_echinococcu	937	24	85.7	582	2	Q6BJL0_DBBHA	Q6BJL0_debaryomyc
865	24	85.7	537	2	Q9B8W3_9CEST	Q9B8W3_taeinia cras	938	24	85.7	582	2	Q5ASV0_CANAL	Q5ASV0_candida alb
866	24	85.7	537	2	Q9B8D1_RHILLO	Q9B8D1_rhizobium l	939	24	85.7	583	2	Q4HC10_9DEIO	Q4HC10_deinococcu
867	24	85.7	538	2	Q6CPW4_KLULA	Q6CPW4_kluyveromyc	940	24	85.7	583	2	Q9KLR7_VIBCH	Q9KLR7_vibrio chol
868	24	85.7	539	2	Q7655A4_ASHGO	Q7655A4_ashbya goes	941	24	85.7	583	2	Q9RVS0_DEIRA	Q9RVS0_deinococcu
869	24	85.7	539	2	Q76B26_TABSA	Q76B26_taeinia saqi	942	24	85.7	584	2	Q5AEK8_CANAL	Q5AEK8_candida alb
870	24	85.7	539	2	Q76B28_TABSA	Q76B28_taeinia saqi	943	24	85.7	584	2	Q5AEZ3_CANAL	Q5AEZ3_candida alb
871	24	85.7	539	2	Q76B29_TABSA	Q76B29_taeinia saqi	944	24	85.7	584	2	Q9KZ90_STRCO	Q9KZ90_streptomyce
872	24	85.7	539	2	Q76B31_TABSA	Q76B31_taeinia saqi	945	24	85.7	584	2	Q82HW1_STRAW	Q82HW1_streptomyce
873	24	85.7	539	2	Q76B33_TABSA	Q76B33_taeinia saqi	946	24	85.7	587	2	Q59127_PYRHO	Q59127_pyrococcu
874	24	85.7	539	2	Q76B35_9CEST	Q76B35_taeinia asia	947	24	85.7	588	2	Q8UOX7_PYRFO	Q8UOX7_pyrococcu
875	24	85.7	539	2	Q7YH64_9CEST	Q7YH64_taeinia asia	948	24	85.7	588	2	Q8UJF1_ARATH	Q8UJF1_arabidopsia
876	24	85.7	539	2	Q955Z2_TABSA	Q955Z2_taeinia saqi	949	24	85.7	589	2	Q6ETK5_ORISA	Q6ETK5_oryza sativ
877	24	85.7	539	2	Q955Z3_9CEST	Q955Z3_taeinia asia	950	24	85.7	590	2	Q5JHH8_PYRKO	Q5JHH8_pyrococcu
878	24	85.7	539	2	Q955Z4_TABSO	Q955Z4_taeinia soli	951	24	85.7	590	2	Q86ZK3_PODAN	Q86ZK3_podospora a
879	24	85.7	539	2	Q955Z5_TABSO	Q955Z5_taeinia soli	952	24	85.7	594	2	Q60WV4_CAEBR	Q60WV4_caenorhabdi
880	24	85.7	539	2	Q955Z6_TABSO	Q955Z6_taeinia soli	953	24	85.7	594	2	Q9DTG1_9CLOS	Q9DTG1_citrus tris
881	24	85.7	539	2	Q955Z7_TABSO	Q955Z7_taeinia soli	954	24	85.7	594	2	Q66223_9CLOS	Q66223_citrus tris
882	24	85.7	539	2	Q955Z8_TABSO	Q955Z8_taeinia soli	955	24	85.7	594	2	Q8B3T5_9CLOS	Q8B3T5_citrus tris
883	24	85.7	539	2	Q955Z9_TABSO	Q955Z9_taeinia soli	956	24	85.7	595	2	Q7T709_9CLOS	Q7T709_citrus tris
884	24	85.7	539	2	Q956A0_TABSO	Q956A0_taeinia soli	957	24	85.7	595	2	Q9HAH3_HUMAN	Q9HAH3_homo sapien
885	24	85.7	539	2	Q956A2_TABSO	Q956A2_taeinia soli	958	24	85.7	596	1	V024_F0WPU	Q915H7_fowlpox vir
886	24	85.7	539	2	Q956A1_TABSO	Q956A1_taeinia soli	959	24	85.7	596	2	Q9VIN9_DROME	Q9VIN9_drosophila
887	24	85.7	539	2	Q5L225_GEOKA	Q5L225_geobacillus	960	24	85.7	596	2	Q70HC6_F0WPU	Q70HC6_fowlpox vir
888	24	85.7	540	2	Q9VRQ8_DROME	Q9VRQ8_drosophila	961	24	85.7	598	1	VE1_HPV65	Q07846_human papil
889	24	85.7	542	2	Q66VZ5_PICPA	Q66VZ5_pichia past	962	24	85.7	599	1	VE1_HPV04	Q07846_human papil
890	24	85.7	543	2	Q4VAV9_DROME	Q4VAV9_drosophila	963	24	85.7	599	2	Q4NIG2_9MICC	Q4NIG2_arthrobacte
891	24	85.7	544	2	Q4WUC6_ASPFU	Q4WUC6_aspergillus	964	24	85.7	600	2	Q6AGQ2_LEIXX	Q6AGQ2_leifsonia x
892	24	85.7	546	2	Q85963_SPHAR	Q85963_sphingomona	965	24	85.7	601	2	Q4Y1X1_PLACH	Q4Y1X1_plasmodium
893	24	85.7	548	2	Q5B4D8_EMENI	Q5B4D8_aspergillus	966	24	85.7	601	2	Q4URV8_XANCP	Q4URV8_xanthomonas
894	24	85.7	548	2	Q9RW08_DEIRA	Q9RW08_deinococcu	967	24	85.7	601	2	Q8PBP1_XANCP	Q8PBP1_xanthomonas
895	24	85.7	549	2	Q4MPX5_BACCE	Q4MPX5_bacillus ce	968	24	85.7	601	2	Q8PN96_XANAC	Q8PN96_xanthomonas
896	24	85.7	549	2	Q6HPG5_BACHK	Q6HPG5_bacillus th	969	24	85.7	604	2	Q7Q6B7_ANOGA	Q7Q6B7_anopheles g
897	24	85.7	549	2	Q73EW9_BACCI	Q73EW9_bacillus ce	970	24	85.7	604	2	Q9V5D9_DROME	Q9V5D9_drosophila
898	24	85.7	549	2	Q811W1_BACCR	Q811W1_bacillus ce	971	24	85.7	604	2	Q86BS2_DROME	Q86BS2_drosophila
899	24	85.7	549	2	Q81V10_BACAN	Q81V10_bacillus an	972	24	85.7	605	2	Q8VZV5_CNPV	Q8VZV5_canarypox v
900	24	85.7	549	2	Q63GZ2_BACCC	Q63GZ2_bacillus ce	973	24	85.7	606	2	Q97A50_THEVO	Q97A50_thermoplaem
901	24	85.7	550	1	HEMA_IADH1	P12582_influenza a	974	24	85.7	606	2	Q54XM6_DICDI	Q54XM6_dictyosteli
902	24	85.7	551	2	Q6Z2W0_ORYSA	Q6Z2W0_oryza sativ	975	24	85.7	608	1	GLPO_STRFN	P35596_streptococc
903	24	85.7	552	2	Q5LTN0_SILPO	Q5LTN0_silicibacte	976	24	85.7	608	2	Q5V345_HALMA	Q5V345_haloarcula
904	24	85.7	553	2	Q4U9L1_THEAN	Q4U9L1_thaieria a	977	24	85.7	608	2	Q4QC9N_LEIMA	Q4QC9N_leishmania
905	24	85.7	553	2	Q5WHJ1_BACSK	Q5WHJ1_bacillus ci	978	24	85.7	609	2	Q8E793_STRAJ	Q8E793_streptococc
906	24	85.7	554	1	COX1A_PARDE	P08305_paracoccu	979	24	85.7	609	2	Q8E1S9_STRAS	Q8E1S9_streptococc
907	24	85.7	554	1	PERF_RAT	P35763_rattus norv	980	24	85.7	611	2	Q6KZT1_PICTO	Q6KZT1_microphilus

981 24 85.7 612 1 GLPO\_STRP3  
 982 24 85.7 612 1 GLPO\_STRP6  
 983 24 85.7 612 1 GLPO\_STRP8  
 984 24 85.7 612 1 GLPO\_STRPY  
 985 24 85.7 612 2 Q4QBB4\_LEIMA  
 986 24 85.7 614 2 Q64DA2\_9ARCH  
 987 24 85.7 615 2 Q9HO66\_HALSA  
 988 24 85.7 616 2 Q4H5N4\_9DEIO  
 989 24 85.7 617 1 CPB1\_CAEJA  
 990 24 85.7 619 1 SELB\_HAEIN  
 991 24 85.7 619 2 Q4QML0\_HAEI8  
 992 24 85.7 619 2 Q65Q14\_MANSM  
 993 24 85.7 623 2 Q8T9F8\_DROWE  
 994 24 85.7 624 2 Q9CK68\_PASWU  
 995 24 85.7 625 2 Q78476\_NEUCR  
 996 24 85.7 626 2 Q9RWJ6\_STAAU  
 997 24 85.7 626 2 Q6GSX3\_STAAS  
 998 24 85.7 626 2 Q6GDA4\_STAAR  
 999 24 85.7 626 2 Q5HCJ6\_STAAC  
 1000 24 85.7 626 2 Q7A2K2\_STAAM

## ALIGNMENTS

RESULT 1  
 Q4S1G2\_TETNG PRELIMINARY; PRT; 95 AA.  
 ID Q4S1G2\_TETNG  
 AC Q4S1G2;  
 DT 13-SEP-2005 (T-EMBLrel. 31, Created)  
 DT 13-SEP-2005 (T-EMBLrel. 31, Last sequence update)  
 DT 13-SEP-2005 (T-EMBLrel. 31, Last annotation update)  
 DE Chromosome 13 SCAR14769, whole genome shotgun sequence.  
 OS ORFNames=GSTENG00025573001;  
 GN Tetraodon nigroviridis (Green puffer).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;  
 OC Tetraodontidae; Tetraodontidae; Tetraodon.  
 OX NCBI\_TaxID=99883;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,  
 RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,  
 RA Nicaud S., Jaffe D., Fisher S., Lufalla G., Dossat C., Segurens B.,  
 RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,  
 RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,  
 RA Blemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,  
 RA Craud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,  
 RA Parra G., Lardier G., Chapple C., McKernan K.J., McSwan P., Bosak S.,  
 RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,  
 RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,  
 RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,  
 RA Wincker P., Lander E.S., Weissenbach J., Roest Crullius H.;  
 RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals  
 the early vertebrate proto-karyotype.";  
 RL Nature 431:946-957(2004).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Genoscope; Whitehead Institute Centre for Genome Research;  
 RG Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.  
 CC -1- CAUTION: The sequence shown here is derived from an  
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 CC preliminary data.  
 DR EMBL; CAAE01014769; 10010 MW; F605503B7359CA25 CRC64;  
 SQ SEQUENCE 95 AA; 10010 MW; F605503B7359CA25 CRC64;

Query Match 100.0%; Score 28; DB 2; Length 95;  
 Best Local Similarity 100.0%; Pred. No. 95;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5  
 |||||

Db 70 HYAMS 74  
 RESULT 2  
 ACP5\_STAAC STANDARD; PRT; 119 AA.  
 ID ACP5\_STAAC  
 AC Q5HED0;  
 DT 13-SEP-2005 (Rel. 48, Created)  
 DT 13-SEP-2005 (Rel. 48, Last sequence update)  
 DT 13-SEP-2005 (Rel. 48, Last annotation update)  
 DE Holo-[acyl-carrier-protein] synthase (EC 2.7.8.7) (Holo-ACP synthase)  
 DE (4'-phosphopantetheinyl transferase acps).  
 GN Name=acps; OrderedLocusNames=SACOL2061;  
 OS Staphylococcus aureus (strain COL).  
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.  
 OX NCBI\_TaxID=93062;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RA Gill S.R., Fouts D.E., Archer G.L., Mongodin E.F., DeBoy R.T.,  
 RA Ravel J., Paulsen I.T., Kolonay J.F., Brinkac L.M., Beanan M.J.,  
 RA Dodson R.J., Daugherty S.C., Madupu R., Angiuoli S.V., Durkin A.S.,  
 RA Haft D.H., Vamathevan J.J., Khouri H., Utterback T.R., Lee C.,  
 RA Dimitrov G., Jiang L., Qin H., Weidman J., Tran K., Kang K.H.,  
 RA Hance I.R., Nelson K.E., Fraser C.M.;  
 RT "Insights on evolution of virulence and resistance from the complete  
 genome analysis of an early methicillin-resistant Staphylococcus  
 aureus strain and a biofilm-producing methicillin-resistant  
 Staphylococcus epidermidis strain.";  
 RL J. Bacteriol. 187:2426-2438(2005).  
 CC -1- FUNCTION: Transfers the 4'-phosphopantetheine moiety from coenzyme  
 CC A to a Ser of acyl-carrier protein (By similarity).  
 CC -1- CATALYTIC ACTIVITY: CoA + apo-[acyl-carrier protein] = adenosine  
 CC 3',5'-bisphosphate + holo-[acyl-carrier protein].  
 CC -1- COFACTOR: Magnesium (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
 CC -1- SIMILARITY: Belongs to the P-Pant transferase superfamily. Acps  
 CC family.  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC -----  
 CC EMBL; CP000046; AAW37023.1; --; Genomic\_DNA.  
 CC TIGR; SACOL2061; --; 1.  
 CC HAMAP; MF\_00101; --; 1.  
 CC InterPro; IPR008278; 4-PPT\_transf.  
 CC InterPro; IPR002582; ACPs.  
 CC InterPro; IPR004568; Pantethn\_trans.  
 CC Pfam; PF01648; ACPs; 1.  
 CC ProDom; PD004282; ACPs; 1.  
 CC TIGRPFAMs; TIGR00516; acps; 1.  
 CC TIGRPFAMs; TIGR00556; pantethn trn; 1.  
 KW Complete proteome; Fatty acid biosynthesis; Lipid synthesis;  
 KW Magnesium; Metal-binding; Transferase.  
 FT METAL 8 59 Magnesium (By similarity).  
 FT METAL 8 59 Magnesium (By similarity).  
 SQ SEQUENCE 119 AA; 13606 MW; 0B828A811774B138 CRC64;  
 Query Match 100.0%; Score 28; DB 1; Length 119;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5  
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 Db 106 HYAMS 110

RESULT 3  
 ACP5\_STAAM STANDARD; PRT; 119 AA.  
 ID ACP5\_STAAM

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AC P63468; Q99514;
AT 28-FEB-2003 (Rel. 41, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DE Holo-[acyl-carrier-protein] synthase (EC 2.7.8.7) (Holo-ACP synthase)
DE (4'-phosphopantetheinyl transferase acps).
GN Name=acps; Synonyms=dpj; OrderedLocNames=SAV2071;
OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158878;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayaashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus.";
RL Lancet 357:1225-1240(2001).
CC -!- FUNCTION: Transfers the 4'-phosphopantetheine moiety from coenzyme
CC A to a Ser of acyl-carrier protein (By similarity).
CC -!- CATALYTIC ACTIVITY: CoA + apo-[acyl-carrier protein] = adenosine
CC 3',5'-bisphosphate + holo-[acyl-carrier protein].
CC -!- COFACTOR: Magnesium (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the P-Pant transferase superfamily. Acps
CC family.
CC
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC removed.
CC -----
CC EMBL; BA000017; BAB58233.1; -; Genomic_DNA.
CC HSSP; P96618; 1F7L.
CC HAMAP; MF 00101; -; 1.
CC InterPro; IPR008278; 4-PPT_transf.
CC InterPro; IPR002582; ACPS_trans.
CC Pfam; PF01648; ACPS; 1.
CC ProDom; PD004282; ACPS; 1.
CC TIGRFAMs; TIGR00516; acps; 1.
CC TIGRFAMs; TIGR00556; pantethn trn; 1.
CC Complete proteome; Fatty acid biosynthesis; Lipid synthesis;
KW Magnesium; Metal-binding; Transferase.
FT METAL 8 8 Magnesium (By similarity).
FT METAL 59 59 Magnesium (By similarity).
SQ SEQUENCE 119 AA; 13634 MW; E2EF3C5A696E7DD2 CRC64;

Query Match 100.0%; Score 28; DB 1; Length 119;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HVAMS 5
DB 106 HVAMS 110

RESULT 4
ACPS_STAN STANDARD; PRT; 119 AA.
ID ACPS_STAN
AT P63468; Q99514;
DT 28-FEB-2003 (Rel. 41, Created)
DE 28-FEB-2003 (Rel. 41, Last sequence update)
DT 13-SEP-2005 (Rel. 45, Last annotation update)
DE Holo-[acyl-carrier-protein] synthase (EC 2.7.8.7) (Holo-ACP synthase)
GN Name=acps; Synonyms=dpj; OrderedLocNames=SA1875;
OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158878;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayaashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus.";
RL Lancet 357:1225-1240(2001).
CC -!- FUNCTION: Transfers the 4'-phosphopantetheine moiety from coenzyme
CC A to a Ser of acyl-carrier protein (By similarity).
CC -!- CATALYTIC ACTIVITY: CoA + apo-[acyl-carrier protein] = adenosine
CC 3',5'-bisphosphate + holo-[acyl-carrier protein].
CC -!- COFACTOR: Magnesium (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the P-Pant transferase superfamily. Acps
CC family.
CC
CC -----
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CC removed.
CC -----
CC EMBL; BA000017; BAB58233.1; -; Genomic_DNA.
CC HSSP; P96618; 1F7L.
CC HAMAP; MF 00101; -; 1.
CC InterPro; IPR008278; 4-PPT_transf.
CC InterPro; IPR002582; ACPS_trans.
CC Pfam; PF01648; ACPS; 1.
CC ProDom; PD004282; ACPS; 1.
CC TIGRFAMs; TIGR00516; acps; 1.
CC TIGRFAMs; TIGR00556; pantethn trn; 1.
CC Complete proteome; Fatty acid biosynthesis; Lipid synthesis;
KW Magnesium; Metal-binding; Transferase.
FT METAL 8 8 Magnesium (By similarity).
FT METAL 59 59 Magnesium (By similarity).
SQ SEQUENCE 119 AA; 13634 MW; E2EF3C5A696E7DD2 CRC64;

Query Match 100.0%; Score 28; DB 1; Length 119;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HVAMS 5
DB 106 HVAMS 110

RESULT 5
ACPS_STAAR STANDARD; PRT; 119 AA.
ID ACPS_STAAR
AT P63468; Q99514;
DT 01-FEB-2005 (Rel. 46, Created)
DE 01-FEB-2005 (Rel. 46, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Holo-[acyl-carrier-protein] synthase (EC 2.7.8.7) (Holo-ACP synthase)
GN Name=acps; Synonyms=dpj; OrderedLocNames=SA1875;
OS Staphylococcus aureus (strain MRSA252).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282458;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=15213324; DOI=10.1073/pnas.0402521101;

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OS Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158879;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayaashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus.";
RL Lancet 357:1225-1240(2001).
CC -!- FUNCTION: Transfers the 4'-phosphopantetheine moiety from coenzyme
CC A to a Ser of acyl-carrier protein (By similarity).
CC -!- CATALYTIC ACTIVITY: CoA + apo-[acyl-carrier protein] = adenosine
CC 3',5'-bisphosphate + holo-[acyl-carrier protein].
CC -!- COFACTOR: Magnesium (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the P-Pant transferase superfamily. Acps
CC family.
CC
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CC removed.
CC -----
CC EMBL; BA000018; BAB43158.1; -; Genomic_DNA.
CC HSSP; P96618; 1F7L.
CC HAMAP; MF 00101; -; 1.
CC InterPro; IPR008278; 4-PPT_transf.
CC InterPro; IPR002582; ACPS_trans.
CC Pfam; PF01648; ACPS; 1.
CC ProDom; PD004282; ACPS; 1.
CC TIGRFAMs; TIGR00516; acps; 1.
CC TIGRFAMs; TIGR00556; pantethn trn; 1.
CC Complete proteome; Fatty acid biosynthesis; Lipid synthesis;
KW Magnesium; Metal-binding; Transferase.
FT METAL 8 8 Magnesium (By similarity).
FT METAL 59 59 Magnesium (By similarity).
SQ SEQUENCE 119 AA; 13634 MW; E2EF3C5A696E7DD2 CRC64;

Query Match 100.0%; Score 28; DB 1; Length 119;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HVAMS 5
DB 106 HVAMS 110

RESULT 5
ACPS_STAAR STANDARD; PRT; 119 AA.
ID ACPS_STAAR
AT P63468; Q99514;
DT 01-FEB-2005 (Rel. 46, Created)
DE 01-FEB-2005 (Rel. 46, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Holo-[acyl-carrier-protein] synthase (EC 2.7.8.7) (Holo-ACP synthase)
GN Name=acps; Synonyms=dpj; OrderedLocNames=SA1875;
OS Staphylococcus aureus (strain MRSA252).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282458;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=15213324; DOI=10.1073/pnas.0402521101;

```

RA Holden M.T.G., Feil E.J., Lindsey J.A., Peacock S.J., Day N.P.J.,  
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,  
RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,  
RA Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,  
RA Felwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jagels K.,  
RA James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,  
RA Ormond D., Quail M.A., Rabinowitsch E., Rutherford K.M., Sanders M.,  
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrall B.G.,  
RA Spratt B.G., Parkhill J.;  
RT "Complete genomes of two clinical *Staphylococcus aureus* strains:  
RT evidence for the rapid evolution of virulence and drug resistance.";  
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).  
CC -!- FUNCTION: Transfers the 4'-phosphopantetheine moiety from coenzyme  
CC A to a Ser of acyl-carrier protein (By similarity).  
CC -!- CATALYTIC ACTIVITY: CoA + apo-[acyl-carrier protein] = adenosine  
CC 3',5'-bisphosphate + holo-[acyl-carrier protein].  
CC -!- COFACTOR: Magnesium (By similarity).  
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
CC -!- SIMILARITY: Belongs to the P-Pant transferase superfamily. Acps  
CC family.  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.  
CC -----  
CC EMBL: BX571856; CAG41140.1; -; Genomic\_DNA.  
CC HAMAP: MF\_00101; -; 1.  
CC InterPro: IPR008278; 4-PPT transf.  
CC InterPro: IPR002582; ACPS\_  
CC InterPro: IPR004568; Pantethn\_trans.  
CC Pfam: PF01648; ACPS; 1.  
CC ProDom: PD004282; ACPS; 1.  
CC TIGRFAMs: TIGR00516; acps; 1.  
CC TIGRFAMs: TIGR00556; pantethn\_trn; 1.  
CC Complete proteome; Fatty acid biosynthesis; Lipid synthesis;  
CC Magnesium; Metal-binding; Transferase.  
CC METAL 8 Magnesium (By similarity).  
CC METAL 59 Magnesium (By similarity).  
CC SEQUENCE 119 AA; 13634 MW; E2EF3C5A696E7DD2 CRC64;  
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CC Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
CC Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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CC QY 1 HYAMS 5  
CC |||||  
CC Db 106 HYAMS 110  
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CC RESULT 6  
CC ACPS STAAAS STANDARD; PRT; 119 AA.  
CC ID ACPS STAAAS STANDARD; PRT; 119 AA.  
CC AC Q6G7N8;  
CC DT 01-FEB-2005 (Rel. 46, Created)  
CC DT 01-FEB-2005 (Rel. 46, Last sequence update)  
CC DT 13-SEP-2005 (Rel. 48, Last annotation update)  
CC DE Holo-[acyl-carrier-protein] synthase (EC 2.7.8.7) (Holo-ACP synthase)  
CC (4'-phosphopantetheinyl transferase acps).  
CC DE Name=acps; Synonyms=dpj; OrderedLocusName=SAS1976;  
CC *Staphylococcus aureus* (strain MSSA476).  
CC OS Bacteria; Firmicutes; Bacillales; *Staphylococcus*.  
CC NCBI\_TaxID=282459;  
CC [1]  
CC NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
CC RP Holden M.T.G., Feil E.J., Lindsey J.A., Peacock S.J., Day N.P.J.,  
CC RA Holden M.T.G., Feil E.J., Lindsey J.A., Peacock S.J., Day N.P.J.,  
CC Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,  
CC Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,  
CC Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,  
CC Felwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jagels K.,  
CC James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,  
CC Ormond D., Quail M.A., Rabinowitsch E., Rutherford K.M., Sanders M.,  
CC Sharp S., Simmonds M., Stevens K., Whitehead S., Barrall B.G.,  
CC Spratt B.G., Parkhill J.;  
CC RT "Complete genomes of two clinical *Staphylococcus aureus* strains:  
CC RT evidence for the rapid evolution of virulence and drug resistance.";  
CC RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).  
CC -!- FUNCTION: Transfers the 4'-phosphopantetheine moiety from coenzyme  
CC A to a Ser of acyl-carrier protein (By similarity).  
CC -!- CATALYTIC ACTIVITY: CoA + apo-[acyl-carrier protein] = adenosine  
CC 3',5'-bisphosphate + holo-[acyl-carrier protein].  
CC -!- COFACTOR: Magnesium (By similarity).  
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
CC -!- SIMILARITY: Belongs to the P-Pant transferase superfamily. Acps  
CC family.  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.  
CC -----  
CC EMBL: BX571856; CAG41140.1; -; Genomic\_DNA.  
CC HAMAP: MF\_00101; -; 1.  
CC InterPro: IPR008278; 4-PPT transf.  
CC InterPro: IPR002582; ACPS\_  
CC InterPro: IPR004568; Pantethn\_trans.  
CC Pfam: PF01648; ACPS; 1.  
CC ProDom: PD004282; ACPS; 1.  
CC TIGRFAMs: TIGR00516; acps; 1.  
CC TIGRFAMs: TIGR00556; pantethn\_trn; 1.  
CC Complete proteome; Fatty acid biosynthesis; Lipid synthesis;  
CC Magnesium; Metal-binding; Transferase.  
CC METAL 8 Magnesium (By similarity).  
CC METAL 59 Magnesium (By similarity).  
CC SEQUENCE 119 AA; 13634 MW; E2EF3C5A696E7DD2 CRC64;  
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CC Query Match 100.0%; Score 28; DB 1; Length 119;  
CC Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
CC Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
CC  
CC QY 1 HYAMS 5  
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CC Db 106 HYAMS 110  
CC  
CC RESULT 7  
CC ACPS STAAAU STANDARD; PRT; 119 AA.  
CC ID ACPS STAAAU STANDARD; PRT; 119 AA.  
CC AC Q9ZAH6;  
CC DT 30-MAY-2000 (Rel. 39, Created)  
CC DT 30-MAY-2000 (Rel. 39, Last sequence update)  
CC DT 13-SEP-2005 (Rel. 48, Last annotation update)  
CC DE Holo-[acyl-carrier-protein] synthase (EC 2.7.8.7) (Holo-ACP synthase)  
CC (4'-phosphopantetheinyl transferase acps).  
CC DE Name=acps; Synonyms=dpj;  
CC *Staphylococcus aureus*.  
CC OS Bacteria; Firmicutes; Bacillales; *Staphylococcus*.  
CC NCBI\_TaxID=1280;  
CC [1]  
CC NUCLEOTIDE SEQUENCE [GENOMIC DNA].  
CC RP STRAIN=NCTC 8325;  
CC RC MEDLINE=98434453; PubMed=9756984; DOI=10.1016/S0378-1119(98)00404-1;  
CC RA Kullik I., Jenni R., Berger-Bachi B.;  
CC RT "Sequence of the putative alanine racemase operon in *Staphylococcus*  
CC *aureus*: insertion of lipoteichoic acid and autolysis.";  
CC RT subunit of lipoteichoic acid and autolysis.";  
CC RL Gene 219:9-17(1998).  
CC -!- FUNCTION: Transfers the 4'-phosphopantetheine moiety from coenzyme  
CC A to a Ser of acyl-carrier protein (By similarity).  
CC -!- CATALYTIC ACTIVITY: CoA + apo-[acyl-carrier protein] = adenosine  
CC 3',5'-bisphosphate + holo-[acyl-carrier protein].  
CC -!- COFACTOR: Magnesium (By similarity).  
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
CC

RA Ormond D., Quail M.A., Rabinowitsch E., Rutherford K.M., Sanders M.,  
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrall B.G.,  
RA Spratt B.G., Parkhill J.;  
RT "Complete genomes of two clinical *Staphylococcus aureus* strains:  
RT evidence for the rapid evolution of virulence and drug resistance.";  
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).  
CC -!- FUNCTION: Transfers the 4'-phosphopantetheine moiety from coenzyme  
CC A to a Ser of acyl-carrier protein (By similarity).  
CC -!- CATALYTIC ACTIVITY: CoA + apo-[acyl-carrier protein] = adenosine  
CC 3',5'-bisphosphate + holo-[acyl-carrier protein].  
CC -!- COFACTOR: Magnesium (By similarity).  
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
CC -!- SIMILARITY: Belongs to the P-Pant transferase superfamily. Acps  
CC family.  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.  
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CC EMBL: BX571857; CAG43783.1; -; Genomic\_DNA.  
CC HAMAP: MF\_00101; -; 1.  
CC InterPro: IPR008278; 4-PPT transf.  
CC InterPro: IPR002582; ACPS\_  
CC InterPro: IPR004568; Pantethn\_trans.  
CC Pfam: PF01648; ACPS; 1.  
CC ProDom: PD004282; ACPS; 1.  
CC TIGRFAMs: TIGR00516; acps; 1.  
CC TIGRFAMs: TIGR00556; pantethn\_trn; 1.  
CC Complete proteome; Fatty acid biosynthesis; Lipid synthesis;  
CC Magnesium; Metal-binding; Transferase.  
CC METAL 8 Magnesium (By similarity).  
CC METAL 59 Magnesium (By similarity).  
CC SEQUENCE 119 AA; 13634 MW; E2EF3C5A696E7DD2 CRC64;  
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CC Query Match 100.0%; Score 28; DB 1; Length 119;  
CC Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
CC Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
CC  
CC QY 1 HYAMS 5  
CC |||||  
CC Db 106 HYAMS 110  
CC  
CC RESULT 7  
CC ACPS STAAU STANDARD; PRT; 119 AA.  
CC ID ACPS STAAU STANDARD; PRT; 119 AA.  
CC AC Q9ZAH6;  
CC DT 30-MAY-2000 (Rel. 39, Created)  
CC DT 30-MAY-2000 (Rel. 39, Last sequence update)  
CC DT 13-SEP-2005 (Rel. 48, Last annotation update)  
CC DE Holo-[acyl-carrier-protein] synthase (EC 2.7.8.7) (Holo-ACP synthase)  
CC (4'-phosphopantetheinyl transferase acps).  
CC DE Name=acps; Synonyms=dpj;  
CC *Staphylococcus aureus*.  
CC OS Bacteria; Firmicutes; Bacillales; *Staphylococcus*.  
CC NCBI\_TaxID=1280;  
CC [1]  
CC NUCLEOTIDE SEQUENCE [GENOMIC DNA].  
CC RP STRAIN=NCTC 8325;  
CC RC MEDLINE=98434453; PubMed=9756984; DOI=10.1016/S0378-1119(98)00404-1;  
CC RA Kullik I., Jenni R., Berger-Bachi B.;  
CC RT "Sequence of the putative alanine racemase operon in *Staphylococcus*  
CC *aureus*: insertion of lipoteichoic acid and autolysis.";  
CC RT subunit of lipoteichoic acid and autolysis.";  
CC RL Gene 219:9-17(1998).  
CC -!- FUNCTION: Transfers the 4'-phosphopantetheine moiety from coenzyme  
CC A to a Ser of acyl-carrier protein (By similarity).  
CC -!- CATALYTIC ACTIVITY: CoA + apo-[acyl-carrier protein] = adenosine  
CC 3',5'-bisphosphate + holo-[acyl-carrier protein].  
CC -!- COFACTOR: Magnesium (By similarity).  
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
CC

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CC CC -!- SIMILARITY: Belongs to the P-Pant transferase superfamily. Acps
CC CC family.
CC CC -----
CC CC This Swiss-Prot entry is copyright. It is produced through a collaboration
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CC CC use as long as its content is in no way modified and this statement is not
CC CC removed.
CC CC -----
CC CC EMBL; Y16431; CAAY6220.1; -; Genomic_DNA.
CC CC HSSP; P96618; 1F7L.
CC CC HAMAP; MF_00101; -; 1.
CC CC InterPro; IPR000278; 4-PPT_transf.
CC CC InterPro; IPR002582; ACPS.
CC CC Pfam; PF01648; ACPS; 1.
CC CC ProDom; PD004282; ACPS; 1.
CC CC TIGRFAMs; TIGR00556; pantethn trn; 1.
CC CC TIGRFAMs; TIGR00516; acps; 1.
CC CC Complete proteome; Fatty acid biosynthesis; Lipid synthesis; Metal-binding;
CC CC Magnesium; Metal-binding; Transferase.
CC CC KW Fatty acid biosynthesis; Lipid synthesis; Magnesium; Metal-binding;
CC CC Transf.
CC CC FT METAL 8 8 Magnesium (By similarity).
CC CC FT METAL 59 59 Magnesium (By similarity).
CC CC SQ SEQUENCE 119 AA; 13606 MW; 0B828A811774B138 CRC64;

Query Match 100.0%; Score 28; DB 1; Length 119;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5
DB 106 HYAMS 110

RESULT 8
ACPS_STAAW STANDARD; PRT; 119 AA.
ID ACPS_STAAW STANDARD; PRT; 119 AA.
AC P63470; Q99S14;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Holo-[acyl-carrier-protein] synthase (EC 2.7.8.7) (Holo-ACP synthase)
DE (4'-phosphopantetheinyl transferase acps).
DE Name=acps; Synonyms=dpj; OrderedLocNames=MW1995;
GN Staphylococcus aureus (strain MW2).
OS Bacteria; Firmicutes; Bacillales; Staphylococcus.
OC NCBI_TaxID=196620;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX MEDLINE=22040717; PubMed=1204378; DOI=10.1016/S0140-6736(02)08713-5;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
RA Yamamoto K., Hiramatsu K.;
RT "Genome and virulence determinants of high virulence community-
RT acquired MRSA.";
RL Lancet 359:1819-1827(2002).
CC -!- FUNCTION: Transfers the 4'-phosphopantetheine moiety from coenzyme
CC A to a Ser of acyl-carrier protein (By similarity).
CC -!- CATALYTIC ACTIVITY: CoA + apo-[acyl-carrier protein] = adenosine
CC 3',5'-bisphosphate + holo-[acyl-carrier protein].
CC -!- COFACTOR: Magnesium (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the P-Pant transferase superfamily. Acps
CC family.
CC -----
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CC CC removed.
CC CC -----
CC CC EMBL; BA000033; BAB95860.1; -; Genomic_DNA.
CC CC HSSP; P96618; 1F7L.
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DR HAMAP; MF_00101; -; 1.
DR InterPro; IPR000278; 4-PPT_transf.
DR InterPro; IPR002582; ACPS.
DR InterPro; IPR004568; Pantethn_trans.
DR Pfam; PF01648; ACPS; 1.
DR ProDom; PD004282; ACPS; 1.
DR TIGRFAMs; TIGR00516; acps; 1.
DR TIGRFAMs; TIGR00556; pantethn trn; 1.
KW Complete proteome; Fatty acid biosynthesis; Lipid synthesis;
KW Magnesium; Metal-binding; Transferase.
FT METAL 8 8 Magnesium (By similarity).
FT METAL 59 59 Magnesium (By similarity).
SQ SEQUENCE 119 AA; 13634 MW; E2EF3C5A696E7DD2 CRC64;

Query Match 100.0%; Score 28; DB 1; Length 119;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5
DB 106 HYAMS 110

RESULT 9
Q4L7V6_STAHJ PRELIMINARY; PRT; 119 AA.
ID Q4L7V6_STAHJ PRELIMINARY; PRT; 119 AA.
AC Q4L7V6;
DT 13-SEP-2005 (TReMBLrel. 31, Created)
DT 13-SEP-2005 (TReMBLrel. 31, Last sequence update)
DE Holo-ACP synthase.
DE Name=dpj; ORFNames=SH0960;
OS Staphylococcus haemolyticus (strain JSC1435).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=279808;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=JSC1435;
RA Takeuchi F., Watanabe S., Baba T., Yuzawa H., Ito T., Cui L.,
RA Morimoto Y., Kuroda M., Takahashi M., Ankaï A., Baba S., Fukui S.,
RA Lee J.C., Hiramatsu K.;
RT "Whole genome sequencing of Staphylococcus haemolyticus uncovers
RT extreme plasticity of its genome and dynamism in the evolution of
RT human-colonizing staphylococcal species.";
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP006716; BAB04269.1; -; Genomic DNA.
SQ SEQUENCE 119 AA; 13732 MW; B12AE9E3B8BB7407 CRC64;

Query Match 100.0%; Score 28; DB 2; Length 119;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5
DB 107 HYAMS 111

RESULT 10
Q4WBD6_ASFPU PRELIMINARY; PRT; 138 AA.
ID Q4WBD6_ASFPU PRELIMINARY; PRT; 138 AA.
AC Q4WBD6;
DT 13-SEP-2005 (TReMBLrel. 31, Created)
DT 13-SEP-2005 (TReMBLrel. 31, Last sequence update)
DE Hypothetical protein.
DE ORFNames=Afu8g01920;
OS Aspergillus fumigatus Af293.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=330879;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Af293;
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RA Niexman W., Pain A., Anderson M.J., Wortman J., Kim H.Stanley.,  
 RA Arroya J., Berrihan M., Abe K., Archer D.B., Bermejo C., Bennett J.,  
 RA Bowyer P., Chen D., Collins M., Coulson R., Davies R., Dyer P.S.,  
 RA Farman M., Fedorova N., Fedorova N., Feldblyum T.V., Fischer R.,  
 RA Foster N., Fraser A., Garcia J.B., Garcia M.J., Goble A.,  
 RA Goldman G.H., Gomi K., Griffith-Jones S., Gwilliam R., Haas B.,  
 RA Haas H., Harris D., Horiuchi H., Huang J., Humphrey S., Jimenez J.,  
 RA Keller N., Khouri H., Kitamoto K., Kobayashi T., Kulkarni R.,  
 RA Kumagai T., Lafton A., Latge J.-P., Li W., Lord A., Lu C.,  
 RA Majoros W.H., May G.S., Miller B.L., Mohamoud Y., Molina M., Monod M.,  
 RA Mouyna I., Mulligan S., Murphy L., O'Neil S., Paulsen I.,  
 RA Penava M.A., Perteau M., Price C., Pritchard B.L., Quail M.A.,  
 RA Rabinowitz E., Rawlins N., Rajandream M.-A., Reichard U.,  
 RA Renauld H., Robson G.D., Rodriguez de Cordoba S., Rodriguez-Pena J.M.,  
 RA Renning C.M., Rutter S., Salzberg S.L., Sanchez M.,  
 RA Sanchez-Ferrero J.C., Saunders D., Seeger K., Squares R., Squares S.,  
 RA Takeuchi M., Tekaita F., Turner G., Vazquez de Aldana C.R., Weidman J.,  
 RA White O., Woodward J., Yu J.-H., Fraser C., Galagan J.E., Asai K.,  
 RA Machida M., Hall N., Barrell B., Denning D.W.,  
 RA "Genomic sequence of the pathogenic and allergenic filamentous fungus  
 RT Aspergillus fumigatus";  
 RL Submitted (May-2005) to the EMBL/GenBank/DBJ databases.  
 CC -!- CAUTION: The sequence shown here is derived from an  
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 CC preliminary data.  
 DR EMBL; AAHF01000014; EAL84976.1; -; Genomic\_DNA.  
 KW Hypothetical protein.  
 SQ SEQUENCE 138 AA; 15418 MW; 3512244A19E4B8C8 CRC64;

Query Match 100.0%; Score 28; DB 2; Length 138;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5  
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 DB 61 HYAMS 65

RESULT 11  
 OS9831\_PYRHO PRELIMINARY; PRT; 143 AA.  
 ID O58831;  
 AC O58831;  
 DT 01-AUG-1998 (TrEMBLrel. 07, Created)  
 DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Hypothetical protein PH1104.  
 GN OrderedLocusNames=PH1104;  
 OS Pyrococcus horikoshii.  
 OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;  
 OC Pyrococcus.  
 OC Pyrococcus.  
 OX NCBI\_TaxID=53953;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=OT3;  
 RX MEDLINE=98344137; PubMed=9679194;  
 RA Kawarabayasi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,  
 RA Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,  
 RA Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,  
 RA Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,  
 RA Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,  
 RA Masuchi Y., Shizuya H., Kikuchi H.,  
 RA "Complete sequence and gene organization of the genome of a hyper-  
 RT thermophilic archaeobacterium, Pyrococcus horikoshii OT3.";  
 RL DNA Res. 5:555-76(1998).  
 DR EMBL; BA000001; BAA30203.1; -; Genomic\_DNA.  
 DR PIR; A71051; A71051.  
 KW Complete proteome; Hypothetical protein.  
 SQ SEQUENCE 143 AA; 16220 MW; 48B66A1605A866E1 CRC64;

Query Match 100.0%; Score 28; DB 2; Length 143;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5  
 |||||  
 DB 128 HYAMS 132

RESULT 12  
 OS9YBD5\_BRUME PRELIMINARY; PRT; 146 AA.  
 ID Q8YBD5;  
 AC Q8YBD5;  
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE PSEUDOAZURIN.  
 GN OrderedLocusNames=BMEII0965;  
 OS Brucella melitensis.  
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
 OC Brucellaceae; Brucella.  
 OX NCBI\_TaxID=29459;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RC STRAIN=16M / ATCC 23456 / Biotype 1;  
 RX PubMed=11756688; DOI=10.1073/pnas.221575398;  
 RA DelVecchio V.G., Kapatral V., Redkar R.J., Patra G., Muejer C., Los T.,  
 RA Ivanova N., Anderson I., Bhattacharyya A., Lykidis A., Reznik G.,  
 RA Jablonaki L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltzman E.,  
 RA Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,  
 RA Haselkorn R., Kyrpides N.C., Overbeek R.,  
 RA "The genome sequence of the facultative intracellular pathogen  
 RT Brucella melitensis.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).  
 DR EMBL; AE009729; AAL54207.1; -; Genomic\_DNA.  
 DR PIR; AD3630; AD3630.  
 DR HSP; P04377; 1PAZ.  
 DR SMR; Q8YBD5; 24-143.  
 DR GO; GO:0005507; F:copper ion binding; IEA.  
 DR GO; GO:0005489; P:electron transporter activity; IEA.  
 DR GO; GO:0006118; P:electron transport; IEA.  
 DR InterPro; IPR002386; Amicyanin.  
 DR InterPro; IPR000923; BlueCu 1.  
 DR InterPro; IPR001235; Copper\_blue.  
 DR InterPro; IPR011572; Copper\_bind; 1.  
 DR Pfam; PF00127; Copper\_bind; 1.  
 DR PRINTS; PR00155; AMICYANIN.  
 DR PRINTS; PR00156; COPPERBLUE.  
 DR ProDom; PD001235; Copper\_blue\_sub; 1.  
 KW Complete proteome.  
 SQ SEQUENCE 146 AA; 15897 MW; 36ADAA0FEE6915E6 CRC64;

Query Match 100.0%; Score 28; DB 2; Length 146;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5  
 |||||  
 DB 104 HYAMS 108

RESULT 13  
 OS9RI70\_STRCO PRELIMINARY; PRT; 185 AA.  
 ID Q9RI70;  
 AC Q9RI70;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Putative aminoglycoside nucleotidyltransferase.  
 GN OrderedLocusNames=SCO0107; ORFNames=SCU11.36c;  
 OS Streptomyces coelicolor.  
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 OC Streptomycineae; Streptomycetaceae; Streptomyces.  
 OX NCBI\_TaxID=1902;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=A3(2) / M145;

```

RX MEDLINE=21996410; PubMed=12000953; DOI=10.1038/417141a;
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kieser T., Larke L., Murphy L.D., Oliver K., O'Neill S.,
RA Rabinowitsch E., Rajandream M.A., Rutherford K.M., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor J.,
RA Warren T., Wietzorrek A., Woodward J.R., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
RT coelicolor A3(2).";
RL Nature 417:141-147(2002).
DR EMBL; AL939104; CAB52921.1; -; Genomic_DNA.
DR PIR; T37007; T37007
DR GO; GO:0016740; F:transferase activity; IEA.
DR InterPro; IPR000669; Mannitol_dh.
DR PROSITE; PS00974; MANNITOL_DHGENASS; UNKNOWN_1.
KW Complete proteome; Transferase.
SQ SEQUENCE 185 AA; 20294 MW; B08AEFD1F4B12C31 CRC64;

Query Match 100.0%; Score 28; DB 2; Length 185;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5
DB 14 HYAMS 18

RESULT 14
Q6M194_METWP
ID Q6M194_METWP PRELIMINARY; PRT; 274 AA.
AC Q6M194;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
GN OrderedLocNames=MWP0023;
OS Methanococcus maripaludis.
OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC Methanococcaceae; Methanococcus.
OC NCBI_TaxID=39152;
RN [1]_TaxID=39152;
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=S2 / LL;
RX PubMed=15466049; DOI=10.1126/JB.186.20.6956-6969.2004;
RA Hendrickson E.L., Kaul R., Zhou Y., Bovee D., Chapman P., Chung J.,
RA Conway de Macario E., Dodsworth J.A., Gillett W., Graham D.E.,
RA Hackett M., Haydock A.K., Kang A., Land M.L., Levy R., Lie T.J.,
RA Major T.A., Moore B.C., Porat I., Palmeiri A., Rouse G.,
RA Saenphimmachak C., Soell D., Van Dien S., Wang T., Whitman W.B.,
RA Xia Q., Zhang Y., Larimer F.W., Olson M.V., Leigh J.A.;
RT "Complete genome sequence of the genetically tractable
RT hydrogeotrophic methanogen Methanococcus maripaludis.";
RL J. Bacteriol. 186:6956-6969(2004).
DR EMBL; BX957219; CAF29579.1; -; Genomic_DNA.
DR InterPro; IPR002825; DUF114.
DR Pfam; PF01972; DUF114; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 274 AA; 31452 MW; E0CD99AD6B8848B9 CRC64;

Query Match 100.0%; Score 28; DB 2; Length 274;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5
DB 120 HYAMS 124

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RESULT 15  
Q5S199\_THET8

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ID Q5S199_THET8 PRELIMINARY; PRT; 275 AA.
AC Q5S199;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Hypothetical protein TTHA1475.
GN OrderedLocNames=TTHA1475;
OS Thermus thermophilus (strain HB8 / ATCC 27634 / DSM 579).
OC Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
OC Thermus.
OX NCBI_TaxID=300852;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=HB8;
RA Masui R., Kurokawa K., Nakagawa N., Tokunaga F., Koyana Y.,
RA Shibata T., Oshima T., Yokoyama S., Yasunaga T., Kuramitsu S.;
RT "Complete genome sequence of Thermus thermophilus HB8.";
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP008226; BAD71298.1; -; Genomic_DNA.
DR InterPro; IPR002825; DUF114.
DR Pfam; PF01972; DUF114; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 275 AA; 31023 MW; 49DED4A2079256F5 CRC64;

Query Match 100.0%; Score 28; DB 2; Length 275;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5
DB 121 HYAMS 125

RESULT 16
Q72IM1_THET2
ID Q72IM1_THET2 PRELIMINARY; PRT; 275 AA.
AC Q72IM1;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Periplasmic serine protease.
GN OrderedLocNames=TTCl111;
OS Thermus thermophilus (strain HB27 / ATCC BAA-163 / DSM 7039).
OC Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
OC Thermus.
OX NCBI_TaxID=262724;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15064768; DOI=10.1038/nbt956;
RA Henne A., Brueggemann H., Raasch C., Wieser A., Hartsch T.,
RA Liebegang H., Johann A., Lienard T., Gohl O., Martinez-Arias R.,
RA Jacobi C., Starkuviene V., Schlenceck S., Dencker S., Huber R.,
RA Klensk H.-P., Kramer W., Merkl R., Gottschalk G., Fritz H.-J.;
RT "The genome sequence of the extreme thermophile Thermus
RT thermophilus.";
RL Nat. Biotechnol. 22:547-553(2004).
DR EMBL; AF017304; AAS81453.1; -; Genomic DNA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR InterPro; IPR002825; DUF114.
DR Pfam; PF01972; DUF114; 1.
KW Complete proteome; Protease.
SQ SEQUENCE 275 AA; 31051 MW; EF05B9130D12FEF2 CRC64;

Query Match 100.0%; Score 28; DB 2; Length 275;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5
DB 121 HYAMS 125

RESULT 17

```



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Q5JFF4 PYRKO
ID Q5JFF4 PYRKO PRELIMINARY; PRT; 280 AA.
AC Q5JFF4_
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=TK0130;
OS Pyrococcus kodakaraensis (Thermococcus kodakaraensis).
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Thermococcus.
NCBI_TaxID=69014;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=KOD1;
RX PubMed=15710748; DOI=10.1101/gr.3003105;
RA Fukui T., Atomi H., Kanai T., Matsumi R., Fujiwara S., Imanaka T.;
RT "Complete genome sequence of the hyperthermophilic archaeon
RT Thermococcus kodakaraensis KOD1 and comparison with Pyrococcus
RT genomes.";
RL Genome Res. 15:352-363(2005).
DR EMBL; BAD84319.1; -; Genomic DNA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR002825; DUF114.
DR InterPro; IPR002142; Peptidase_S49.
DR Pfam; PF01972; DUF114; 1.
DR ProDom; PD002897; Peptidase_S49; 1.
DR Complete proteome; Hypothetical protein.
SQ SEQUENCE 280 AA; 31521 MW; BBE521F46EE4BC37 CRC64;

Query Match 100.0%; Score 28; DB 2; Length 280;
Best Local Similarity 100.0%; Pred. No. 2.9e+02; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0;

QY 1 HYAMS 5
DB 126 HYAMS 130

RESULT 18
Q8U454 PYRFU
ID Q8U454 PYRFU PRELIMINARY; PRT; 280 AA.
AC Q8U454_
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical protein PF0240.
GN OrderedLocusNames=PF0240;
OS Pyrococcus furiosus.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus.
NCBI_TaxID=2261;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Vc1 / DSM 3638 / ATCC 43587 / JCM 8422;
RA Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.;
RT "The complete sequence of the Pyrococcus furiosus genome.";
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB010149; AAL80364.1; -; Genomic_DNA.
DR InterPro; IPR002825; DUF114.
DR Pfam; PF01972; DUF114; 1.
DR Complete proteome.
SQ SEQUENCE 280 AA; 31627 MW; 451EFAA1057C4579 CRC64;

Query Match 100.0%; Score 28; DB 2; Length 280;
Best Local Similarity 100.0%; Pred. No. 2.9e+02; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0;

QY 1 HYAMS 5
DB 126 HYAMS 130
```

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RESULT 19
Q9V218 PYRAB
ID Q9V218 PYRAB PRELIMINARY; PRT; 280 AA.
AC Q9V218_
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=PYRAB02560; ORFNames=PAB2437;
OS Pyrococcus abyssi.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus.
NCBI_TaxID=29292;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=GES / Orsay;
RX MEDLINE=22511545; PubMed=12622808;
RX DOI=10.1046/j.1365-2958.2003.03381.x;
RA Cohen G.N., Barbe V., Flament D., Galperin M., Heilig R., Lecompte O.,
RA Poch O., Prieur D., Querellou J., Ripp R., Thierry J.-C.,
RA Van der Oost J., Weissenbach J., Zivanovic Y., Forterre P.;
RT "An integrated analysis of the genome of the hyperthermophilic
RT archaeon Pyrococcus abyssi.";
RL Mol. Microbiol. 47:1495-1512(2003).
DR EMBL; AJ248283; CAB49180.1; -; Genomic_DNA.
DR PIR; E75216; E75216.
DR InterPro; IPR002825; DUF114.
DR Pfam; PF01972; DUF114; 1.
DR Complete proteome; Hypothetical protein.
KW SEQUENCE 280 AA; 31874 MW; 04DA90632B363177 CRC64;

Query Match 100.0%; Score 28; DB 2; Length 280;
Best Local Similarity 100.0%; Pred. No. 2.9e+02; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0;

QY 1 HYAMS 5
DB 126 HYAMS 130

RESULT 20
Q58020 PYRHO
ID Q58020 PYRHO PRELIMINARY; PRT; 280 AA.
AC Q58020_
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein PH0282.
GN OrderedLocusNames=PH0282;
OS Pyrococcus horikoshii.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus.
NCBI_TaxID=53953;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=OT3;
RX MEDLINE=98344137; PubMed=9679194;
RX Kawarabayashi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
RX Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
RX Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
RX Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,
RX Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
RX Masuchi Y., Shizuya H., Kikuchi H.;
RT "Complete sequence and gene organization of the genome of a hyper-
RT thermophilic archaeobacterium, Pyrococcus horikoshii OT3.";
RL DNA Res. 5:55-76(1998).
DR EMBL; BA000001; BAA29354.1; -; Genomic_DNA.
DR PIR; C71453; C71453.
DR InterPro; IPR002825; DUF114.
DR Pfam; PF01972; DUF114; 1.
DR Complete proteome; Hypothetical protein.
KW SEQUENCE 280 AA; 31784 MW; 6A8D616ED465D375 CRC64;
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Query Match 100.0%; Score 28; DB 2; Length 280;  
 Best Local Similarity 100.0%; Pred. No. 2.9e+02; Mismatches 0; Indels 0; Gaps 0;  
 Matches 5; Conservative 0

QY 1 HYAMS 5  
 |||||  
 Db 126 HYAMS 130

## RESULT 21

Q9X018 THEME PRELIMINARY; PRT; 284 AA.  
 AC Q9X018;  
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Hypothetical protein.  
 GN OrderedLocusNames=TM0916;  
 OS Thermotoga maritima.  
 OC Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga.  
 OX NCBI\_TaxID=2336;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=MSB8 / DSM 3109 / ATCC 43589;  
 RX MEDLINE=99287316; PubMed=10360571; DOI=10.1038/20601;  
 RA Nelson K.E., Clayton R.A., Gill S.R., Gwin M.L., Dodson R.J.,  
 Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,  
 McDonald L.A., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,  
 Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.L.,  
 Heidelberg J.F., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,  
 Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;  
 RT "Evidence for lateral gene transfer between Archaea and Bacteria from  
 genome sequence of Thermotoga maritima."  
 RL Nature 399:323-329 (1999).  
 RL EMBL; AE001755; AAD35997.1; -; Genomic\_DNA.  
 DR PIR; C72320; C72320.  
 DR TIGR; TM0916; -;  
 DR GO; GO:0008233; F:peptidase activity; IEA.  
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.  
 DR InterPro; IPR002825; DUF114.  
 DR InterPro; IPR002142; Peptidase\_S49.  
 DR Pfam; PF01972; DUF114; 1.  
 DR ProDom; PD002897; Peptidase\_S49; 1.  
 KW Complete proteome; Hypothetical protein.  
 SQ SEQUENCE 284 AA; 32142 MW; 2D0B0B47CDF66121 CRC64;

Query Match 100.0%; Score 28; DB 2; Length 284;  
 Best Local Similarity 100.0%; Pred. No. 2.9e+02; Mismatches 0; Indels 0; Gaps 0;  
 Matches 5; Conservative 0

QY 1 HYAMS 5  
 |||||  
 Db 125 HYAMS 129

## RESULT 22

Y137 METJA  
 ID Y137 METJA STANDARD; PRT; 286 AA.  
 AC Q57601;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 10-MAY-2005 (Rel. 47, Last annotation update)  
 DE Hypothetical protein MJ0137.  
 GN OrderedLocusNames=MJ0137;  
 OS Methanococcus jannaschii.  
 OC Archaea; Euryarchaeota; Methanococci; Methanococcales;  
 OC Methanocaldococcaceae; Methanocaldococcus.  
 OX NCBI\_TaxID=2190;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;  
 RX MEDLINE=96337999; PubMed=8688087;

RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,  
 RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,  
 RA Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,  
 RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,  
 RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,  
 RA Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,  
 RA Cotton M.D., Roberts K.M., Hrust M.A., Kaine B.P., Borodovsky M.,  
 RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;  
 RT "Complete genome sequence of the methanogenic archaeon, Methanococcus  
 jannaschii."  
 RL Science 273:1058-1073 (1996).  
 CC -; SIMILARITY: To M.jannaschii MJ1495.  
 CC -----  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
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 CC removed.  
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DR EMBL; U67471; AAB98120.1; -; Genomic\_DNA.  
 DR PIR; A64317; A64317.  
 DR TIGR; MJ0137; -;  
 DR InterPro; IPR002825; DUF114.  
 DR Pfam; PF01972; DUF114; 1.  
 KW Complete proteome; Hypothetical protein; Transmembrane.  
 FT TRANSMEM 8  
 SQ SEQUENCE 286 AA; 32166 MW; A43DD345B569C55F CRC64;

Query Match 100.0%; Score 28; DB 1; Length 286;  
 Best Local Similarity 100.0%; Pred. No. 3e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5  
 |||||  
 Db 131 HYAMS 135

## RESULT 23

O66996 AQUAE PRELIMINARY; PRT; 288 AA.  
 AC O66996;  
 DT 01-AUG-1998 (TrEMBLrel. 07, Created)  
 DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Hypothetical protein aq\_814.  
 GN OrderedLocusNames=AQ\_814;  
 OS Aquifex aeolicus.  
 OC Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.  
 OX NCBI\_TaxID=63363;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=VFS;  
 RX MEDLINE=98196666; PubMed=9537320; DOI=10.1038/32831;  
 RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,  
 RA Graham D.E., Overbeek R., Snead M.A., Keller M., Aufay M., Huber R.,  
 RA Feldman R.A., Short J.M., Olsen G.J., Swanson R.V.;  
 RT "The complete genome of the hyperthermophilic bacterium Aquifex  
 aeolicus."  
 RL Nature 392:353-358 (1998).  
 RL EMBL; AE000708; AAC06959.1; -; Genomic\_DNA.  
 DR PIR; A70371; A70371.  
 DR InterPro; IPR002825; DUF114.  
 DR Pfam; PF01972; DUF114; 1.  
 KW Complete proteome.  
 SQ SEQUENCE 288 AA; 32624 MW; 3D862535B32AF730 CRC64;

Query Match 100.0%; Score 28; DB 2; Length 288;  
 Best Local Similarity 100.0%; Pred. No. 3e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5  
 |||||  
 Db 128 HYAMS 132

RG US DOE Joint Genome Institute (JGI-PGF);  
RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler C., Glavina T.,  
RA Hammon N., Ibrani S., Pitluck S., Richardson P.;

Query Match 100.0%; Score 28; DB 1; Length 292;  
 Best Local Similarity 100.0%; Pred. No. 3e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5  
 DB 135 HYAMS 139

## RESULT 27

Q4UVS4 XANCP  
 ID Q4UVS4\_XANCP PRELIMINARY; PRT; 292 AA.  
 AC Q4UVS4;  
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
 DE Hypothetical protein.  
 GN ORFNames=XC1786;  
 OS Xanthomonas campestris pv. campestris str. 8004.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;  
 OC Xanthomonadaceae; Xanthomonas.  
 OX NCBI\_TaxID=314565;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=8004;  
 RA Qian W., Jia Y.-T., Ren S.-X., He Y.-Q., Feng J.-X., Lu L.-F.,  
 RA Sun Q.-H., Ying G., Tang D.-J., Wu W., Wang L.-F., Jiang B.-L.,  
 RA Zeng S.-Y., Gu W.-Y., Lu G., Rong L., Tian Y.-C., Yao Z.-J., Fu G.,  
 RA Chen B.-S., Fang R.-X., Qiang B.-Q., Chen Z., Zhao G.-P., Tang J.-L.,  
 RA He C.-Z.;  
 RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; CP000050; AY48849.1; -; Genomic\_DNA.  
 KW Hypothetical protein.  
 SQ SEQUENCE 292 AA; 31427 MW; 24A2E29CEA2A858 CRC64;

Query Match 100.0%; Score 28; DB 2; Length 292;  
 Best Local Similarity 100.0%; Pred. No. 3e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5  
 DB 70 HYAMS 74

## RESULT 28

Q8P8B3 XANCP  
 ID Q8P8B3\_XANCP PRELIMINARY; PRT; 292 AA.  
 AC Q8P8B3;  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE Hypothetical protein XCC2330.  
 GN OrderedLocusNames=XCC2330;  
 OS Xanthomonas campestris [pv. campestris].  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;  
 OC Xanthomonadaceae; Xanthomonas.  
 OX NCBI\_TaxID=340;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=ATCC 33913 / NCPPB 528;  
 RX MEDLINE=22022145; PubMed=12024217; DOI=10.1038/417459a;  
 RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,  
 RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A.,  
 RA Almeida N.E., Jr., Alves L.M.C., do Amaral A.M., Bertolini M.C.,  
 RA Camargo L.E.A., Camarotte G., Cannavan F., Cardozo J., Chambergo F.,  
 RA Ciapina L.P., Ciccarelli R.M.B., Coutinho L.L., Cursino-Santos J.R.,  
 RA El-Dorri H., Faria J.B., Ferreira A.J.S., Ferreira R.C.C.,  
 RA Ferro M.I.T., Fornighieri E.F., Franco M.C., Greggio C.C., Gruber A.,  
 RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,  
 RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,  
 RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,  
 RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,  
 RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,

RA Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,  
 RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,  
 RA Setubal J.C., Kitajima J.P.;  
 RT "Comparison of the genomes of two Xanthomonas pathogens with differing  
 host specificities";  
 RL Nature 417:459-463(2002).  
 DR EMBL; AE012341; AAM41608.1; -; Genomic\_DNA.  
 KW Complete proteome; Hypothetical protein.  
 SQ SEQUENCE 292 AA; 31426 MW; 24A2E29CEA2A858 CRC64;

Query Match 100.0%; Score 28; DB 2; Length 292;  
 Best Local Similarity 100.0%; Pred. No. 3e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5  
 DB 70 HYAMS 74

## RESULT 29

Q9Y9S6 AERPE  
 ID Q9Y9S6\_AERPE PRELIMINARY; PRT; 295 AA.  
 AC Q9Y9S6;  
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Hypothetical protein APE2212.  
 GN OrderedLocusNames=APE2212;  
 OS Aeropyrum pernix.  
 OC Archaea; Crenarchaeota; Thermoprotei; Desulfurococcales;  
 OC Desulfurococaceae; Aeropyrum.  
 OX NCBI\_TaxID=56636;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=K1;  
 RX MEDLINE=99310339; PubMed=10382966;  
 RA Kavarabayasi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y.,  
 RA Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kosugi H.,  
 RA Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,  
 RA Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y.,  
 RA Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Kubota K.,  
 RA Nakamura Y., Nomura N., Sako Y., Kikuchi H.;  
 RT "Complete genome sequence of an aerobic hyper-thermophilic  
 crenarchaeon, Aeropyrum pernix K1";  
 RL DNA Res. 6:83-101(1999).  
 DR EMBL; BA000002; BAA81224.1; -; Genomic\_DNA.  
 DR PIR; H72529; H72529.  
 DR InterPro; IPR002825; DUF114.  
 DR Pfam; PF01972; DUF114; 1.  
 KW Complete proteome; Hypothetical protein.  
 SQ SEQUENCE 295 AA; 32651 MW; 64D00C0E5C8D439 CRC64;

Query Match 100.0%; Score 28; DB 2; Length 295;  
 Best Local Similarity 100.0%; Pred. No. 3e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5  
 DB 129 HYAMS 133

## RESULT 30

Q8YQJ8 ANASP  
 ID Q8YQJ8\_ANASP PRELIMINARY; PRT; 297 AA.  
 AC Q8YQJ8;  
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Alr3825 protein.  
 GN OrderedLocusNames=alr3825;  
 OS Anabaena sp. (strain PCC 7120).  
 OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.  
 OX NCBI\_TaxID=103690;

```

RN NUCLEOTIDE SEQUENCE.
RX MEDLINE=21595285; PubMed=11759840;
RA Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
RA Watanabe A., Iriiguchi M., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kohara M., Matsumoto M., Matsumoto A., Muraki A.,
RA Nakazaki N., Shimo S., Sugimoto M., Takazawa M., Yamada M.,
RA Yasuda M., Tabata S.,
RT "Complete genomic sequence of the filamentous nitrogen-fixing
RT cyanobacterium Anabaena sp. strain PCC 7120.";
RL DNA Res. 8:205-213 (2001).
DR EMBL; BA000019; BAB75524.1; -; Genomic_DNA.
DR PIR; AB2284; AB2284.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0005508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR002825; DUF114.
DR InterPro; IPR002142; Peptidase_S49.
DR Pfam; PF01972; DUF114; 1.
DR ProDom; PD002897; Peptidase_S49; 1.
KW Complete proteome.
SQ SEQUENCE 297 AA; 33313 MW; 927BBF4D2BF29D1A CRC64;

Query Match 100.0%; Score 28; DB 2; Length 297;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5
DB 122 HYAMS 126

RESULT 31
QSNMN3_ZYMO
ID QSNMN3_ZYMO PRELIMINARY; PRT; 337 AA.
AC QSNMN3;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Membrane protein.
GN OrderedLocusNames=ZM01403;
OS Zymomonas mobilis.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Sphingomonadales;
OC Sphingomonadaceae; Zymomonas.
OX NCBI_TaxID=542;
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=ATCC 31821 / ZM4 / CP4;
RX PubMed=1592456; DOI=10.1038/nbt1045;
RA Seo J.-S., Chong H., Park H.S., Yoon K.-O., Jung C., Kim J.J.,
RA Hong J.H., Kim H., Kim J.-H., Kil J.-I., Park C.J., Oh H.-M.,
RA Lee J.-S., Jin S.-J., Um H.-W., Lee H.-J., Oh S.-J., Kim J.Y.,
RA Kang H.B., Lee S.X., Lee K.J., Kang H.S.;
RT "The genome sequence of the ethanologenic bacterium Zymomonas mobilis
RT ZM4.";
RL Nat. Biotechnol. 23:63-68 (2005).
DR EMBL; AE008692; AAU90027.1; -; Genomic_DNA.
DR GO; GO:0004222; F:metalloendopeptidase activity; IEA.
DR GO; GO:0005508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR002886; Peptidase_M23B.
DR Pfam; PF01551; Peptidase_M23; 1.
KW Complete proteome.
SQ SEQUENCE 337 AA; 36470 MW; 05E56803AA5160E2 CRC64;

Query Match 100.0%; Score 28; DB 2; Length 337;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5
DB 108 HYAMS 112

RESULT 32
QSNMN3_ZYMO
ID QSNMN3_ZYMO PRELIMINARY; PRT; 337 AA.
AC QSNMN3;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Membrane protein.
GN OrderedLocusNames=ZM01403;
OS Zymomonas mobilis.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Sphingomonadales;
OC Sphingomonadaceae; Zymomonas.
OX NCBI_TaxID=542;
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=ATCC 31821 / ZM4 / CP4;
RX PubMed=1592456; DOI=10.1038/nbt1045;
RA Seo J.-S., Chong H., Park H.S., Yoon K.-O., Jung C., Kim J.J.,
RA Hong J.H., Kim H., Kim J.-H., Kil J.-I., Park C.J., Oh H.-M.,
RA Lee J.-S., Jin S.-J., Um H.-W., Lee H.-J., Oh S.-J., Kim J.Y.,
RA Kang H.B., Lee S.X., Lee K.J., Kang H.S.;
RT "The genome sequence of the ethanologenic bacterium Zymomonas mobilis
RT ZM4.";
RL Nat. Biotechnol. 23:63-68 (2005).
DR EMBL; AE008692; AAU90027.1; -; Genomic_DNA.
DR GO; GO:0004222; F:metalloendopeptidase activity; IEA.
DR GO; GO:0005508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR002886; Peptidase_M23B.
DR Pfam; PF01551; Peptidase_M23; 1.
KW Complete proteome.
SQ SEQUENCE 337 AA; 36470 MW; 05E56803AA5160E2 CRC64;

Query Match 100.0%; Score 28; DB 1; Length 345;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5
DB 137 HYAMS 141

RESULT 33
QSNMN3_ZYMO
ID QSNMN3_ZYMO PRELIMINARY; PRT; 424 AA.
AC QSNMN3;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Na+/H+ antiporter NhaP.
GN Name=nhaP; OrderedLocusNames=PA3887;
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;

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RA Bremer M.;
RT "Primary structure and evolution of intermediate filament proteins
RL from the lungfish Protopterus aethiopicus.";
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ785790; CAH05046.1; -; mRNA.
DR GO; GO:0003882; C:intermediate filament; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR001664; IF.
DR InterPro; IPR002957; Keratin I.
DR Pfam; PF00038; Filament; I.
DR PRINTS; PR01248; TYPEIKERATIN.
KW Keratin.
SQ SEQUENCE 456 AA; 49809 MW; 8B30D2AB26DF78BC CRC64;

Query Match 100.0%; Score 28; DB 2; Length 456;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5
Db |||||
4 HYAMS 8

RESULT 37
ID Q89UC7_BRAJA PRELIMINARY; PRT; 464 AA.
AC Q89UC7;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Bll1490 protein.
GN OrderedLocusNames=bll1490;
OS Bradyrhizobium japonicum.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bradyrhizobiaceae; Bradyrhizobium.
OX NCBI_TaxID=375;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=USDA 110;
RX MEDLINE=22484998; PubMed=12597275;
RA Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
RA Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
RA Kohara M., Matsumoto M., Shimo S., Tsuruoka H., Wada T., Yamada M.,
RA Tabata S.;
RT "Complete genomic sequence of nitrogen-fixing symbiotic bacterium
RT Bradyrhizobium japonicum USDA110.";
RL DNA Res. 9:189-197(2002).
DR EMBL; BA000040; BAC46755.1; -; Genomic_DNA.
KW Complete proteome.
SQ SEQUENCE 464 AA; 50203 MW; 733DFC702255DD3E CRC64;

Query Match 100.0%; Score 28; DB 2; Length 464;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5
Db |||||
309 HYAMS 313

RESULT 38
DNAME LEIXX
ID DNAME LEIXX STANDARD; PRT; 473 AA.
AC Q6AHN6;
DT 10-MAY-2005 (Rel. 47, Created)
DT 10-MAY-2005 (Rel. 47, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Chromosomal replication initiator protein dnaA.
GN Name=dnaA; OrderedLocusNames=Lxx00010;
OS Leifsonia xyl (subsp. xyl).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Micrococccineae; Microbacteriaceae; Leifsonia.

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OX NCBI_TaxID=59736;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=CTCB07;
RX PubMed=15305603;
RA Monteiro-Vitorello C.B., Camargo L.E.A., Van Sluys M.A.,
RA Kitajima J.P., Truffi D., do Amaral A.M., Harakava R.,
RA de Oliveira J.C.F., Wood D., de Oliveira M.C., Miyaki C.Y.,
RA Takita M.A., da Silva A.C.R., Furlan L.R., Cartaro D.M., Camarotte G.,
RA Almeida N.F. Jr., Carrer H., Coutinho L.L., El-Doroty H.A.,
RA Ferri M.I.T., Gagliardi P.R., Gigliotti E., Goldman M.H.S.,
RA Goldman G.H., Kimura E.T., Ferro E.S., Kuramae E.E., Lemos E.G.M.,
RA Lemos M.V.F., Mauro S.M.Z., Machado M.A., Marino C.L., Menck C.F.,
RA Nunes L.R., Oliveira R.C., Pereira G.G., Siqueira W., de Souza A.A.,
RA Tsai S.M., Zanca A.S., Simpson A.J.G., Brumley S.M., Setubal J.C.;
RT "The genome sequence of the Gram-positive sugarcane pathogen Leifsonia
RT xyl subsp. xyl";
RL Mol. Plant Microbe Interact. 17:827-836(2004).
CC -!- FUNCTION: Plays an important role in the initiation and regulation
CC of chromosomal replication. Binds to the origin of replication; it
CC binds specifically double-stranded DNA at a 9 bp consensus (dnaA
CC box): 5'-TTATC[CA]A[CA]A-3'. DnaA binds to ATP and to acidic
CC phospholipids (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the dnaA family.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; AE016822; AAT88109.1; -; Genomic_DNA.
DR HAMAP; MF_00377; -; 1.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR001957; Bac_DnaA.
DR Pfam; PF00308; Bac_DnaA; 1.
DR PRINTS; PR00051; DNAA.
DR SMART; SM00382; AAA; 1.
DR TIGRPFAMs; TIGR00362; DnaA; 1.
DR PROSITE; PS01008; DNAA; 1.
KW ATP-binding; Complete proteome; DNA replication; DNA-binding;
KW Nucleotide-binding.
FT NP_BIND 174 181 ATP (Potential).
SQ SEQUENCE 473 AA; 53010 MW; 0CCE6EB3D5F2CC0 CRC64;

Query Match 100.0%; Score 28; DB 1; Length 473;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5
Db |||||
189 HYAMS 193

RESULT 39
QSF80_GLUOX
ID QSF80_GLUOX PRELIMINARY; PRT; 545 AA.
AC QSF80;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Acid phosphatase (EC 3.1.3.2).
GN OrderedLocusNames=GOX0994;
OS Gluconobacter oxydans (Gluconobacter suboxydans).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales;
OC Acetobacteraceae; Gluconobacter.
OX NCBI_TaxID=442;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=621H;
RX PubMed=15665924; DOI=10.1038/nbt1062;
RA Prust C., Hoffmeister M., Liesegang H., Wierzer A., Fricke W.F.,

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RA Ehrenreich A., Gottschalk G., Deppenmeier U.;  
 RT "Complete genome sequence of the acetic acid bacterium *Gluconobacter*  
 RT oxydans";  
 RL Nat. Biotechnol. 23:195-200 (2005).  
 DR EMBL; CP000009; AAW60766.1; -; Genomic DNA.  
 DR GO; GO:0003993; F:acid phosphatase activity; IEA.  
 DR GO; GO:0016788; F:hydrolase activity, acting on ester bonds; IEA.  
 DR InterPro; IPR007312; Pesterase. 1.  
 DR Pfam; PF04185; Phosphoesterase. 1.  
 KW Complete proteome; Hydrolase.  
 SQ SEQUENCE 545 AA; 57888 MW; D025969CAFCF8CA CRC64;  
 Query Match 100.0%; Score 28; DB 2; Length 545;  
 Best Local Similarity 100.0%; Pred. No. 5.7e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 HYAMS 5  
 DB 182 HYAMS 186  
 RESULT 40  
 NUSM CANPA STANDARD; PRT; 555 AA.  
 AC P48919;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 05-JUL-2004 (Rel. 44, Last sequence update)  
 DT 10-MAY-2005 (Rel. 47, Last annotation update)  
 DE NADH-ubiquinone oxidoreductase chain 5 (EC 1.6.5.3) (NADH  
 DE dehydrogenase subunit 5).  
 DE Name=ND5; Synonyms=NAD5;  
 OS Candida parapsilosis (Yeast).  
 OG Mitochondrion.  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; mitosporic Saccharomycetales; Candida.  
 OC NCBI\_TaxID=5480;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=SR23 / CBS 7157;  
 RX MEDLINE=94364940; PubMed=7521869;  
 RA Nosek J., Fukuhara H.;  
 RT "NADH dehydrogenase subunit genes in the mitochondrial DNA of  
 RT yeasts";  
 RL J. Bacteriol. 176:5622-5630 (1994).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=SR23 / CBS 7157;  
 RA Nosek J., Novotna M., Hlavatovicova Z., Ussery D.W., Fajkus J.,  
 RA Tomaska L.;  
 RT "Complete DNA sequence of the linear mitochondrial genome of the  
 RT pathogenic yeast *Candida parapsilosis*.";  
 RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.  
 CC -1- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial  
 CC inner membrane (Probable).  
 CC -1- SIMILARITY: Belongs to the complex I subunit 5 family.  
 CC  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC  
 CC EMBL; X74411; CAE54609.1; -; Genomic DNA.  
 DR InterPro; IPR010934; NADH5\_C.  
 DR InterPro; IPR003945; NADH5\_Oxred5.  
 DR InterPro; IPR003916; NADHub\_Oxred5.  
 DR InterPro; IPR001750; Oxidored\_g1.  
 DR InterPro; IPR001516; Oxidored\_g1\_N.  
 DR Pfam; PF06455; NADH5\_C; 1.  
 DR Pfam; PF00361; Oxidored\_g1; 1.  
 DR Pfam; PF00662; Oxidored\_g1\_N; 1.  
 DR PRINTS; PR01434; NADHDHGNASE5.

DR TIGRFAMs; TIGR01974; NDH\_I\_L; 1.  
 KW Inner membrane; Membrane; Mitochondrion; NAD; Oxidoreductase;  
 KW Transmembrane; Ubiquinone.  
 SQ SEQUENCE 555 AA; 62518 MW; 604232CEB556ACD CRC64;  
 Query Match 100.0%; Score 28; DB 1; Length 555;  
 Best Local Similarity 100.0%; Pred. No. 5.9e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 HYAMS 5  
 DB 434 HYAMS 438  
 RESULT 41  
 QSN753 ORYSA PRELIMINARY; PRT; 566 AA.  
 AC QSN753;  
 DT 01-FEB-2005 (TrEMBLrel. 29, Created)  
 DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)  
 DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)  
 DE Pentatricopeptide (PPR) repeat-containing protein-like.  
 GN Name=OSJNBa0085D07.42;  
 OS Oryza sativa (japonica cultivar-group).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC Ehrhartoideae; Oryzaceae; Oryza.  
 OC NCBI\_TaxID=39947;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Sasaki T., Matsumoto T., Yamamoto K., Sakata K., Baba T., Katayose Y.,  
 RA Wu J., Nilmura Y., Cheng Z., Nagamura Y., Antonio B.A., Kanamori H.,  
 RA Hosokawa S., Masukawa M., Arikawa K., Chiden Y., Hayashi M.,  
 RA Okamoto M., Ando T., Aoki H., Arita K., Hamada M., Hayada C.,  
 RA Hijishita S., Honda M., Ichikawa Y., Idonuma A., Iijima M., Ikeda M.,  
 RA Ikeno M., Itoh S., Itoh T., Itoh Y., Itoh Y., Iwabuchi A., Kamiya K.,  
 RA Karsawa W., Katagiri S., Kikuta A., Kobayashi N., Kono I.,  
 RA Machita K., Maehara T., Mizuno H., Mizubayashi T., Mukai Y.,  
 RA Nagasaki H., Nakashima M., Nakama Y., Nakamichi Y., Nakamura M.,  
 RA Namiki N., Negishi M., Ohta I., Ono N., Saji S., Sakai K., Shibata M.,  
 RA Shimokawa T., Shomura A., Song J., Takazaki Y., Terasawa K., Tsuji K.,  
 RA Waki K., Yamagata H., Yamane H., Yoshiki S., Yoshihara R., Yukawa K.,  
 RA Zhong H., Iwama H., Endo T., Ito H., Hahn J.H., Kim H.I., Eun M.Y.,  
 RA Yano M., Jiang J., Gojobori T.;  
 RT "The genome sequence and structure of rice chromosome 1.";  
 RL Nature 420:312-316 (2002).  
 DR EMBL; AP004331; BAD82703.1; -; Genomic DNA.  
 DR Gramene; OSN753;  
 DR InterPro; IPR002885; PPR.  
 DR InterPro; IPR011990; TPR-like\_helical.  
 DR Pfam; PF01535; PPR; 12.  
 DR TIGRFAMs; TIGR00756; PPR; 10.  
 KW Repeat.  
 SQ SEQUENCE 566 AA; 63368 MW; 4A0874266C57CA6C CRC64;  
 Query Match 100.0%; Score 28; DB 2; Length 566;  
 Best Local Similarity 100.0%; Pred. No. 6e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 HYAMS 5  
 DB 20 HYAMS 24  
 RESULT 42  
 Q4RKT5 TETNG PRELIMINARY; PRT; 699 AA.  
 AC Q4RKT5;  
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
 DE Chromosome 1 SCAF15025, whole genome shotgun sequence.  
 DE (Fragment).



GN ORFNames=GSTENG00032795001;  
OS Tetraodon nigroviridis (Green puffer).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;  
OC Tetraodontidae; Tetraodontidae; Tetraodon.  
OX NCBI\_TaxID=99883;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,  
RA Mauceli E., Bouneau L., Fischer C., Ozou-Costaz C., Bernot A.,  
RA Nicod S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,  
RA Delsalva C., Salanoubat M., Levy M., Boudet N., Castellano S.,  
RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,  
RA Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,  
RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Guzy J.,  
RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,  
RA Kellis M., Wolff J.N., Guigo R., Zody M.C., Mesirov J.,  
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,  
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,  
RA Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.,  
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals  
RT the early vertebrate proto-karyotype.";  
RL Nature 431:946-957(2004).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RG Genoscope; Whitehead Institute Centre for Genome Research;  
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.  
CC -!- CAUTION: The sequence shown here is derived from an  
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
CC preliminary data.  
DR EMBL; CAEE01015025; CAG10997.1; -; Genomic\_DNA.  
DR InterPro: IPR001810; F-box.  
DR InterPro: IPR001611; LRR.  
DR InterPro: IPR007089; LRR\_cys.  
DR InterPro: IPR006553; LRR\_cys\_sub.  
DR Pfam: PF00646; F-box; 1.  
DR Pfam: PF00560; LRR 1; 2.  
DR SMART: SM00256; FBOX; 1.  
DR SMART: SM00367; LRR\_CC; 4.  
DR PROSITE; PS50181; FBOX; 1.  
KW Ub1 conjugation pathway.  
FT NON TER 1  
SQ SEQUENCE 699 AA; 78857 MW; 1710D1412288BD31 CRC64;  
Query Match 100.0%; Score 28; DB 2; Length 699;  
Best Local Similarity 100.0%; Pred. No. 7.4e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 HYAMS 5  
DB 539 HYAMS 543  
RESULT 43  
COG6\_YEAST STANDARD; PRT; 839 AA.  
ID F53959;  
AC F53959;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 10-MAY-2005 (Rel. 47, Last annotation update)  
DE Conserved oligomeric Golgi complex component 6 (Complexed with DOR1  
DE protein 2)  
GN Name=COG6; Synonyms=COD2, TFI2; OrderedLocusNames=YNL041C;  
GN ORFNames=N2675;  
OS Saccharomyces cerevisiae (Baker's yeast).  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.  
OX NCBI\_TaxID=4932;  
RN [1]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
RX MEDLINE=97313269; PubMed=9169873;  
RA Philippen P., Kleine K., Poehlmann R., Duesterhoeft A., Hamberg K.,

RA Hegemann J.H., Obermaier B., Urrestazu L.A., Aert R., Albermann K.,  
RA Altmann R., Andre B., Baladron V., Ballesta J.P.G., Becam A.-M.,  
RA Beinhaus J.D., Boskovic J., Buitrago M.J., Bussereau F., Coster F.,  
RA Crouzet M., D'Angelo M., Del Pero F., De Antoni A., del Rey F.,  
RA Drougnon F., Domdey H., Dubois E., Fiedler T.A., Fleig U., Floeth M.,  
RA Fritz C., Galland C., Garcia-Cantalejo J.M., Glandsdorff N.,  
RA Goffeau A., Guellder U., Herbert C.J., Heumann K., Heuss-Neitzel D.,  
RA Hilbert H., Hinni K., Iraqui Housaini I., Jacquet M., Jimenez A.,  
RA Joniaux J.-L., Karpfinger-Hartl L., Lanfranchi G., Lepingle A.,  
RA Levesque H., Lyck R., Maftahi M., Mallet L., Maurer C.T.C.,  
RA Messenguy F., Mewes H.-W., Moestl D., Nasr F., Nicaud J.-M.,  
RA Neththal R.K., Pandolfo D., Pierard A., Piravandi E., Planta R.J.,  
RA Pohl T.M., Purnelle B., Rebeschung C., Remacha M.A., Revuelta J.L.,  
RA Rinke M., Saiz J.E., Sartorello F., Scherens B., Sen-Gupta M.,  
RA Soler-Mira A., Urbanus J.H.M., Valle G., Van Dyck L., Verhasselet P.,  
RA Vierendeels F., Visser S., Voet M., Volckaert G., Wach A.,  
RA Wambutt R., Wedler H., Zollner A., Hani J.;  
RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome XIV  
RT and its evolutionary implications.";  
RL Nature 387:93-98(1997).  
RN [2]  
RP SUBUNIT.  
RX MEDLINE=21563418; PubMed=11703943; DOI=10.1016/S1534-5807(01)00063-3;  
RA Whyte J.R., Munro S.;  
RA "The Sec34/35 Golgi transport complex is related to the exocyst,  
RT defining a family of complexes involved in multiple steps of membrane  
RT traffic.";  
RL Dev. Cell 1:527-537(2001).  
CC -!- SUBUNIT: Component of the Sec34/Sec35 complex which consists of  
CC eight different proteins.  
CC -!- INTERACTION:  
CC Q04934:IVY1; NExp=1; IntAct=EBI-4829, EBI-35255;  
CC Q02199:NUP49; NExp=1; IntAct=EBI-4829, EBI-12315;  
CC Q06708:VAC14; NExp=1; IntAct=EBI-4829, EBI-27189;  
CC -!- SIMILARITY: Belongs to the COG6 family.  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.  
CC -----  
DR EMBL; Z71317; CAA95908.1; -; Genomic\_DNA.  
DR PIR; S62963; S62963.  
DR InterPro: IPR03959; -.  
DR GernOnline: 143048; -.  
DR Ensembl; YNL041C; Saccharomyces cerevisiae.  
DR SGD; S000004986; COG6.  
DR GO; GO:0017119; C:Golgi transport complex; IPI.  
DR GO; GO:0006891; P:intra-Golgi transport; IGI.  
DR InterPro: IPR010490; COG6.  
DR Pfam; PF06419; COG6; 1.  
KW Complete proteome; Golgi stack; Membrane; Protein transport;  
KW Transport.  
SQ SEQUENCE 839 AA; 96976 MW; 6484A40F999AD787 CRC64;  
Query Match 100.0%; Score 28; DB 1; Length 839;  
Best Local Similarity 100.0%; Pred. No. 9e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 HYAMS 5  
DB 78 HYAMS 82  
RESULT 44  
Q6CHS4\_YARLI  
ID Q6CHS4\_YARLI PRELIMINARY; PRT; 1012 AA.  
AC Q6CHS4;  
DT 25-OCT-2004 (TRENBLrel. 28, Created)  
DT 25-OCT-2004 (TRENBLrel. 28, Last sequence update)  
DT 25-OCT-2004 (TRENBLrel. 28, Last annotation update)  
DE Yarrowia lipolytica chromosome A of strain CLIB99 of Yarrowia

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DE lipolytica.
GN OrderedLocuNames=YALIOA05533g;
OS Yarrowia lipolytica (Candida lipolytica).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Dipodascaceae; Yarrowia.
RN NCBI_TaxID=4952;
RX NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RP PubMed=15229592; DOI=10.1038/nature02579;
RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,
RA Coffard N., Frangul N., Aigle M., Anthouard V., Babour A., Barbe V.,
RA Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,
RA Boisarame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA Nicaud J.-M., Nikolski M., Ostas S., Ozier-Kalogeropoulos O.,
RA Pellenz S., Potier S., Richard G.-F., Straub M.-L., Suleau A.,
RA Swennen D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA Zenlou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,
RA Bouchier C., Caudron B., Scarpelli C., Gallardin C., Weissenbach J.,
RA Wincker P., Souciet J.-L.;
RL Nature 430:35-44 (2004).
RT "Genome evolution in yeasts.";
DR EMBL; CP382127; CAG83712.1; -; Genomic DNA.
DR GO; GO:0005515; F:protein binding; IEA.
DR GO; GO:0004252; F:serine-type endopeptidase activity; IEA.
DR GO; GO:0007596; P:blood coagulation; IEA.
DR GO; GO:0030195; P:negative regulation of blood coagulation; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001478; PDZ.
DR InterPro; IPR001940; Peptidase_S1C.
DR PRINTS; PR00834; PROTEASES1C.
KW Complete proteome.
SQ SEQUENCE 1012 AA; 113158 MW; E12C7D18F427807C CRC64;

Query Match 100.0%; Score 28; DB 2; Length 1012;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5
DB 36 HYAMS 40

RESULT 45
SC24B HUMAN
ID SC24B HUMAN STANDARD; PRT; 1268 AA.
AC O95487;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Protein transport protein Sec24B (SEC24-related protein B).
GN Name=SEC24B;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=B-cell;
RX MEDLINE=99175155; PubMed=10075675; DOI=10.1074/jbc.274.12.7833;
RA Pagano A., Letourneur F., Garcia-Satofania D., Carpentier J.-L.,
RA Orci L., Paccard J.-P.;
RT "Sec24 proteins and sorting at the endoplasmic reticulum.";
RL J. Biol. Chem. 274:7833-7840(1999).
CC -! FUNCTION: Component of the COPII coat, that covers ER-derived
CC vesicles involved in transport from the endoplasmic reticulum to
CC the Golgi apparatus. COPII acts in the cytoplasm to promote the
CC transport of secretory, plasma membrane, and vacuolar proteins
CC from the endoplasmic reticulum to the Golgi complex.

-! SUBUNIT: COPII is composed of at least five proteins: the Sec23/24
complex, the Sec13/31 complex and Sar1. Sec24B is capable of
forming heterodimers with Sec24A.
-! INTERACTION:
CC 15436:SEC23A; NbExp=1; IntAct=EBI-81101, EBI-81088;
-! SUBCELLULAR LOCATION: Cytoplasmic and perinuclear.
CC -! TISSUE SPECIFICITY: Expressed in fibroblasts, hepatocytes, and
lymphocytes.
CC -! SIMILARITY: Belongs to the SEC23/SEC24 family. SEC24 subfamily.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.
EMBL; AJ131245; CAA10335.1; -; mRNA.
HSP; P40482; 1M2V.
IntAct; O95487; -
Ensembl; ENSG00000138802; Homo sapiens.
HGNC; HGNC:10704; SEC24B.
MIM; 607184; -
GO; GO:0030138; C:COPII-coated vesicle; TAS.
GO; GO:0016020; C:membrane; TAS.
GO; GO:005215; F:transporter activity; TAS.
GO; GO:0016192; P:vesicle-mediated transport; TAS.
InterPro; IPR007123; Gelsolin.
InterPro; IPR012990; Sec23_24_beta_S.
InterPro; IPR006900; Sec23_helical.
InterPro; IPR006896; Sec23_trunk.
InterPro; IPR006895; Znf_Sec23_Sec24.
Pfam; PF00626; Gelsolin; 1.
Pfam; PF08033; Sec23_RS; 1.
Pfam; PF04815; Sec23_helical; 1.
Pfam; PF04811; Sec23_trunk; 1.
Pfam; PF04810; zf-Sec23_Sec24; 1.
KW Endoplasmic reticulum; ER-Golgi transport; Golgi stack;
Multigene family; Protein transport; Transport.
REGION 605 629 Zinc finger-like.
FT COMPLETAS 379 387 Poly-Glu.
SQ SEQUENCE 1268 AA; 137789 MW; 7FCA4907CBB32FF9 CRC64;

Query Match 100.0%; Score 28; DB 1; Length 1268;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5
DB 182 HYAMS 186

RESULT 46
QSVLT1 DROME
ID QSVLT1 DROME PRELIMINARY; PRT; 1675 AA.
AC QSVLT1; QSVLT2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE CG31756-PA.
GN ORFNames=CG31756, CG8683;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscophila;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers J.-H.C., Blazef R.G., Champe M., Pfeiffer B.D.,

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RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,  
RA Ballew R.M., Basu A., Bakendahl J., Bayraktaroglu L., Beasley E.M.,  
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,  
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
RA Cherry J.M., Cawley S., Dahike C., Davenport L.B., Davies P.,  
RA de Pablo B., Delcher A., Deng Z., Mays A.C., Dew I., Dietz S.M.,  
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,  
RA Foster C., Gabriellista C.C., Garg N.S., Gelbart W.M., Glasser K.,  
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,  
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
RA Jalali M., Kalush P., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulip D., Lai Z.,  
RA Lasko P., Lei Y., Levitsky A.C., Li J.H., Li Z., Liang Y., Lin X.,  
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,  
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
RA Wang Z.-Y., Waasman D.A., Weinstein G.M., Weissenbach J.,  
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
RT "The genome sequence of *Drosophila melanogaster*,"  
RL Science 287:2185-2195(2000).  
RL [2]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=22426065; PubMed=12537568;  
RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,  
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,  
RA George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,  
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,  
RA Svirskas R., Taber P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,  
RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;  
RT "Finishing a whole-genome shotgun: release 3 of the *Drosophila*  
RT *melanogaster* euchromatic genome sequence,"  
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).  
RL [3]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=22426070; PubMed=12537573;  
RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Svirskas R.,  
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,  
RA Ashburner M., Celniker S.E.;  
RT "The transposable elements of the *Drosophila melanogaster* euchromatin:  
RT a Genomics perspective,"  
RL Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).  
RL [4]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=22426069; PubMed=12537572;  
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,  
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,  
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,  
RA Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,  
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.O.,  
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,  
RA Lewis S.E.;  
RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a  
RT systematic review,"  
RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).  
RL [5]  
RP NUCLEOTIDE SEQUENCE.  
RG Berkeley *Drosophila* Genome Project;  
RA Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,  
RA Hoskins R., Stapleton M., Pacleb J., Park S., Svirskas R., Smith E.,  
RA Yu C., Rubin G.;

RT "Drosophila melanogaster release 4 sequence,";  
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
RL [6]  
RP NUCLEOTIDE SEQUENCE.  
RG FlyBase;  
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.  
CC -!- INTERACTION:  
CC Q9VVP8:skl; NbExp=1; IntAct=EBI-168399, EBI-129806;  
CC Q9VVP8:skl; NbExp=1; IntAct=EBI-168399, EBI-125392;  
DR EMBL: AE003620; AAF52603.3; -; Genomic\_DNA.  
DR IntAct; Q9VLP1; -;  
DR Ensembl; CG313949; NbExp=1; IntAct=EBI-168399, EBI-129806;  
DR FlyBase; FBgn0031985; CG8683.  
DR GO; GO:0005488; F:binding; IEA.  
DR GO; GO:0007076; P:mitotic chromosome condensation; IEA.  
DR InterPro; IPR011989; ARM-like.  
DR InterPro; IPR000357; HEAT.  
DR Pfam; PF02985; HEAT; 2.  
SQ SEQUENCE 1675 AA; 185904 MW; EAS3DD1943FF96E CRC64;  
Query Match 100.0%; Score 28; DB 2; Length 1675;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 HYAMS 5  
Db 572 HYAMS 576  
RESULT 47  
Q86DB6 HALRO PRELIMINARY; PRT; 19 AA.  
AC Q86DB6;  
DT 01-JUN-2003 (TRENBLrel. 24, Created)  
DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)  
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)  
DE Homeobox protein Otx (Fragment).  
GN Name:Hroth;  
OS Halocynthia roretzi (Sea squirt).  
OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;  
OC Stolidobranchia; Pyrosidae; Halocynthia.  
OX NCBI\_TaxId=7729;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=22586101; PubMed=12701103; DOI=10.1002/dvdy.10295;  
RA Oda-Ishii I., Saiga H.;  
RT "Genomic organization and promoter and transcription regulatory  
RT regions for the expression in the anterior brain (sensory vesicle) of  
RT Hroth, the otx homologue of the ascidian, *Halocynthia roretzi*,"  
RL Dev. Dyn. 227:1104-1113(2003).  
DR EMBL; AB104851; BAC76068.1; -; Genomic\_DNA.  
DR GO; GO:0005634; C:nucleus; IEA.  
KW Nuclear protein.  
FT NON TER 19  
SQ SEQUENCE 19 AA; 2041 MW; 2D9CAB7036EAF8D CRC64;  
Query Match 89.3%; Score 25; DB 2; Length 19;  
Best Local Similarity 80.0%; Pred. No. 90;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 HYAMS 5  
Db 8 HYAMN 12  
RESULT 48  
Q8TFAS AERHY PRELIMINARY; PRT; 56 AA.  
AC Q8TFAS;  
DT 05-JUL-2004 (TRENBLrel. 27, Created)  
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)  
DE Hypothetical protein.

OS Aeromonas hydrophila.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;  
 OC Aeromonadaceae; Aeromonas.  
 OX NCBI\_TaxID=644;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=PPD134/91;  
 RX MEDLINE=2024644; PubMed=10784058;  
 RA Zhang Y.L., Ong C.T., Leung K.Y.;  
 RT "Molecular analysis of genetic differences between virulent and  
 RT avirulent strains of Aeromonas hydrophila isolated from diseased  
 RT fish."  
 RL Microbiology 146:999-1009(2000).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=PPD134/91;  
 RA Lau Y.L., Leung K.Y.;  
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY422732; AAR06612.1; -; Genomic\_DNA.  
 KW Hypothetical protein.  
 SQ SEQUENCE 56 AA; 6246 MW; 13F2CF2A13635440 CRC64;  
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 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 HYAMS 5  
 DB 23 HYALS 27  
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 AC Q8GWL8;  
 DT 01-WAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-WAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 01-WAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Hypothetical protein At5g47830/MCA23\_17;  
 GS Name=At5g47830/MCA23\_17;  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;  
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 OC eurosids II; Brassicales; Brassicaceae; Arabidopsi8.  
 OX NCBI\_TaxID=3702;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Seki M., Iida K., Satou M., Sakurai T., Akiyama K., Iehida J.,  
 RA Nakajima M., Enju A., Kamiya A., Narusaka M., Carninci P., Kawai J.,  
 RA Hayashizaki Y., Shinozaki K.;  
 RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AK118767; BAC43360.1; -; mRNA.  
 KW Hypothetical protein.  
 SQ SEQUENCE 60 AA; 6671 MW; 6D4ECA745A15FEF7 CRC64;  
 Query Match 89.3%; Score 25; DB 2; Length 60;  
 Best Local Similarity 80.0%; Pred. No. 2.9e+02;  
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 DB 2 HYAMN 6  
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 AC Q4TDA6;  
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
 DE Chromosome undetermined SCAF6391, whole genome shotgun sequence.  
 DE (Fragment).

GN ORPNames=GSTENG0002894001;  
 OS Tetraodon nigroviridis (Green puffer).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;  
 OC Tetraodontidae; Tetraodontidae; Tetraodon.  
 OX NCBI\_TaxID=99883;  
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 RP NUCLEOTIDE SEQUENCE.  
 RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,  
 RA Mauceli E., Bounneau L., Fischer C., Ozouf-Costaz C., Bernot A.,  
 RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,  
 RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,  
 RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,  
 RA Bieumont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,  
 RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,  
 RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,  
 RA Kellis M., Wolff J.N., Guigo R., Zody M.C., Mesirov J.,  
 RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,  
 RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,  
 RA Wincker P., Lander E.S., Weissenbach J., Roest Crolius H.;  
 RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals  
 RT the early vertebrate proto-karyotype.";  
 RL Nature 431:946-957(2004).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 DR Genoscope; Whitehead Institute Centre for Genome Research;  
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.  
 CC -!- CAUTION: The sequence shown here is derived from an  
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 CC preliminary data.  
 DR EMBL; CAAG01006391; CAF89126.1; -; Genomic\_DNA.  
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 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 HYAMS 5  
 DB 5 HYSMS 9  
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GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: April 6, 2006, 08:58:56 ; Search time 6.69492 Seconds  
(without alignments)  
61.745 Million cell updates/sec

Title: US-10-089-500-3

Perfect score: 28

Sequence: 1 HVAMS 5

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Issued Patents AA:\*

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2: /cgn2\_6/prodata/1/1aa/6 COMB.pep.\*

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4: /cgn2\_6/prodata/1/1aa/PCUS COMB.pep.\*

5: /cgn2\_6/prodata/1/1aa/RE COMB.pep.\*

6: /cgn2\_6/prodata/1/1aa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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6	28	100.0	130	2	US-09-764-304-18
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8	28	100.0	211	2	US-09-270-767-49495
9	28	100.0	351	2	US-09-270-767-42774
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15	25	89.3	272	2	US-09-771-161A-149
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19	25	89.3	318	2	US-09-134-001C-3852
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21	25	89.3	348	2	US-09-270-767-44839
22	25	89.3	352	2	US-09-711-164-448
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94	89.3	343	2	US-09-394-455-34	Sequence 34, Appli
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103	24	85.7	351	2	US-09-394-455-4	Sequence 4, Appli	176	23	82.1	166	2	US-09-489-039A-10135	Sequence 10135, A
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139	24	85.7	727	2	US-08-650-599A-4	Sequence 4, Appli	212	23	82.1	988	2	US-09-402-181B-112	Sequence 112, App
140	24	85.7	727	2	US-09-490-517-4	Sequence 4, Appli	213	23	82.1	988	2	US-09-721-456-112	Sequence 112, App
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146	24	85.7	852	2	US-10-160-187-2	Sequence 2, Appli	219	22	78.6	9	2	US-08-159-339A-251	Sequence 251, App
147	24	85.7	949	2	US-09-198-452A-478	Sequence 478, App	220	22	78.6	11	1	US-08-479-614-14	Sequence 14, Appli
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151	24	85.7	1132	1	US-08-446-010B-18	Sequence 18, Appli	224	22	78.6	67	2	US-09-248-796A-24187	Sequence 24187, A
152	24	85.7	1132	1	US-08-805-445-18	Sequence 18, Appli	225	22	78.6	69	2	US-09-513-990C-7289	Sequence 7289, Ap
153	24	85.7	1132	1	US-08-064-067D-18	Sequence 18, Appli	226	22	78.6	69	2	US-09-248-796A-22607	Sequence 22607, A
154	24	85.7	1132	1	US-09-066-208-18	Sequence 18, Appli	227	22	78.6	72	2	US-09-949-016-9040	Sequence 9040, Ap
155	24	85.7	1142	1	US-08-097-997A-11	Sequence 11, Appli	228	22	78.6	76	2	US-09-248-796A-23877	Sequence 23877, A
156	24	85.7	1142	2	US-08-665-574C-11	Sequence 11, Appli	229	22	78.6	79	2	US-08-630-172-8	Sequence 8, Appli
157	24	85.7	1142	2	US-08-946-994-11	Sequence 11, Appli	230	22	78.6	79	2	US-09-375-419-8	Sequence 8, Appli
158	24	85.7	1142	2	US-09-771-161A-211	Sequence 211, App	231	22	78.6	85	2	US-09-720-532A-3	Sequence 3, Appli
159	24	85.7	1151	2	US-08-840-006-6	Sequence 6, Appli	232	22	78.6	105	2	US-09-107-583A-6671	Sequence 6671, Ap
160	24	85.7	1153	1	US-08-097-997A-14	Sequence 14, Appli	233	22	78.6	110	2	US-09-270-767-38240	Sequence 38240, Ap
161	24	85.7	1153	2	US-08-665-574C-14	Sequence 14, Appli	234	22	78.6	110	2	US-09-270-767-53457	Sequence 53457, A
162	24	85.7	1153	2	US-08-946-994-14	Sequence 14, Appli	235	22	78.6	111	2	US-09-270-767-33793	Sequence 33793, A
163	24	85.7	1154	1	US-08-357-598-7	Sequence 7, Appli	236	22	78.6	111	2	US-09-270-767-49010	Sequence 49010, A
164	24	85.7	1154	1	US-08-446-010B-24	Sequence 24, Appli	237	22	78.6	114	2	US-09-248-796A-25363	Sequence 25363, A
165	24	85.7	1154	1	US-09-003-289-7	Sequence 7, Appli	238	22	78.6	122	2	US-09-328-352-7146	Sequence 7146, Ap
166	24	85.7	1154	4	PCT-US95-16435-7	Sequence 7, Appli	239	22	78.6	123	2	US-10-104-047-2234	Sequence 2234, Ap
167	24	85.7	1200	2	US-08-840-006-5	Sequence 5, Appli	240	22	78.6	128	2	US-09-270-767-32549	Sequence 32549, A
168	24	85.7	1264	2	US-09-252-991A-30264	Sequence 30264, A	241	22	78.6	136	2	US-09-903-540-10776	Sequence 10776, A
169	24	85.7	2472	2	US-09-538-092-1312	Sequence 1312, Ap	242	22	78.6	139	2	US-09-903-650B-27	Sequence 27, Appli
170	23	82.1	78	2	US-09-489-039A-9486	Sequence 9486, Ap	243	22	78.6	140	2	US-09-471-276-850	Sequence 850, App
171	23	82.1	96	2	US-09-270-767-62012	Sequence 62012, A	244	22	78.6	155	2	US-09-252-991A-18638	Sequence 18638, A
172	23	82.1	101	2	US-09-199-637A-399	Sequence 399, App	245	22	78.6	169	2	US-09-252-991A-30273	Sequence 30273, A
173	23	82.1	103	2	US-09-543-681A-5517	Sequence 5517, App	246	22	78.6	200	2	US-09-252-991A-29032	Sequence 29032, A

247	22	78.6	200	2	US-09-270-767-31918	Sequence 31918, A	320	22	78.6	389	2	US-09-270-767-45357	Sequence 45357, A
248	22	78.6	200	2	US-09-270-767-47135	Sequence 47135, A	321	22	78.6	401	2	US-09-489-039A-14203	Sequence 14203, A
249	22	78.6	204	2	US-09-248-796A-16426	Sequence 16426, A	322	22	78.6	404	2	US-09-248-796A-20215	Sequence 20215, A
250	22	78.6	215	2	US-09-229-583A-5	Sequence 5, Appli	323	22	78.6	406	2	US-09-248-796A-16826	Sequence 16826, A
251	22	78.6	215	2	US-10-187-904-5	Sequence 5, Appli	324	22	78.6	409	2	US-09-569-804-21	Sequence 21, Appl
252	22	78.6	216	2	US-09-229-583A-3	Sequence 3, Appli	325	22	78.6	413	2	US-09-543-681A-5108	Sequence 5108, Ap
253	22	78.6	216	2	US-09-489-039A-9538	Sequence 9538, Ap	326	22	78.6	421	2	US-09-093-448-4	Sequence 4, Appli
254	22	78.6	216	2	US-10-187-904-3	Sequence 3, Appli	327	22	78.6	421	2	US-09-134-001C-5201	Sequence 5201, Ap
255	22	78.6	217	2	US-09-229-583A-6	Sequence 6, Appli	328	22	78.6	421	2	US-09-813-555-4	Sequence 4, Appli
256	22	78.6	217	2	US-10-187-904-6	Sequence 6, Appli	329	22	78.6	421	2	US-09-523-263B-18	Sequence 18, Appl
257	22	78.6	222	1	US-08-871-033-3	Sequence 3, Appli	330	22	78.6	421	2	US-09-902-540-10244	Sequence 10244, A
258	22	78.6	222	1	US-09-212-167-3	Sequence 3, Appli	331	22	78.6	421	2	US-10-299-867-18	Sequence 18, Appl
259	22	78.6	223	1	US-08-871-033-4	Sequence 4, Appli	332	22	78.6	422	2	US-09-025-580-3	Sequence 3, Appli
260	22	78.6	223	1	US-09-212-167-4	Sequence 4, Appli	333	22	78.6	422	2	US-09-457-040B-38	Sequence 38, Appl
261	22	78.6	227	1	US-08-254-493-1	Sequence 1, Appli	334	22	78.6	422	2	US-09-642-749-3	Sequence 3, Appli
262	22	78.6	227	1	US-08-253-751-6	Sequence 6, Appli	335	22	78.6	422	2	US-09-771-161A-269	Sequence 269, App
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264	22	78.6	227	2	US-08-403-253A-6	Sequence 6, Appli	337	22	78.6	422	2	US-09-165-522-5	Sequence 5, Appli
265	22	78.6	227	2	US-08-435-816A-6	Sequence 6, Appli	338	22	78.6	422	2	US-09-165-522-8	Sequence 8, Appli
266	22	78.6	227	2	US-09-350-202-6	Sequence 6, Appli	339	22	78.6	422	2	US-09-165-522-12	Sequence 12, Appl
267	22	78.6	227	2	US-08-592-711-6	Sequence 6, Appli	340	22	78.6	424	2	US-09-909-650B-30	Sequence 30, Appl
268	22	78.6	227	2	US-09-349-915B-6	Sequence 6, Appli	341	22	78.6	429	2	US-09-489-039A-8684	Sequence 8684, Ap
269	22	78.6	230	1	US-08-408-222B-1	Sequence 1, Appli	342	22	78.6	431	2	US-09-198-452A-831	Sequence 831, App
270	22	78.6	230	1	US-09-134-000C-4397	Sequence 4397, Ap	343	22	78.6	434	2	US-09-328-352-4563	Sequence 4563, Ap
271	22	78.6	237	2	US-10-010-160-12	Sequence 12, Appl	344	22	78.6	434	2	US-10-140-372-6	Sequence 6, Appli
272	22	78.6	256	2	US-09-949-016-7486	Sequence 7486, Ap	345	22	78.6	435	2	US-09-438-185A-784	Sequence 784, App
273	22	78.6	258	2	US-09-328-352-6852	Sequence 6852, Ap	346	22	78.6	443	2	US-09-342-325C-42	Sequence 42, Appl
274	22	78.6	261	2	US-09-468-738A-29	Sequence 29, Appl	347	22	78.6	443	2	US-10-244-367-42	Sequence 42, Appl
275	22	78.6	261	2	US-09-940-019-29	Sequence 29, Appl	348	22	78.6	446	2	US-09-540-236-2532	Sequence 2532, Ap
276	22	78.6	261	2	US-09-940-037A-29	Sequence 29, Appl	349	22	78.6	449	1	US-08-657-392-2	Sequence 2, Appli
277	22	78.6	261	2	US-09-305-390-18	Sequence 18, Appl	350	22	78.6	449	4	PCT-US94-02539-2	Sequence 2, Appli
278	22	78.6	261	2	US-10-004-115B-36	Sequence 36, Appl	351	22	78.6	455	2	US-09-489-039A-9969	Sequence 9969, Ap
279	22	78.6	262	2	US-09-154-083-24	Sequence 24, Appl	352	22	78.6	456	2	US-09-252-991A-25142	Sequence 25142, A
280	22	78.6	262	2	US-09-710-279-204	Sequence 204, App	353	22	78.6	458	2	US-09-282-305-2	Sequence 2, Appli
281	22	78.6	267	2	US-09-134-001C-5042	Sequence 5042, Ap	354	22	78.6	458	1	US-08-673-312-2	Sequence 2, Appli
282	22	78.6	268	1	US-08-824-874-1	Sequence 1, Appli	355	22	78.6	459	2	US-09-489-039A-10537	Sequence 10537, A
283	22	78.6	268	2	US-09-210-084-1	Sequence 1, Appli	356	22	78.6	463	2	US-09-883-720-2	Sequence 2, Appli
284	22	78.6	268	2	US-09-764-762-1	Sequence 1, Appli	357	22	78.6	464	2	US-09-025-580-28	Sequence 28, Appl
285	22	78.6	270	2	US-09-949-016-7712	Sequence 7712, Ap	358	22	78.6	464	2	US-09-457-040B-5	Sequence 5, Appli
286	22	78.6	281	2	US-09-252-991A-33047	Sequence 33047, A	359	22	78.6	464	2	US-09-538-092-1204	Sequence 1204, Ap
287	22	78.6	282	2	US-09-543-681A-4715	Sequence 4715, Ap	360	22	78.6	464	2	US-09-642-749-28	Sequence 28, Appl
288	22	78.6	282	2	US-09-270-767-41535	Sequence 41535, A	361	22	78.6	464	2	US-09-165-522-2	Sequence 2, Appli
289	22	78.6	285	2	US-09-489-039A-13506	Sequence 13506, A	362	22	78.6	466	2	US-09-328-352-8242	Sequence 8242, Ap
290	22	78.6	286	1	US-08-358-117-2	Sequence 2, Appli	363	22	78.6	466	2	US-09-909-650B-31	Sequence 31, Appl
291	22	78.6	286	2	US-09-502-540-9958	Sequence 9958, Ap	364	22	78.6	469	2	US-09-252-991A-28286	Sequence 28286, A
292	22	78.6	290	2	US-09-543-681A-7967	Sequence 7967, Ap	365	22	78.6	469	2	US-09-489-039A-8689	Sequence 8689, Ap
293	22	78.6	293	2	US-09-509-908-2	Sequence 2, Appli	366	22	78.6	469	2	US-09-270-767-45360	Sequence 45360, A
294	22	78.6	293	2	US-09-991-181-309	Sequence 309, App	367	22	78.6	471	1	US-08-657-392-31	Sequence 31, Appl
295	22	78.6	293	2	US-09-990-444-309	Sequence 309, App	368	22	78.6	471	4	PCT-US94-02539-31	Sequence 31, Appl
296	22	78.6	293	2	US-09-997-333-309	Sequence 309, App	369	22	78.6	482	2	US-09-538-092-454	Sequence 454, App
297	22	78.6	293	2	US-09-992-598-309	Sequence 309, App	370	22	78.6	488	2	US-09-556-877-297	Sequence 297, App
298	22	78.6	298	2	US-09-328-352-6064	Sequence 6064, Ap	371	22	78.6	488	2	US-09-620-412C-297	Sequence 297, App
299	22	78.6	303	2	US-09-949-016-6717	Sequence 6717, Ap	372	22	78.6	488	2	US-09-598-419-297	Sequence 297, App
300	22	78.6	308	2	US-09-248-796A-17690	Sequence 17690, A	373	22	78.6	501	2	US-08-906-791-2	Sequence 2, Appli
301	22	78.6	311	2	US-08-608-284B-18	Sequence 18, Appl	374	22	78.6	501	2	US-09-111-730-1	Sequence 1, Appli
302	22	78.6	315	2	US-09-252-991A-26740	Sequence 26740, A	375	22	78.6	508	2	US-09-111-730-2	Sequence 2, Appli
303	22	78.6	316	2	US-09-252-991A-30325	Sequence 30325, A	376	22	78.6	508	2	US-09-949-016-5994	Sequence 10466, A
304	22	78.6	317	1	US-08-726-306A-168	Sequence 168, App	377	22	78.6	523	2	US-09-949-016-10466	Sequence 10466, A
305	22	78.6	345	1	US-08-479-614-5	Sequence 5, Appli	378	22	78.6	526	2	US-09-252-991A-21748	Sequence 21748, A
306	22	78.6	345	1	US-09-739-455-5	Sequence 5, Appli	379	22	78.6	531	2	US-09-252-991A-26690	Sequence 26690, A
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308	22	78.6	347	2	US-10-153-919-5	Sequence 5, Appli	381	22	78.6	548	2	US-09-252-991A-21629	Sequence 21629, A
309	22	78.6	347	2	US-10-153-919-15	Sequence 15, Appl	382	22	78.6	555	2	US-09-543-681A-6372	Sequence 6372, Ap
310	22	78.6	351	2	US-09-283-305-4	Sequence 4, Appli	383	22	78.6	566	2	US-09-491-522-7	Sequence 7, Appli
311	22	78.6	351	2	US-09-883-720-4	Sequence 4, Appli	384	22	78.6	566	2	US-09-949-016-7010	Sequence 7010, Ap
312	22	78.6	353	2	US-09-134-000C-5843	Sequence 5843, Ap	385	22	78.6	566	2	US-09-949-016-8505	Sequence 8505, Ap
313	22	78.6	361	1	US-08-479-614-2	Sequence 2, Appli	386	22	78.6	566	2	US-09-949-002-452	Sequence 452, App
314	22	78.6	361	2	US-09-328-352-7863	Sequence 7863, Ap	387	22	78.6	566	2	US-09-252-991A-32979	Sequence 32979, A
315	22	78.6	362	1	US-08-479-614-8	Sequence 8, Appli	388	22	78.6	595	2	US-09-248-796A-20439	Sequence 20439, A
316	22	78.6	362	1	US-09-252-991A-18016	Sequence 18016, A	389	22	78.6	602	2	US-09-252-991A-22527	Sequence 22527, A
317	22	78.6	379	2	US-09-492-709A-355	Sequence 355, App	390	22	78.6	605	2	US-10-363-937-3	Sequence 3, Appli
318	22	78.6	381	2	US-09-568-804-17	Sequence 17, Appl	391	22	78.6	608	2	US-09-902-540-14034	Sequence 14034, A
319	22	78.6	381	2	US-09-949-016-8976	Sequence 8976, Ap	392	22	78.6	621	2	US-09-551-778-2	Sequence 2, Appli



393	22	78.6	621	2	US-09-551-778-4	Sequence 4, Appli	466	21	75.0	68	2	US-09-270-767-34897	Sequence 34897, A
394	22	78.6	621	2	US-10-047-593-2	Sequence 2, Appli	467	21	75.0	68	2	US-09-270-767-50114	Sequence 50114, A
395	22	78.6	621	2	US-10-047-593-4	Sequence 4, Appli	468	21	75.0	69	2	US-09-270-767-35850	Sequence 35850, A
396	22	78.6	654	2	US-10-172-502-10	Sequence 10, Appli	469	21	75.0	69	2	US-09-270-767-51067	Sequence 51067, A
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398	22	78.6	664	2	US-09-949-016-8598	Sequence 8598, Ap	471	21	75.0	70	2	US-08-134-001C-3950	Sequence 3950, Ap
399	22	78.6	664	2	US-09-949-016-9005	Sequence 9005, Ap	472	21	75.0	72	2	US-09-621-976-7160	Sequence 7160, Ap
400	22	78.6	664	2	US-09-949-016-9226	Sequence 9226, Ap	473	21	75.0	74	2	US-09-248-796A-27760	Sequence 27760, A
401	22	78.6	677	2	US-09-543-681A-7936	Sequence 7936, Ap	474	21	75.0	77	2	US-09-134-000C-6211	Sequence 6211, Ap
402	22	78.6	682	2	US-09-489-039A-11284	Sequence 11284, A	475	21	75.0	79	2	US-09-382-155-5	Sequence 5, Appli
403	22	78.6	705	2	US-09-328-352-7436	Sequence 7436, Ap	476	21	75.0	79	2	US-09-074-044A-5	Sequence 5, Appli
404	22	78.6	711	1	US-08-235-838-7	Sequence 7, Appli	477	21	75.0	81	2	US-09-205-258-1152	Sequence 1152, Ap
405	22	78.6	711	1	US-08-465-473B-7	Sequence 7, Appli	478	21	75.0	81	2	US-10-004-860-1152	Sequence 1152, Ap
406	22	78.6	716	1	US-08-766-982-1	Sequence 1, Appli	479	21	75.0	91	2	US-09-543-681A-6313	Sequence 6313, Ap
407	22	78.6	716	1	US-09-296-219-1	Sequence 1, Appli	480	21	75.0	92	2	US-09-621-976-5018	Sequence 5018, Ap
408	22	78.6	749	2	US-09-562-737-97	Sequence 97, Appli	481	21	75.0	95	2	US-09-134-000C-3831	Sequence 3831, Ap
409	22	78.6	774	2	US-09-538-092-591	Sequence 591, App	482	21	75.0	100	2	US-09-840-459-36	Sequence 36, Appli
410	22	78.6	783	2	US-09-540-236-2284	Sequence 2284, Ap	483	21	75.0	100	2	US-09-497-625A-36	Sequence 36, Appli
411	22	78.6	848	2	US-09-489-039A-13773	Sequence 13773, A	484	21	75.0	102	2	US-08-923-992A-20	Sequence 20, Appli
412	22	78.6	896	2	US-09-270-767-46130	Sequence 46130, A	485	21	75.0	103	2	US-09-107-532A-5377	Sequence 5377, Ap
413	22	78.6	969	2	US-09-321-987B-5	Sequence 5, Appli	486	21	75.0	103	2	US-09-248-796A-26050	Sequence 26050, A
414	22	78.6	1009	2	US-09-252-991A-24492	Sequence 24492, A	487	21	75.0	106	2	US-09-583-110-4852	Sequence 4852, Ap
415	22	78.6	1020	2	US-09-538-092-911	Sequence 911, App	488	21	75.0	106	2	US-09-107-433-4219	Sequence 4219, Ap
416	22	78.6	1032	2	US-09-949-016-10553	Sequence 10553, A	489	21	75.0	110	2	US-08-466-886-32	Sequence 32, Appli
417	22	78.6	1157	2	US-09-538-092-1328	Sequence 1328, Ap	490	21	75.0	110	2	US-08-469-617-32	Sequence 32, Appli
418	22	78.6	1205	2	US-09-491-522-11	Sequence 11, Appli	491	21	75.0	110	2	US-08-469-630-32	Sequence 32, Appli
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420	22	78.6	1211	2	US-09-949-016-11401	Sequence 11401, A	493	21	75.0	110	2	US-08-252-778-32	Sequence 32, Appli
421	22	78.6	1211	2	US-09-949-002-401	Sequence 401, App	494	21	75.0	111	2	US-08-923-992A-14	Sequence 14, Appli
422	22	78.6	1211	2	US-09-949-002-555	Sequence 555, App	495	21	75.0	111	2	US-08-923-992A-15	Sequence 15, Appli
423	22	78.6	1250	1	US-08-441-139-9	Sequence 9, Appli	496	21	75.0	114	2	US-08-483-749A-10	Sequence 10, Appli
424	22	78.6	1250	2	US-09-487-558B-364	Sequence 364, App	497	21	75.0	115	1	US-08-468-661-1	Sequence 1, Appli
425	22	78.6	1250	2	US-09-770-170-2	Sequence 2, Appli	498	21	75.0	115	1	US-08-466-272A-1	Sequence 1, Appli
426	22	78.6	1418	2	US-09-252-991A-32367	Sequence 32367, A	499	21	75.0	115	1	US-08-478-857-1	Sequence 1, Appli
427	21	75.0	10	2	US-08-908-469-86	Sequence 86, Appli	500	21	75.0	115	1	US-08-379-057-31	Sequence 31, Appli
428	21	75.0	10	2	US-08-908-469-87	Sequence 87, Appli	501	21	75.0	115	1	US-08-428-197-42	Sequence 42, Appli
429	21	75.0	10	2	US-08-908-469-88	Sequence 88, Appli	502	21	75.0	115	1	US-09-130-783-1	Sequence 1, Appli
430	21	75.0	10	2	US-08-908-469-89	Sequence 89, Appli	503	21	75.0	115	2	US-09-583-110-3719	Sequence 2719, Ap
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432	21	75.0	10	2	US-08-908-469-91	Sequence 91, Appli	505	21	75.0	115	2	US-09-583-110-4727	Sequence 4727, Ap
433	21	75.0	10	2	US-08-908-469-128	Sequence 128, App	506	21	75.0	115	2	US-09-583-110-5007	Sequence 5007, Ap
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435	21	75.0	20	1	US-08-416-950-7	Sequence 7, Appli	508	21	75.0	115	2	US-09-919-039-207	Sequence 207, App
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437	21	75.0	20	1	US-08-468-279-35	Sequence 35, Appli	510	21	75.0	115	2	US-09-840-459-83	Sequence 83, Appli
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439	21	75.0	20	2	US-08-463-486-18	Sequence 18, Appli	512	21	75.0	117	2	US-09-107-433-4108	Sequence 4108, Ap
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442	21	75.0	20	2	US-08-197-484-101	Sequence 101, App	515	21	75.0	117	2	US-09-107-433-4332	Sequence 4332, Ap
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446	21	75.0	20	4	PCT-US94-02195-18	Sequence 18, Appli	519	21	75.0	118	2	US-08-908-469-112	Sequence 112, App
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448	21	75.0	20	2	US-09-270-767-33986	Sequence 33986, A	521	21	75.0	118	2	US-08-908-469-118	Sequence 118, App
449	21	75.0	21	2	US-09-270-767-49203	Sequence 49203, A	522	21	75.0	118	2	US-08-192-102-5	Sequence 5, Appli
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455	21	75.0	49	2	US-09-004-406C-21	Sequence 21, Appli	528	21	75.0	119	2	US-08-270-767-58598	Sequence 58598, A
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458	21	75.0	52	2	US-09-205-658-82	Sequence 82, Appli	531	21	75.0	119	2	US-09-756-398B-5	Sequence 5, Appli
459	21	75.0	60	2	US-09-461-325-168	Sequence 168, App	532	21	75.0	120	2	US-08-767-128-28	Sequence 28, Appli
460	21	75.0	60	2	US-10-012-542-168	Sequence 168, App	533	21	75.0	120	2	US-08-923-992A-16	Sequence 16, Appli
461	21	75.0	60	2	US-10-115-123-168	Sequence 168, App	534	21	75.0	120	2	US-08-923-992A-17	Sequence 17, Appli
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463	21	75.0	65	2	US-08-918-148-73	Sequence 73, Appli	536	21	75.0	122	2	US-08-483-749A-2	Sequence 2, Appli
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565	21	75.0	151	2	US-09-963-620-15	Sequence 15, Appl	638	21	75.0	253	2	US-09-071-035-12	Sequence 12, Appl
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567	21	75.0	151	2	US-09-934-773-15	Sequence 15, Appl	640	21	75.0	254	2	US-10-087-167-6	Sequence 6, Appl
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577	21	75.0	158	2	US-09-519-232-50	Sequence 50, Appl	650	21	75.0	267	1	US-08-667-809B-2	Sequence 2, Appl
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582	21	75.0	162	2	US-10-012-819-202	Sequence 202, App	655	21	75.0	274	2	US-09-543-681A-5511	Sequence 5511, Ap
583	21	75.0	162	2	US-10-101-464A-766	Sequence 766, App	656	21	75.0	278	2	US-09-051-755-5	Sequence 5, Appl
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585	21	75.0	165	2	US-09-519-232-34	Sequence 34, Appl	658	21	75.0	278	2	US-09-134-000C-5006	Sequence 5006, Ap
586	21	75.0	165	2	US-09-519-232-38	Sequence 38, Appl	659	21	75.0	279	2	US-10-087-167-8	Sequence 8, Appl
587	21	75.0	165	2	US-09-519-232-40	Sequence 40, Appl	660	21	75.0	280	2	US-09-660-587-42	Sequence 42, Appl
588	21	75.0	165	2	US-09-519-232-42	Sequence 42, Appl	661	21	75.0	280	2	US-09-314-701-48	Sequence 48, Appl
589	21	75.0	165	2	US-09-519-232-48	Sequence 48, Appl	662	21	75.0	280	2	US-09-811-007A-42	Sequence 42, Appl
590	21	75.0	165	2	US-09-519-232-58	Sequence 58, Appl	663	21	75.0	280	2	US-10-314-639-48	Sequence 48, Appl
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593	21	75.0	171	2	US-09-382-153-23	Sequence 23, Appl	666	21	75.0	283	2	US-09-328-352-5674	Sequence 5674, Ap
594	21	75.0	171	2	US-09-074-044A-23	Sequence 23, Appl	667	21	75.0	283	2	US-10-087-167-10	Sequence 10, Appl
595	21	75.0	171	2	US-09-902-540-13819	Sequence 13819, A	668	21	75.0	285	2	US-09-318-661-4	Sequence 4, Appl
596	21	75.0	175	2	US-09-134-000C-6776	Sequence 6776, Ap	669	21	75.0	285	2	US-09-883-758-4	Sequence 4, Appl
597	21	75.0	176	2	US-09-232-446B-4	Sequence 4, Appl	670	21	75.0	286	2	US-09-107-532A-7153	Sequence 7153, Ap
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610	21	75.0	207	2	US-09-538-092-880	Sequence 880, App	683	21	75.0	303	2	US-09-328-352-8214	Sequence 8214, Ap
611	21	75.0	208	2	US-09-621-976-6798	Sequence 6798, Ap	684	21	75.0	305	2	US-09-315-794-22	Sequence 22, Appl

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688	21	75.0	308	2	US-09-252-991A-31589	Sequence 31589, A	761	21	75.0	413	2	US-09-270-767-34924	Sequence 34924, A
689	21	75.0	309	2	US-09-107-534A-6629	Sequence 6629, App	762	21	75.0	413	2	US-09-270-767-50141	Sequence 50141, A
690	21	75.0	310	2	US-09-583-110-3105	Sequence 3105, App	763	21	75.0	413	2	US-09-949-016-8261	Sequence 8261, App
691	21	75.0	311	2	US-09-252-991A-17320	Sequence 17320, A	764	21	75.0	414	2	US-09-888-664A-13	Sequence 13, Appl
692	21	75.0	312	2	US-08-653-648A-16	Sequence 16, Appl	765	21	75.0	414	2	US-10-274-978-14	Sequence 14, Appl
693	21	75.0	313	2	US-09-564-418-7	Sequence 7, Appl	766	21	75.0	414	2	US-10-697-263-14	Sequence 14, Appl
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695	21	75.0	315	2	US-09-107-433-3914	Sequence 3914, App	768	21	75.0	422	1	US-08-484-575A-6	Sequence 6, Appl
696	21	75.0	316	2	US-09-328-352-5223	Sequence 5223, App	769	21	75.0	422	2	US-08-477-459-6	Sequence 6, Appl
697	21	75.0	317	2	US-09-489-039A-9500	Sequence 9500, App	770	21	75.0	422	2	US-08-479-869-6	Sequence 6, Appl
698	21	75.0	318	2	US-08-653-648A-7	Sequence 7, Appl	771	21	75.0	422	2	US-08-486-414-6	Sequence 6, Appl
699	21	75.0	319	2	US-09-564-418-13	Sequence 13, Appl	772	21	75.0	422	2	US-09-489-039A-10905	Sequence 10905, A
700	21	75.0	320	2	US-09-252-991A-29428	Sequence 29428, A	773	21	75.0	422	4	PCT-US94-01826A-6	Sequence 6, Appl
701	21	75.0	321	2	US-09-688-019-2	Sequence 2, Appl	774	21	75.0	422	4	PCT-US94-02252A-6	Sequence 6, Appl
702	21	75.0	322	2	US-09-252-991A-28222	Sequence 28222, A	775	21	75.0	425	2	US-09-233-549-6	Sequence 6, Appl
703	21	75.0	323	2	US-09-605-703B-2166	Sequence 2166, App	776	21	75.0	427	1	US-08-476-008-59	Sequence 59, Appl
704	21	75.0	324	2	US-09-252-991A-27569	Sequence 27569, A	777	21	75.0	427	1	US-08-306-063-59	Sequence 59, Appl
705	21	75.0	325	2	US-09-605-703B-580	Sequence 580, App	778	21	75.0	427	1	US-08-833-485-59	Sequence 59, Appl
706	21	75.0	326	2	US-09-605-703B-582	Sequence 582, App	779	21	75.0	427	2	US-09-137-440-59	Sequence 59, Appl
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708	21	75.0	328	2	US-09-248-796A-18110	Sequence 18110, A	781	21	75.0	431	2	US-09-489-039A-12670	Sequence 12670, A
709	21	75.0	329	2	US-09-543-681A-5373	Sequence 5373, App	782	21	75.0	437	2	US-09-477-135A-136	Sequence 136, App
710	21	75.0	330	2	US-09-825-414-11	Sequence 11, Appl	783	21	75.0	438	2	US-09-489-039A-13834	Sequence 13834, A
711	21	75.0	331	2	US-09-540-236-2888	Sequence 2888, App	784	21	75.0	444	2	US-09-602-787A-70	Sequence 70, Appl
712	21	75.0	332	2	US-09-248-796A-14436	Sequence 14436, A	785	21	75.0	444	2	US-09-107-532A-3952	Sequence 3952, App
713	21	75.0	333	2	US-09-540-236-3102	Sequence 3102, App	786	21	75.0	444	2	US-09-248-796A-23963	Sequence 23963, A
714	21	75.0	334	2	US-09-328-352-6329	Sequence 6329, App	787	21	75.0	447	2	US-09-109-204-3	Sequence 3, Appl
715	21	75.0	335	2	US-09-583-110-2773	Sequence 2773, App	788	21	75.0	447	2	US-09-490-032-3	Sequence 3, Appl
716	21	75.0	336	2	US-09-710-279-3076	Sequence 3076, App	789	21	75.0	458	2	US-09-543-681A-6324	Sequence 6324, App
717	21	75.0	337	2	US-09-107-433-4806	Sequence 4806, App	790	21	75.0	459	2	US-09-134-001C-3178	Sequence 3178, App
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985 21 75.0 818 2 US-09-949-016-8579 Sequence 8579, Ap  
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1000 21 75.0 969 2 US-09-949-016-8059 Sequence 8059, Ap

## ALIGNMENTS

RESULT 1  
US-09-770-834-6  
; Sequence 6, Application US/09770834  
; Patent No. 6684162  
; GENERAL INFORMATION:  
; APPLICANT: Parrie, Kevin  
; APPLICANT: Somers, William  
; APPLICANT: Tam, Amy  
; APPLICANT: Lin, Laura  
; APPLICANT: Stahl, Mark  
; APPLICANT: Powers, Robert  
; APPLICANT: Xu, Guan-Yi  
; TITLE OF INVENTION: CRYSTAL STRUCTURE OF ACPS/ACP COMPLEX, SOLUTION STRUCTURE  
; TITLE OF INVENTION: OF B. SUBTILIS ACP, AND USES THEREOF  
; FILE REFERENCE: 2368/14  
; CURRENT APPLICATION NUMBER: US/09/770,834  
; CURRENT FILING DATE: 2001-10-12  
; PRIOR APPLICATION NUMBER: US 60/202,466  
; PRIOR FILING DATE: 2000-05-08  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn version 3.0  
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; LENGTH: 119  
; TYPE: PRT  
; ORGANISM: Staphylococcus sp.  
US-09-770-834-6

Query Match 100.0%; Score 28; DB 2; Length 119;  
Best Local Similarity 100.0%; Pred. No. 20;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2  
US-09-771-383-5  
; Sequence 5, Application US/09771383  
; Patent No. 6957150  
; GENERAL INFORMATION:  
; APPLICANT: Parrie, Kevin  
; APPLICANT: Somers, William  
; APPLICANT: Tam, Amy

; APPLICANT: Lin, Laura  
; APPLICANT: Stahl, Mark  
; TITLE OF INVENTION: CRYSTAL STRUCTURE OF ACYL CARRIER PROTEIN SYNTHASE  
; TITLE OF INVENTION: AND ACYL CARRIER PROTEIN SYNTHASE COMPLEX  
; FILE REFERENCE: 2368/12  
; CURRENT APPLICATION NUMBER: US/09/771,383  
; CURRENT FILING DATE: 2001-01-25  
; PRIOR APPLICATION NUMBER: US 60/178,639  
; PRIOR FILING DATE: 2000-01-28  
; NUMBER OF SEQ ID NOS: 13  
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US-09-771-383-5

Query Match 100.0%; Score 28; DB 2; Length 119;  
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RESULT 3  
US-09-225-322B-8  
; Sequence 8, Application US/09225322B  
; Patent No. 6437098  
; GENERAL INFORMATION:  
; APPLICANT: SHITARA, KENYA  
; APPLICANT: HANAI, NOBUO  
; APPLICANT: HASEGAWA, MAMORU  
; APPLICANT: MIYAJI, HIROMASA  
; APPLICANT: KIWANA, YOSHIHISA  
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY  
; FILE REFERENCE: 249-101  
; CURRENT APPLICATION NUMBER: US/09/225,322B  
; CURRENT FILING DATE: 1999-01-05  
; PRIOR APPLICATION NUMBER: US 08/454,680  
; PRIOR FILING DATE: 1995-05-31  
; PRIOR APPLICATION NUMBER: US 08/408,133  
; PRIOR FILING DATE: 1995-03-21  
; PRIOR APPLICATION NUMBER: US 08/292,178  
; PRIOR FILING DATE: 1994-08-17  
; PRIOR APPLICATION NUMBER: US07/947,674  
; PRIOR FILING DATE: 1992-09-17  
; PRIOR APPLICATION NUMBER: JP 3-238375  
; PRIOR FILING DATE: 1991-09-18  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 8  
; LENGTH: 130  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: cDNA KM-641  
US-09-225-322B-8

Query Match 100.0%; Score 28; DB 2; Length 130;  
Best Local Similarity 100.0%; Pred. No. 22;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5  
Db 41 HYAMS 45

RESULT 4  
US-09-225-322B-18  
; Sequence 18, Application US/09225322B  
; Patent No. 6437098

```

; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUWANA, YOSHIHISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/09/225,322B
; CURRENT FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: US 08/454,680
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
; PRIOR APPLICATION NUMBER: US07/947,674
; PRIOR FILING DATE: 1992-09-17
; PRIOR APPLICATION NUMBER: JP 3-238375
; PRIOR FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 18
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: cDNA KM-641
US-09-225-322B-18

Query Match          100.0%; Score 28; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 HYAMS 5
Db      41 HYAMS 45

RESULT 5
US-09-764-304-8
; Sequence 8, Application US/09764304
; Patent No. 6495666
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUWANA, YOSHIHISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/09/764,304
; CURRENT FILING DATE: 2001-01-19
; EARLIER APPLICATION NUMBER: 09/225,322
; EARLIER FILING DATE: 1999-01-05
; EARLIER APPLICATION NUMBER: US 08/454,680
; EARLIER FILING DATE: 1995-05-31
; EARLIER APPLICATION NUMBER: US 08/408,133
; EARLIER FILING DATE: 1995-03-21
; EARLIER APPLICATION NUMBER: US 08/292,178
; EARLIER FILING DATE: 1994-08-17
; EARLIER APPLICATION NUMBER: US07/947,674
; EARLIER FILING DATE: 1992-09-17
; EARLIER APPLICATION NUMBER: JP 3-238375
; EARLIER FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 18
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: cDNA KM-641
US-09-764-304-8

Query Match          100.0%; Score 28; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 HYAMS 5
Db      41 HYAMS 45

RESULT 5
US-09-764-304-8
; Sequence 8, Application US/09764304
; Patent No. 6495666
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUWANA, YOSHIHISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/09/764,304
; CURRENT FILING DATE: 2001-01-19
; EARLIER APPLICATION NUMBER: 09/225,322
; EARLIER FILING DATE: 1999-01-05
; EARLIER APPLICATION NUMBER: US 08/454,680
; EARLIER FILING DATE: 1995-05-31
; EARLIER APPLICATION NUMBER: US 08/408,133
; EARLIER FILING DATE: 1995-03-21
; EARLIER APPLICATION NUMBER: US 08/292,178
; EARLIER FILING DATE: 1994-08-17
; EARLIER APPLICATION NUMBER: US07/947,674
; EARLIER FILING DATE: 1992-09-17
; EARLIER APPLICATION NUMBER: JP 3-238375
; EARLIER FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 8
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: cDNA KM-641

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US-09-764-304-8

Query Match          100.0%; Score 28; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 HYAMS 5
Db      41 HYAMS 45

RESULT 6
US-09-764-304-18
; Sequence 18, Application US/09764304
; Patent No. 6495666
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUWANA, YOSHIHISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/09/764,304
; CURRENT FILING DATE: 2001-01-19
; EARLIER APPLICATION NUMBER: 09/225,322
; EARLIER FILING DATE: 1999-01-05
; EARLIER APPLICATION NUMBER: US 08/454,680
; EARLIER FILING DATE: 1995-05-31
; EARLIER APPLICATION NUMBER: US 08/408,133
; EARLIER FILING DATE: 1995-03-21
; EARLIER APPLICATION NUMBER: US 08/292,178
; EARLIER FILING DATE: 1994-08-17
; EARLIER APPLICATION NUMBER: US07/947,674
; EARLIER FILING DATE: 1992-09-17
; EARLIER APPLICATION NUMBER: JP 3-238375
; EARLIER FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 18
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: cDNA KM-641
US-09-764-304-18

Query Match          100.0%; Score 28; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 HYAMS 5
Db      41 HYAMS 45

RESULT 7
US-09-270-767-34278
; Sequence 34278, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 34278
; LENGTH: 211
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:

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; OTHER INFORMATION: Xaa means any amino acid  
US-09-270-767-34278

Query Match 100.0%; Score 28; DB 2; Length 211;  
Best Local Similarity 100.0%; Pred. No. 37;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5  
|||||  
Db 154 HYAMS 158

## RESULT 8

US-09-270-767-49495  
; Sequence 49495, Application US/09270767  
; Patent No. 6703491

; GENERAL INFORMATION:

; APPLICANT: Homburger et al.  
; TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*  
; FILE REFERENCE: File Reference: 7326-094  
; CURRENT APPLICATION NUMBER: US/09/270,767  
; CURRENT FILING DATE: 1999-03-17

; NUMBER OF SEQ ID NOS: 62517  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 49495

; LENGTH: 211  
; TYPE: PRT

; ORGANISM: *Drosophila melanogaster*  
; FEATURE:

; OTHER INFORMATION: Xaa means any amino acid  
US-09-270-767-49495

Query Match 100.0%; Score 28; DB 2; Length 211;  
Best Local Similarity 100.0%; Pred. No. 37;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5  
|||||  
Db 154 HYAMS 158

## RESULT 9

US-09-270-767-42774  
; Sequence 42774, Application US/09270767  
; Patent No. 6703491

; GENERAL INFORMATION:

; APPLICANT: Homburger et al.  
; TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*  
; FILE REFERENCE: File Reference: 7326-094  
; CURRENT APPLICATION NUMBER: US/09/270,767  
; CURRENT FILING DATE: 1999-03-17

; NUMBER OF SEQ ID NOS: 62517  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 42774

; LENGTH: 351  
; TYPE: PRT

; ORGANISM: *Drosophila melanogaster*  
; FEATURE:

; OTHER INFORMATION: Xaa means any amino acid  
US-09-270-767-42774

Query Match 100.0%; Score 28; DB 2; Length 351;  
Best Local Similarity 100.0%; Pred. No. 63;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5  
|||||  
Db 247 HYAMS 251

## RESULT 10

US-09-824-734-4

; Sequence 4, Application US/09824734

; Patent No. 6727408  
; GENERAL INFORMATION:

; APPLICANT: ZHU, JIAN-KANG  
; APPLICANT: SHI, HUAZHONG  
; APPLICANT: ISHITANI, MANABU  
; APPLICANT: STEVENSON, BECKY  
; TITLE OF INVENTION: PROTEINS AND DNA RELATED TO SALT TOLERANCE IN PLANTS

; FILE REFERENCE: 205644US20

; CURRENT APPLICATION NUMBER: US/09/824,734

; CURRENT FILING DATE: 2001-04-04

; PRIOR APPLICATION NUMBER: US 60/194,648

; PRIOR FILING DATE: 2000-04-04

; NUMBER OF SEQ ID NOS: 20

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 4

; LENGTH: 424

; TYPE: PRT

; ORGANISM: *Pseudomonas aeruginosa*

US-09-824-734-4

Query Match 100.0%; Score 28; DB 2; Length 424;

Best Local Similarity 100.0%; Pred. No. 77;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5

|||||

Db 272 HYAMS 276

## RESULT 11

US-09-902-540-10862

; Sequence 10862, Application US/09902540

; Patent No. 6833447

; GENERAL INFORMATION:

; APPLICANT: Goldman, Barry S.

; APPLICANT: Hinkle, Gregory J.

; APPLICANT: Slater, Steven C.

; APPLICANT: Wiegand, Roger C.

; TITLE OF INVENTION: *Myxococcus xanthus* Genome Sequences and Uses Thereof

; FILE REFERENCE: 38-10(15849)B

; CURRENT APPLICATION NUMBER: US/09/902,540

; CURRENT FILING DATE: 2001-07-10

; PRIOR APPLICATION NUMBER: 60/217,883

; PRIOR FILING DATE: 2000-07-10

; NUMBER OF SEQ ID NOS: 16825

; SEQ ID NO 10862

; LENGTH: 496

; TYPE: PRT

; ORGANISM: *Myxococcus xanthus*

US-09-902-540-10862

Query Match 100.0%; Score 28; DB 2; Length 496;

Best Local Similarity 100.0%; Pred. No. 91;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5

|||||

Db 225 HYAMS 229

## RESULT 12

US-09-252-991A-20338

; Sequence 20338, Application US/09252991A

; Patent No. 6551795

; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252,991A

; CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18



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; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 20338
; LENGTH: 514
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-20338

Query Match      100.0%; Score 28; DB 2; Length 514;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 HYAMS 5
      |||||
Db      362 HYAMS 366

RESULT 13
US-08-335-865J-4
; Sequence 4, Application US/08335865J
; Patent No. 6107472
; GENERAL INFORMATION:
; APPLICANT: Stackner, Steven A.; Hovens, Christopher M.,
; APPLICANT: Wilks, Andrew F.
; TITLE OF INVENTION: RECEPTOR-TYPE TYROSINE KINASE-LIKE MOLECULES
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski L.L.P.
; STREET: 666 Fifth Ave
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 720 KB storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: ASCII/wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/335,865J
; FILING DATE: 19-January-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/AU93/00210
; FILING DATE: 10-May-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PL2358
; FILING DATE: 11-May-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6107472man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD-5277
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3100
; TELEFAX: (212) 752-5958
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-335-865J-4

Query Match      89.3%; Score 25; DB 2; Length 23;
Best Local Similarity 80.0%; Pred. No. 18;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 HYAMS 5
      |||||
Db      18 HYALS 22

; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 20338
; LENGTH: 514
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-20338

Query Match      100.0%; Score 28; DB 2; Length 514;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 HYAMS 5
      |||||
Db      362 HYAMS 366

RESULT 14
US-09-710-279-908
; Sequence 908, Application US/09710279
; Patent No. 6703492
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/09/710,279
; CURRENT FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 908
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-09-710-279-908

Query Match      89.3%; Score 25; DB 2; Length 116;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 HYAMS 5
      |||||
Db      34 HYAMT 38

RESULT 15
US-09-771-161A-149
; Sequence 149, Application US/09771161A
; Patent No. 6936450
; GENERAL INFORMATION:
; APPLICANT: LEVINE, et al.
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
; FILE REFERENCE: 802620-2005.1
; CURRENT APPLICATION NUMBER: US/09/771,161A
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/724,676
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 136776
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 135619
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 149
; LENGTH: 272
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-771-161A-149

Query Match      89.3%; Score 25; DB 2; Length 272;
Best Local Similarity 80.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 HYAMS 5
      |||||
Db      92 HYALS 96

RESULT 16
US-09-248-796A-16865
; Sequence 16865, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
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; FILE REFERENCE: 107196.132  
; CURRENT APPLICATION NUMBER: US/09/248,796A  
; CURRENT FILING DATE: 1999-02-12  
; PRIOR APPLICATION NUMBER: US 60/074,725  
; PRIOR FILING DATE: 1998-02-13  
; PRIOR APPLICATION NUMBER: US 60/096,409  
; PRIOR FILING DATE: 1998-08-13  
; NUMBER OF SEQ ID NOS: 28208  
; SEQ ID NO 16865  
; LENGTH: 306  
; TYPE: PRT  
; ORGANISM: Candida albicans  
; FEATURE:  
; NAME/KEY: UNSURE  
; LOCATION: (6)-(51)  
; OTHER INFORMATION: Identity of amino acid sequences at the above locations are unknown

US-09-248-796A-16865  
  
Query Match 89.3%; Score 25; DB 2; Length 306;  
Best Local Similarity 80.0%; Pred. No. 2.8e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5  
|||:|  
DB 83 HYALS 87

RESULT 17  
US-09-710-279-1072  
; Sequence 1072, Application US/09710279  
; Patent No. 6703492  
; GENERAL INFORMATION:  
; APPLICANT: KIMMERLY, WILLIAM JOHN  
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS  
; FILE REFERENCE: PU3480US  
; CURRENT APPLICATION NUMBER: US/09/710,279  
; CURRENT FILING DATE: 2000-11-09  
; PRIOR APPLICATION NUMBER: 60/164,258  
; PRIOR FILING DATE: 1999-11-09  
; NUMBER OF SEQ ID NOS: 4472  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1072  
; LENGTH: 308  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: amino acid sequence  
US-09-710-279-1072

Query Match 89.3%; Score 25; DB 2; Length 308;  
Best Local Similarity 80.0%; Pred. No. 2.9e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5  
|||:|  
DB 209 HYALS 213

RESULT 18  
US-09-710-279-2706  
; Sequence 2706, Application US/09710279  
; Patent No. 6703492  
; GENERAL INFORMATION:  
; APPLICANT: KIMMERLY, WILLIAM JOHN  
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS  
; FILE REFERENCE: PU3480US  
; CURRENT APPLICATION NUMBER: US/09/710,279  
; CURRENT FILING DATE: 2000-11-09  
; PRIOR APPLICATION NUMBER: 60/164,258  
; PRIOR FILING DATE: 1999-11-09  
; NUMBER OF SEQ ID NOS: 4472  
; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 2706  
; LENGTH: 308  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: amino acid sequence  
US-09-710-279-2706

Query Match 89.3%; Score 25; DB 2; Length 308;  
Best Local Similarity 80.0%; Pred. No. 2.9e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5  
|||:|  
DB 209 HYALS 213

RESULT 19  
US-09-134-001C-3852  
; Sequence 3852, Application US/09134001C  
; Patent No. 6380370  
; GENERAL INFORMATION:  
; APPLICANT: Lynn Doucette-Stamm et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS  
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: GTC-007  
; CURRENT APPLICATION NUMBER: US/09/134,001C  
; CURRENT FILING DATE: 1998-08-13  
; PRIOR APPLICATION NUMBER: US 60/064,964  
; PRIOR FILING DATE: 1997-11-08  
; PRIOR APPLICATION NUMBER: US 60/055,779  
; PRIOR FILING DATE: 1997-08-14  
; NUMBER OF SEQ ID NOS: 5674  
; SEQ ID NO 3852  
; LENGTH: 318  
; TYPE: PRT  
; ORGANISM: Staphylococcus epidermidis  
US-09-134-001C-3852

Query Match 89.3%; Score 25; DB 2; Length 318;  
Best Local Similarity 80.0%; Pred. No. 3e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5  
|||:|  
DB 219 HYALS 223

RESULT 20  
US-09-248-796A-14325  
; Sequence 14325, Application US/09248796A  
; Patent No. 6747137  
; GENERAL INFORMATION:  
; APPLICANT: Keith Weinstock et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN  
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.132  
; CURRENT APPLICATION NUMBER: US/09/248,796A  
; CURRENT FILING DATE: 1999-02-12  
; PRIOR APPLICATION NUMBER: US 60/074,725  
; PRIOR FILING DATE: 1998-02-13  
; PRIOR APPLICATION NUMBER: US 60/096,409  
; PRIOR FILING DATE: 1998-08-13  
; NUMBER OF SEQ ID NOS: 28208  
; SEQ ID NO 14325  
; LENGTH: 318  
; TYPE: PRT  
; ORGANISM: Candida albicans  
US-09-248-796A-14325

Query Match 89.3%; Score 25; DB 2; Length 318;  
Best Local Similarity 80.0%; Pred. No. 3e+02;

```
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 HYAMS 5
Db 199 HYALS 203

RESULT 21
US-09-270-767-44839
; Sequence 44839, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 44839
; LENGTH: 348
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-44839

Query Match 89.3%; Score 25; DB 2; Length 348;
Best Local Similarity 80.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 HYAMS 5
Db 193 HYAMA 197

RESULT 22
US-09-711-164-448
; Sequence 448, Application US/09711164
; Patent No. 6589738
; GENERAL INFORMATION:
; APPLICANT: Forsyth, R. Allyn
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; TITLE OF INVENTION: GENES ESSENTIAL FOR MICROBIAL PROLIFERATION AND ANTISENSE THEREOF
; FILE REFERENCE: ELITRA.008A
; CURRENT APPLICATION NUMBER: US/09/711,164
; CURRENT FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: US 60/164415
; PRIOR FILING DATE: 1999-11-9
; NUMBER OF SEQ ID NOS: 469
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 448
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Escherichia coli
US-09-711-164-448

Query Match 89.3%; Score 25; DB 2; Length 352;
Best Local Similarity 80.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 HYAMS 5
Db 245 HYAMT 249

RESULT 23
US-09-543-681A-5431
; Sequence 5431, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
```

```
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 5431
; LENGTH: 359
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-5431

Query Match 89.3%; Score 25; DB 2; Length 359;
Best Local Similarity 80.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 HYAMS 5
Db 250 HYAMT 254

RESULT 24
US-09-500-569-16
; Sequence 16, Application US/09500569
; Patent No. 6329204
; GENERAL INFORMATION:
; APPLICANT: Cahoon, Rebecca E.
; APPLICANT: Rafalski, Antoni
; APPLICANT: Shen, Jennie
; TITLE OF INVENTION: Plant Caffeic acid 3-O-Methyltransferase Homologs
; FILE REFERENCE: BB1327 US NA
; CURRENT APPLICATION NUMBER: US/09/500,569
; CURRENT FILING DATE: 2000-02-09
; EARLIER APPLICATION NUMBER: 60/119,587
; EARLIER FILING DATE: 1999-February-10
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 16
; LENGTH: 371
; TYPE: PRT
; ORGANISM: Oryza sativa
US-09-500-569-16

Query Match 89.3%; Score 25; DB 2; Length 371;
Best Local Similarity 80.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 HYAMS 5
Db 291 HYALS 295

RESULT 25
US-09-971-823B-16
; Sequence 16, Application US/09971823B
; Patent No. 6610521
; GENERAL INFORMATION:
; APPLICANT: Cahoon, Rebecca E.
; TITLE OF INVENTION: Plant Caffeic acid 3-O-Methyltransferase Homologs
; FILE REFERENCE: BB1327 US NA
; CURRENT APPLICATION NUMBER: US/09/971,823B
; CURRENT FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/119,587
; PRIOR FILING DATE: 1999-02-10
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 16
; LENGTH: 371
; TYPE: PRT
; ORGANISM: Oryza sativa
US-09-971-823B-16
```

Query Match 89.3%; Score 25; DB 2; Length 371;  
Best Local Similarity 80.0%; Pred. No. 3.5e+02; Mismatches 0; Indels 0; Gaps 0;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5  
DB 291 HYALS 295

RESULT 26  
US-09-489-039A-10078  
; Sequence 10078, Application US/09489039A  
; Patent No. 6610836  
; GENERAL INFORMATION:  
; APPLICANT: Gary Breton et. al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA  
; FILE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 2709.2004001  
; CURRENT APPLICATION NUMBER: US/09/489,039A  
; CURRENT FILING DATE: 2000-01-27  
; PRIOR APPLICATION NUMBER: US 60/117,747  
; PRIOR FILING DATE: 1999-01-29  
; NUMBER OF SEQ ID NOS: 14342  
; SEQ ID NO 10078  
; LENGTH: 410  
; TYPE: PRT  
; ORGANISM: Klebsiella pneumoniae  
US-09-489-039A-10078

Query Match 89.3%; Score 25; DB 2; Length 410;  
Best Local Similarity 80.0%; Pred. No. 3.9e+02; Mismatches 0; Indels 0; Gaps 0;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5  
DB 391 HYAMA 395

RESULT 27  
US-08-311-731A-48  
; Sequence 48, Application US/08311731A  
; Patent No. 6581266  
; GENERAL INFORMATION:  
; APPLICANT: SMITH, DOUGLAS  
; APPLICANT: MAO, JEN-I  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES  
; TITLE OF INVENTION: RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LAPRAE FOR  
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS  
; NUMBER OF SEQUENCES: 411  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.  
; STREET: 600 ATLANTIC AVENUE  
; CITY: BOSTON  
; STATE: MASSACHUSETTS  
; COUNTRY: USA  
; ZIP: 02210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/311,731A  
; FILING DATE:  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: GATES, EDWARD R.  
; REGISTRATION NUMBER: 31,616  
; REFERENCE/DOCKET NUMBER: C0044/7125  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617/720-3500  
; TELEFAX: 617/720-2441

; INFORMATION FOR SEQ ID NO: 48:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 439 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: YES  
; ORIGINAL SOURCE:  
; ORGANISM: MYCOBACTERIUM LEPRAE  
US-08-311-731A-48

Query Match 89.3%; Score 25; DB 2; Length 439;  
Best Local Similarity 80.0%; Pred. No. 4.2e+02; Mismatches 1; Mismatches 0; Indels 0; Gaps 0;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5  
DB 366 HYAMT 370

RESULT 28  
US-09-543-681A-8179  
; Sequence 8179, Application US/09543681A  
; Patent No. 6605709  
; GENERAL INFORMATION:  
; APPLICANT: GARY BRETON  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS  
; FILE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 2709.1002-001  
; CURRENT APPLICATION NUMBER: US/09/543,681A  
; CURRENT FILING DATE: 2000-04-05  
; PRIOR APPLICATION NUMBER: US 60/128,706  
; PRIOR FILING DATE: 1999-04-09  
; NUMBER OF SEQ ID NOS: 8344  
; SEQ ID NO 8179  
; LENGTH: 440  
; TYPE: PRT  
; ORGANISM: Proteus mirabilis  
US-09-543-681A-8179

Query Match 89.3%; Score 25; DB 2; Length 440;  
Best Local Similarity 80.0%; Pred. No. 4.2e+02; Mismatches 1; Mismatches 0; Indels 0; Gaps 0;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5  
DB 106 HYAMN 110

RESULT 29  
US-09-248-796A-19817  
; Sequence 19817, Application US/09248796A  
; Patent No. 6747137  
; GENERAL INFORMATION:  
; APPLICANT: Keith Weinstock et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS  
; FILE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.132  
; CURRENT APPLICATION NUMBER: US/09/248,796A  
; CURRENT FILING DATE: 1999-02-12  
; PRIOR APPLICATION NUMBER: US 60/074,725  
; PRIOR FILING DATE: 1998-02-13  
; PRIOR APPLICATION NUMBER: US 60/096,409  
; PRIOR FILING DATE: 1998-08-13  
; NUMBER OF SEQ ID NOS: 28208  
; SEQ ID NO 19817  
; LENGTH: 440  
; TYPE: PRT  
; ORGANISM: Candida albicans  
US-09-248-796A-19817

Query Match 89.3%; Score 25; DB 2; Length 440;  
Best Local Similarity 80.0%; Pred. No. 4.2e+02; Mismatches 1; Mismatches 0; Indels 0; Gaps 0;

```
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 HVAMS 5
Db 344 HYAMN 348

RESULT 30
US-09-328-352-4712
; Sequence 4712, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 4712
; LENGTH: 473
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-4712

Query Match 89.3%; Score 25; DB 2; Length 473;
Best Local Similarity 80.0%; Pred. No. 4.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 HVAMS 5
Db 462 HYALS 466

RESULT 31
US-09-198-956-2
; Sequence 2, Application US/09198956
; Patent No. 6165769
; GENERAL INFORMATION:
; APPLICANT: Andersen, Lene N.
; APPLICANT: Schulein, Martin
; APPLICANT: Lange, Niels Erik K.
; APPLICANT: Bjornvad, Mads E.
; APPLICANT: Schnorr, Kirk
; TITLE OF INVENTION: Pectin Degrading Enzymes From Bacillus
; TITLE OF INVENTION: Licheniformis
; FILE REFERENCE: 5377,200-US
; CURRENT APPLICATION NUMBER: US/09/198,956
; CURRENT FILING DATE: 1998-11-24
; EARLIER APPLICATION NUMBER: 1344/97
; EARLIER FILING DATE: 1997-11-24
; EARLIER APPLICATION NUMBER: 60/067,240
; EARLIER FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 494
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-09-198-956-2

Query Match 89.3%; Score 25; DB 2; Length 494;
Best Local Similarity 80.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 HVAMS 5
Db 99 HYALS 103

RESULT 32
US-09-670-141-2
; Sequence 2, Application US/09670141
```

```
; Patent No. 6429000
; GENERAL INFORMATION:
; APPLICANT: Andersen, Lene N.
; APPLICANT: Schulein, Martin
; APPLICANT: Lange, Niels Erik K.
; APPLICANT: Bjornvad, Mads E.
; APPLICANT: Schnorr, Kirk
; TITLE OF INVENTION: Pectin Degrading Enzymes From Bacillus
; TITLE OF INVENTION: Licheniformis
; FILE REFERENCE: 5377,200-US
; CURRENT APPLICATION NUMBER: US/09/670,141
; CURRENT FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: 09/198,956
; PRIOR FILING DATE: 1998-11-24
; PRIOR APPLICATION NUMBER: 1344/97
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/067,240
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 494
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-09-670-141-2

Query Match 89.3%; Score 25; DB 2; Length 494;
Best Local Similarity 80.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 HVAMS 5
Db 99 HYALS 103

RESULT 33
US-08-335-865J-9
; Sequence 9, Application US/08335865J
; Patent No. 6107472
; GENERAL INFORMATION:
; APPLICANT: Stacker, Steven A.; Hovens, Christopher M.,
; APPLICANT: Wilks, Andrew F.
; TITLE OF INVENTION: RECEPTOR-TYPE TYROSINE KINASE-LIKE MOLECULES
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski L.L.P.
; STREET: 666 Fifth Ave
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 720 KB storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: ASCII/Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/335,865J
; FILING DATE: 19-January-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/AU93/00210
; FILING DATE: 10-May-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PL2358
; FILING DATE: 11-May-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6107472man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD-5277
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3100
; TELEFAX: (212) 752-5958
```

; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 566  
; TYPE: amino acid  
; TOPOLOGY: linear  
; ORIGINAL SOURCE: mouse  
US-08-335-865J-9

Query Match 89.3%; Score 25; DB 2; Length 566;  
Best Local Similarity 80.0%; Pred. No. 5.5e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5  
|||:  
Db 49 HYALS 53

RESULT 34  
US-08-335-865J-21  
; Sequence 21, Application US/08335865J  
; Patent No. 6107472  
; GENERAL INFORMATION:  
; APPLICANT: Stacke, Steven A.; Hovens, Christopher M.,  
; APPLICANT: Wilks, Andrew F.  
; TITLE OF INVENTION: RECEPTOR-TYPE TYROSINE KINASE-LIKE MOLECULES  
; NUMBER OF SEQUENCES: 21  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fulbright & Jaworski L.L.P.  
; STREET: 666 Fifth Ave  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10103

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.5 inch, 720 KB storage  
; COMPUTER: IBM PS/2  
; OPERATING SYSTEM: PC-DOS  
; SOFTWARE: ASCII/Wordperfect  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/335,865J  
; FILING DATE: 19-January-1995  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/AU93/00210  
; FILING DATE: 10-May-1993  
; APPLICATION NUMBER: PL2358  
; FILING DATE: 11-May-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hanson, No. 6107472man D.  
; REGISTRATION NUMBER: 30,946  
; REFERENCE/DOCKET NUMBER: LUD-5277  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 318-3100  
; TELEFAX: (212) 752-5958  
; INFORMATION FOR SEQ ID NO: 21:

SEQUENCE CHARACTERISTICS:  
; LENGTH: 593  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; ORIGINAL SOURCE: human  
US-08-335-865J-21

Query Match 89.3%; Score 25; DB 2; Length 593;  
Best Local Similarity 80.0%; Pred. No. 5.7e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5  
|||:  
Db 76 HYALS 80

RESULT 35  
US-08-335-865J-20  
; Sequence 20, Application US/08335865J  
; Patent No. 6107472  
; GENERAL INFORMATION:  
; APPLICANT: Stacke, Steven A.; Hovens, Christopher M.,  
; APPLICANT: Wilks, Andrew F.  
; TITLE OF INVENTION: RECEPTOR-TYPE TYROSINE KINASE-LIKE MOLECULES  
; NUMBER OF SEQUENCES: 21  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fulbright & Jaworski L.L.P.  
; STREET: 666 Fifth Ave  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10103

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.5 inch, 720 KB storage  
; COMPUTER: IBM PS/2  
; OPERATING SYSTEM: PC-DOS  
; SOFTWARE: ASCII/Wordperfect  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/335,865J  
; FILING DATE: 19-January-1995  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/AU93/00210  
; FILING DATE: 10-May-1993  
; APPLICATION NUMBER: PL2358  
; FILING DATE: 11-May-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hanson, No. 6107472man D.  
; REGISTRATION NUMBER: 30,946  
; REFERENCE/DOCKET NUMBER: LUD-5277  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 318-3100  
; TELEFAX: (212) 752-5958  
; INFORMATION FOR SEQ ID NO: 20:

SEQUENCE CHARACTERISTICS:  
; LENGTH: 606  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; ORIGINAL SOURCE: human  
US-08-335-865J-20

Query Match 89.3%; Score 25; DB 2; Length 606;  
Best Local Similarity 80.0%; Pred. No. 5.9e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5  
|||:  
Db 90 HYALS 94

RESULT 36  
US-09-771-161A-240  
; Sequence 240, Application US/09771161A  
; Patent No. 6936450  
; GENERAL INFORMATION:  
; APPLICANT: LEVINE, et al.  
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES  
; FILE REFERENCE: 802620-2005.1  
; CURRENT APPLICATION NUMBER: US/09/771,161A  
; CURRENT FILING DATE: 2001-01-26  
; PRIOR APPLICATION NUMBER: 09/724,676  
; PRIOR FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: 136776  
; PRIOR FILING DATE: 2000-06-15  
; PRIOR APPLICATION NUMBER: 135619  
; PRIOR FILING DATE: 2000-04-12  
; NUMBER OF SEQ ID NOS: 273

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; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 240
; LENGTH: 606
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-771-161A-240

Query Match      89.3%; Score 25; DB 2; Length 606;
Best Local Similarity 80.0%; Pred. No. 5.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 HYAMS 5
      |||||
Db      90 HVALS 94

RESULT 37
US-09-771-161A-241
; Sequence 241, Application US/09771161A
; Patent No. 6936450
; GENERAL INFORMATION:
; APPLICANT: LEVINE, et al.
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
; FILE REFERENCE: 802620-2005.1
; CURRENT APPLICATION NUMBER: US/09/771,161A
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/724,676
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 136776
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 135619
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 241
; LENGTH: 606
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-771-161A-241

Query Match      89.3%; Score 25; DB 2; Length 606;
Best Local Similarity 80.0%; Pred. No. 5.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 HYAMS 5
      |||||
Db      90 HVALS 94

RESULT 38
US-09-252-991A-24741
; Sequence 24741, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 24741
; LENGTH: 628
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-24741

Query Match      89.3%; Score 25; DB 2; Length 628;
Best Local Similarity 80.0%; Pred. No. 6.1e+02;
```

```
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 HYAMS 5
      |||||
Db      604 HYAMA 608

RESULT 39
US-09-147-236-7
; Sequence 7, Application US/09147236A
; Patent No. 6316251
; GENERAL INFORMATION:
; APPLICANT: TONOUCHI, Naoto
; APPLICANT: TSUCHIDA, Takayasu
; APPLICANT: YOSHINAGA, Fumihito
; APPLICANT: TAHARA, Naoki
; APPLICANT: HAYASHI, Takahisa
; TITLE OF INVENTION: NOVEL GENE, GROUP OF GENES, AND NOVEL BETA-GLUCOSIDASE
; FILE REFERENCE: 6537-011-0PCT
; CURRENT APPLICATION NUMBER: US/09/147,236A
; EARLIER APPLICATION NUMBER: PCT/JP97/03633
; PRIOR FILING DATE: 1999-04-08
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 735
; TYPE: PRT
; ORGANISM: Acetobacter xylinum
; FEATURE:
; OTHER INFORMATION: n at positions 15741 and 15767 may be a, g, t, or
; OTHER INFORMATION: c
US-09-147-236-7

Query Match      89.3%; Score 25; DB 2; Length 735;
Best Local Similarity 80.0%; Pred. No. 7.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 HYAMS 5
      |||||
Db      199 HYAMN 203

RESULT 40
US-09-522-474-7
; Sequence 7, Application US/09522474
; Patent No. 6573076
; GENERAL INFORMATION:
; APPLICANT: TONOUCHI, Naoto
; APPLICANT: TSUCHIDA, Takayasu
; APPLICANT: YOSHINAGA, Fumihiro
; APPLICANT: TAHARA, Naoki
; APPLICANT: HAYASHI, Takahisa
; TITLE OF INVENTION: NOVEL GENE, GROUP OF GENES, AND NOVEL BETA-GLUCOSIDASE
; FILE REFERENCE: 6537-011-0PCT
; CURRENT APPLICATION NUMBER: US/09/522,474
; CURRENT FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US/09/147,236
; PRIOR FILING DATE: 1999-04-08
; PRIOR APPLICATION NUMBER: PCT/JP97/03633
; PRIOR FILING DATE: 1997-10-09
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 735
; TYPE: PRT
; ORGANISM: Acetobacter xylinum
; FEATURE:
; OTHER INFORMATION: n at positions 15741 and 15767 may be a, g, t, or
; OTHER INFORMATION: c
US-09-522-474-7

Query Match      89.3%; Score 25; DB 2; Length 735;
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Best Local Similarity 80.0%; Pred. No. 7.2e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5  
DB 199 HYAMN 203

RESULT 41  
US-09-095-881-14  
; Sequence 14, Application US/09095881  
; Patent No. 6489137  
; GENERAL INFORMATION:  
; APPLICANT: Seeley, Todd  
; TITLE OF INVENTION: DETECTION OF LOSS OF THE WILD-TYPE  
; FILE REFERENCE: 1405.003 / 200130.437  
; CURRENT APPLICATION NUMBER: US/09/095,881  
; CURRENT FILING DATE: 1998-06-11  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 14  
; LENGTH: 46  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-09-095-881-14

Query Match 85.7%; Score 24; DB 2; Length 46;  
Best Local Similarity 100.0%; Pred. No. 65;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAM 4  
DB 28 HYAM 31

RESULT 42  
US-09-621-976-6089  
; Sequence 6089, Application US/09621976  
; Patent No. 6639063  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Jobert, S.  
; APPLICANT: Giordano, J.Y.  
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.  
; FILE REFERENCE: GENSET.054PR2  
; CURRENT APPLICATION NUMBER: US/09/621,976  
; CURRENT FILING DATE: 2000-07-21  
; NUMBER OF SEQ ID NOS: 19335  
; SOFTWARE: Patent.pm  
; SEQ ID NO 6089  
; LENGTH: 61  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; NAME/KEY: UNSURE  
; LOCATION: 29  
; OTHER INFORMATION: Xaa = \*, Glu  
US-09-621-976-6089

Query Match 85.7%; Score 24; DB 2; Length 61;  
Best Local Similarity 100.0%; Pred. No. 88;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAM 4  
DB 46 HYAM 49

RESULT 43  
US-09-489-039A-13625  
; Sequence 13625, Application US/09489039A  
; Patent No. 6610836

; GENERAL INFORMATION:  
; APPLICANT: Gary Breton et. al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA  
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 2709.2004001  
; CURRENT APPLICATION NUMBER: US/09/489,039A  
; CURRENT FILING DATE: 2000-01-27  
; PRIOR APPLICATION NUMBER: US 60/117,747  
; PRIOR FILING DATE: 1999-01-29  
; NUMBER OF SEQ ID NOS: 14342  
; SEQ ID NO 13625  
; LENGTH: 63  
; TYPE: PRT  
; ORGANISM: Klebsiella pneumoniae  
US-09-489-039A-13625

Query Match 85.7%; Score 24; DB 2; Length 63;  
Best Local Similarity 100.0%; Pred. No. 91;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAM 4  
DB 23 HYAM 26

RESULT 44  
US-09-270-767-62479  
; Sequence 62479, Application US/09270767  
; Patent No. 6703491  
; GENERAL INFORMATION:  
; APPLICANT: Homburger et al.  
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
; FILE REFERENCE: File Reference: 7326-094  
; CURRENT APPLICATION NUMBER: US/09/270,767  
; CURRENT FILING DATE: 1999-03-17  
; NUMBER OF SEQ ID NOS: 62517  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 62479  
; LENGTH: 68  
; TYPE: PRT  
; ORGANISM: Drosophila melanogaster  
; FEATURE:  
; OTHER INFORMATION: Xaa means any amino acid  
US-09-270-767-62479

Query Match 85.7%; Score 24; DB 2; Length 68;  
Best Local Similarity 100.0%; Pred. No. 99;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAM 4  
DB 54 HYAM 57

RESULT 45  
US-09-248-796A-26555  
; Sequence 26555, Application US/09248796A  
; Patent No. 6747137  
; GENERAL INFORMATION:  
; APPLICANT: Keith Weinstock et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN  
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.132  
; CURRENT APPLICATION NUMBER: US/09/248,796A  
; CURRENT FILING DATE: 1999-02-12  
; PRIOR APPLICATION NUMBER: US 60/074,725  
; PRIOR FILING DATE: 1998-02-13  
; PRIOR APPLICATION NUMBER: US 60/096,409  
; PRIOR FILING DATE: 1998-08-13  
; NUMBER OF SEQ ID NOS: 28208  
; SEQ ID NO 26555  
; LENGTH: 77  
; TYPE: PRT



; ORGANISM: Candida albicans  
US-09-248-796A-26555

Query Match 85.7%; Score 24; DB 2; Length 77;  
Best Local Similarity 80.0%; Pred. No. 1.1e+02;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HYAMS 5  
Db 72 HYMS 76

## RESULT 46

US-08-858-207A-504  
; Sequence 504, Application US/08858207A  
; Patent No. 6348328  
; GENERAL INFORMATION:  
; APPLICANT: Black, Michael  
; APPLICANT: Hodgson, John  
; APPLICANT: Knowles, David  
; APPLICANT: Nicholas, Richard  
; APPLICANT: Stodola, Robert  
; TITLE OF INVENTION: No. 6348328e1 Compounds  
; NUMBER OF SEQUENCES: 552  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SmithKline Beecham Corporation  
; STREET: 709 Swedeland Road  
; CITY: King of Prussia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19406-0939  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: Fast-Seq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/858,207A  
; FILING DATE: 09-MAY-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/017670  
; FILING DATE: 14-MAY-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Gimml, Edward R  
; REGISTRATION NUMBER: 38,891  
; REFERENCE/DOCKET NUMBER: P50475  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 610-270-4478  
; TELEFAX: 610-270-5090  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 504:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 88 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: No. 6348328e

US-08-858-207A-504  
Query Match 85.7%; Score 24; DB 2; Length 88;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HYAM 4  
Db 16 HYAM 19

## RESULT 47

US-10-104-047-3071  
; Sequence 3071, Application US/10104047  
; Patent No. 6943241

; GENERAL INFORMATION:  
; APPLICANT: HELIX RESEARCH INSTITUTE  
; TITLE OF INVENTION: No. 6943241e1 full length cDNA  
; FILE REFERENCE: H1-A0105  
; CURRENT APPLICATION NUMBER: US/10/104,047  
; CURRENT FILING DATE: 2002-03-25  
; PRIOR APPLICATION NUMBER:  
; PRIOR FILING DATE:  
; NUMBER OF SEQ ID NOS: 4096  
; SOFTWARE: PatentIn ver. 2.1  
; SEQ ID NO 3071  
; LENGTH: 108  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-104-047-3071

Query Match 85.7%; Score 24; DB 2; Length 108;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HYAM 4  
Db 54 HYAM 57

## RESULT 48

US-10-104-047-3241  
; Sequence 3241, Application US/10104047  
; Patent No. 6943241  
; GENERAL INFORMATION:  
; APPLICANT: HELIX RESEARCH INSTITUTE  
; TITLE OF INVENTION: No. 6943241e1 full length cDNA  
; FILE REFERENCE: H1-A0105  
; CURRENT APPLICATION NUMBER: US/10/104,047  
; CURRENT FILING DATE: 2002-03-25  
; PRIOR APPLICATION NUMBER:  
; PRIOR FILING DATE:  
; NUMBER OF SEQ ID NOS: 4096  
; SOFTWARE: PatentIn ver. 2.1  
; SEQ ID NO 3241  
; LENGTH: 137  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-104-047-3241

Query Match 85.7%; Score 24; DB 2; Length 137;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HYAM 4  
Db 83 HYAM 86

## RESULT 49

US-08-943-136-4  
; Sequence 4, Application US/08943136  
; Patent No. 6291208  
; GENERAL INFORMATION:  
; APPLICANT: Anand, Naveen N  
; APPLICANT: Barber, Brian H  
; APPLICANT: Cates, George A  
; APPLICANT: Caterini, Judith E  
; APPLICANT: Klein, Michel H  
; TITLE OF INVENTION: CHIMERIC ANTIBODIES FOR DELIVERY OF  
; TITLE OF INVENTION: ANTIGENS TO SELECTED CELLS OF THE IMMUNE SYSTEM  
; NUMBER OF SEQUENCES: 20  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sim & McBurney  
; STREET: 6th Floor, 330 University Avenue  
; CITY: Toronto  
; STATE: Ontario  
; COUNTRY: Canada

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; ZIP: MSG 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/943,136
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/483,576
; FILING DATE: 07-JUNE-1995
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-733
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 140 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-943-136-4

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Query Match      85.7%; Score 24; DB 2; Length 140;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 HYAM 4
Db      124 HYAM 127

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RESULT 50
US-08-973-518-4
; Sequence 4, Application US/08973518
; Patent No. 6328962
; GENERAL INFORMATION:
; APPLICANT: Anand, Naveen N
; APPLICANT: Barber, Brian H
; APPLICANT: Cates, George A
; APPLICANT: Caterini, Judith E
; APPLICANT: Klein, Michel H
; TITLE OF INVENTION: CHIMERIC ANTIBODIES FOR DELIVERY OF
; TITLE OF INVENTION: ANTIGENS TO SELECTED CELLS OF THE IMMUNE SYSTEM
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: 6th Floor, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: MSG 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/973,518
; FILING DATE: 07-APR-1998
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-781
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155

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; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 140 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-973-518-4
; Query Match      85.7%; Score 24; DB 2; Length 140;
; Best Local Similarity 100.0%; Pred. No. 2.1e+02;
; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
; Qy      1 HYAM 4
; Db      124 HYAM 127
; Search completed: April 6, 2006, 09:00:39
; Job time : 14.6949 secs

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GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: April 6, 2006, 09:13:24 ; Search time 40.4237 Seconds

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Title: US-10-089-500-3

Perfect score: 28

Sequence: 1 HVAMS 5

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Maximum Match 100%

Listing first 1000 summaries

Database : Published Applications AA Main:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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4	28	100.0	119	4	US-10-282-122A-44196
5	28	100.0	119	4	US-10-282-122A-71569
6	28	100.0	119	5	US-10-717-138-6
7	28	100.0	130	3	US-09-762-304-8
8	28	100.0	130	3	US-09-764-304-18
9	28	100.0	130	4	US-10-265-713-8
10	28	100.0	130	4	US-10-265-713-18
11	28	100.0	130	4	US-10-166-626-8
12	28	100.0	130	4	US-10-166-626-18
13	28	100.0	156	5	US-10-450-763-59338
14	28	100.0	412	4	US-10-369-493-10250
15	28	100.0	424	3	US-09-824-734-4
16	28	100.0	424	4	US-10-749-386-4
17	28	100.0	1031	4	US-10-437-963-189155
18	28	100.0	1569	6	US-11-097-143-18732
19	25	89.3	53	4	US-10-424-599-240643
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21	25	89.3	57	4	US-10-424-599-181420
22	25	89.3	57	4	US-10-425-115-249920
23	25	89.3	58	4	US-10-424-599-177790
24	25	89.3	58	4	US-10-335-977-8261
25	25	89.3	70	4	US-10-424-599-214263
26	25	89.3	77	4	US-10-424-599-199143
27	25	89.3	84	4	US-10-425-115-313005

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29	25	89.3	86	4	US-10-424-599-180930	Sequence 180930,
30	25	89.3	86	4	US-10-424-599-231987	Sequence 231987,
31	25	89.3	89	4	US-10-424-599-184650	Sequence 184650,
32	25	89.3	99	4	US-10-425-115-270245	Sequence 270245,
33	25	89.3	100	4	US-10-437-963-172988	Sequence 172988,
34	25	89.3	107	4	US-10-437-963-165791	Sequence 165791,
35	25	89.3	113	5	US-10-501-282-1606	Sequence 1606, Ap
36	25	89.3	126	4	US-10-282-122A-77481	Sequence 77481, A
37	25	89.3	131	4	US-10-437-963-106924	Sequence 106924,
38	25	89.3	131	4	US-10-425-115-360208	Sequence 360208,
39	25	89.3	133	5	US-10-501-282-1614	Sequence 1614, Ap
40	25	89.3	134	5	US-10-501-282-1608	Sequence 1608, Ap
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42	25	89.3	136	4	US-10-424-599-177566	Sequence 177566,
43	25	89.3	148	4	US-10-424-599-188149	Sequence 188149,
44	25	89.3	150	3	US-09-764-868-938	Sequence 938, App
45	25	89.3	174	5	US-10-450-763-52145	Sequence 52145, A
46	25	89.3	174	4	US-10-425-115-225898	Sequence 225898,
47	25	89.3	180	4	US-10-275-589-3	Sequence 3, Appli
48	25	89.3	181	4	US-10-275-589-2	Sequence 2, Appli
49	25	89.3	191	4	US-10-275-589-1	Sequence 1, Appli
50	25	89.3	191	4	US-10-425-115-269047	Sequence 269047,
51	25	89.3	192	4	US-10-437-963-203843	Sequence 203843,
52	25	89.3	201	4	US-10-437-963-117523	Sequence 117523,
53	25	89.3	204	4	US-10-275-589-10	Sequence 10, Appl
54	25	89.3	205	4	US-10-424-599-177794	Sequence 177794,
55	25	89.3	210	4	US-10-437-963-150670	Sequence 150670,
56	25	89.3	214	5	US-10-501-282-4938	Sequence 4938, Ap
57	25	89.3	215	5	US-10-501-282-4940	Sequence 4940, Ap
58	25	89.3	218	4	US-10-275-589-8	Sequence 8, Appli
59	25	89.3	221	4	US-10-451-467A-130	Sequence 130, App
60	25	89.3	230	5	US-10-732-923-20929	Sequence 20929, A
61	25	89.3	236	4	US-10-238-075-1019	Sequence 1019, Ap
62	25	89.3	245	4	US-10-767-701-55900	Sequence 55900, A
63	25	89.3	259	5	US-10-220-335-196	Sequence 196, App
64	25	89.3	272	3	US-09-771-161A-149	Sequence 149, App
65	25	89.3	286	4	US-10-425-115-252561	Sequence 252561,
66	25	89.3	296	4	US-10-437-963-177489	Sequence 177489,
67	25	89.3	318	4	US-10-724-972A-5558	Sequence 5558, Ap
68	25	89.3	349	4	US-10-335-977-6766	Sequence 6766, Ap
69	25	89.3	350	4	US-10-437-963-150112	Sequence 150112,
70	25	89.3	352	4	US-10-287-274-448	Sequence 448, App
71	25	89.3	352	4	US-10-282-122A-42718	Sequence 42718, A
72	25	89.3	352	4	US-10-282-122A-56085	Sequence 56085, A
73	25	89.3	352	4	US-10-282-122A-73027	Sequence 73027, A
74	25	89.3	352	4	US-10-282-122A-75084	Sequence 75084, A
75	25	89.3	352	4	US-10-282-122A-75831	Sequence 75831, A
76	25	89.3	353	4	US-10-282-122A-72686	Sequence 72686, A
77	25	89.3	354	4	US-10-282-122A-69126	Sequence 69126, A
78	25	89.3	356	4	US-10-282-122A-59523	Sequence 59523, A
79	25	89.3	358	4	US-10-282-122A-55684	Sequence 55684, A
80	25	89.3	359	4	US-10-282-122A-75949	Sequence 75949, A
81	25	89.3	361	4	US-10-282-122A-42851	Sequence 42851, A
82	25	89.3	367	4	US-10-282-122A-66664	Sequence 66664, A
83	25	89.3	367	5	US-10-495-455-24	Sequence 24, Appl
84	25	89.3	367	5	US-10-495-455-36	Sequence 36, Appl
85	25	89.3	371	4	US-10-464-610-16	Sequence 16, Appl
86	25	89.3	408	4	US-10-275-589-9	Sequence 9, Appli
87	25	89.3	414	4	US-10-275-589-7	Sequence 7, Appli
88	25	89.3	442	4	US-10-282-122A-54210	Sequence 54210, A
89	25	89.3	442	4	US-10-437-963-129724	Sequence 129724,
90	25	89.3	464	4	US-10-369-493-2216	Sequence 2216, Ap
91	25	89.3	475	5	US-10-915-366-2	Sequence 2, Appli
92	25	89.3	496	6	US-11-097-143-4809	Sequence 4809, Ap
93	25	89.3	564	4	US-10-437-963-183104	Sequence 183104,
94	25	89.3	594	5	US-10-972-073-16	Sequence 16, Appl
95	25	89.3	594	5	US-10-972-078-16	Sequence 16, Appl
96	25	89.3	604	5	US-10-264-237-2102	Sequence 2102, Ap
97	25	89.3	604	5	US-10-847-972-83	Sequence 83, Appl
98	25	89.3	604	5	US-10-972-073-14	Sequence 14, Appl
99	25	89.3	604	5	US-10-972-078-14	Sequence 14, Appl
100	25	89.3	604	5	US-10-503-870A-10	Sequence 10, Appl

101	25	89.3	604	5	US-10-745-237-312	Sequence 312, App	174	24	85.7	124	5	US-10-963-903-92	Sequence 92, Appl
102	25	89.3	606	3	US-09-771-161A-240	Sequence 240, App	175	24	85.7	126	4	US-10-424-599-248021	Sequence 248021,
103	25	89.3	606	3	US-09-771-161A-241	Sequence 241, App	176	24	85.7	127	3	US-09-778-927A-69	Sequence 69, Appl
104	25	89.3	606	5	US-10-482-029-36	Sequence 36, Appl	177	24	85.7	137	4	US-10-104-047-3241	Sequence 3241, Ap
105	25	89.3	607	4	US-10-275-589-6	Sequence 6, Appl	178	24	85.7	137	4	US-10-437-963-127823	Sequence 127823,
106	25	89.3	607	4	US-10-618-941-116	Sequence 116, App	179	24	85.7	138	4	US-10-425-115-289256	Sequence 289256,
107	25	89.3	610	4	US-10-236-417-98	Sequence 98, Appl	180	24	85.7	140	2	US-08-973-518-4	Sequence 4, Appl
108	25	89.3	631	4	US-10-323-167-8	Sequence 167, App	181	24	85.7	140	3	US-09-007-093-4	Sequence 4, Appl
109	25	89.3	635	6	US-11-097-143-15207	Sequence 15207, A	182	24	85.7	140	3	US-09-771-161A-103	Sequence 103, App
110	25	89.3	648	5	US-10-501-283-5536	Sequence 5536, Ap	183	24	85.7	140	4	US-10-428-754-4	Sequence 4, Appl
111	25	89.3	655	4	US-10-425-114-65646	Sequence 65646, A	184	24	85.7	145	4	US-10-425-114-60054	Sequence 60054, A
112	25	89.3	680	4	US-10-437-963-185054	Sequence 185054,	185	24	85.7	145	4	US-10-767-701-39101	Sequence 39101, A
113	25	89.3	716	5	US-10-501-282-5538	Sequence 5538, Ap	186	24	85.7	149	4	US-10-425-115-272662	Sequence 272662,
114	25	89.3	840	4	US-10-369-493-18521	Sequence 18521, A	187	24	85.7	149	5	US-10-926-683-898	Sequence 898, App
115	25	89.3	861	6	US-11-097-143-12084	Sequence 12084, A	188	24	85.7	151	4	US-10-425-114-53147	Sequence 53147, A
116	25	89.3	893	4	US-10-156-761-7726	Sequence 7726, Ap	189	24	85.7	151	4	US-10-425-114-58296	Sequence 58296, A
117	25	89.3	979	6	US-11-097-143-10662	Sequence 10662, A	190	24	85.7	159	4	US-10-425-115-298972	Sequence 298972,
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119	25	89.3	1012	4	US-10-369-493-18704	Sequence 18704, A	192	24	85.7	161	4	US-10-425-115-204361	Sequence 204361,
120	25	89.3	1070	6	US-11-097-143-15468	Sequence 15468, A	193	24	85.7	168	4	US-10-369-493-22329	Sequence 22329, A
121	25	89.3	1099	4	US-10-437-963-176244	Sequence 176244,	194	24	85.7	175	4	US-10-767-701-54218	Sequence 54218, A
122	25	89.3	1103	4	US-10-757-262-12	Sequence 12, Appl	195	24	85.7	178	5	US-10-732-923-1464	Sequence 1464, Ap
123	25	89.3	1296	6	US-11-097-143-23101	Sequence 23101, A	196	24	85.7	178	5	US-10-732-923-1465	Sequence 1465, Ap
124	25	89.3	1770	5	US-10-732-923-17002	Sequence 17002, A	197	24	85.7	181	4	US-10-168-624B-2	Sequence 2, Appl
125	25	89.3	2211	5	US-10-732-923-17003	Sequence 17003, A	198	24	85.7	182	4	US-10-767-701-33206	Sequence 33206, A
126	25	89.3	2640	5	US-10-450-763-56084	Sequence 56084, A	199	24	85.7	183	5	US-10-450-763-38095	Sequence 38095, A
127	25	89.3	3390	4	US-10-369-493-21101	Sequence 21101, A	200	24	85.7	187	5	US-10-732-923-3739	Sequence 3739, Ap
128	24	85.7	5	4	US-10-663-244-37	Sequence 37, Appl	201	24	85.7	193	4	US-10-282-122A-57723	Sequence 57723, A
129	24	85.7	12	5	US-10-996-316-191	Sequence 191, App	202	24	85.7	196	4	US-10-437-963-109874	Sequence 109874,
130	24	85.7	22	5	US-10-792-582-486	Sequence 486, App	203	24	85.7	204	5	US-10-430-381-8	Sequence 8, Appl
131	24	85.7	27	4	US-10-424-599-155245	Sequence 155245,	204	24	85.7	207	6	US-11-006-098-196	Sequence 196, App
132	24	85.7	41	4	US-10-424-599-270897	Sequence 270897,	205	24	85.7	207	6	US-11-006-098-198	Sequence 198, App
133	24	85.7	42	4	US-10-425-115-290419	Sequence 290419,	206	24	85.7	209	5	US-10-732-923-20763	Sequence 20763, A
134	24	85.7	42	4	US-10-424-599-269350	Sequence 269350,	207	24	85.7	210	4	US-10-296-115-759	Sequence 759, App
135	24	85.7	44	4	US-10-050-882-94	Sequence 94, Appl	208	24	85.7	212	4	US-10-425-115-192944	Sequence 192944,
136	24	85.7	44	4	US-10-724-972A-6319	Sequence 6319, Ap	209	24	85.7	213	3	US-09-138-559-3	Sequence 3, Appl
137	24	85.7	44	5	US-10-963-903-94	Sequence 94, Appl	210	24	85.7	213	4	US-10-091-613-3	Sequence 3, Appl
138	24	85.7	46	3	US-09-095-881-14	Sequence 14, Appl	211	24	85.7	213	4	US-10-451-467A-604	Sequence 604, App
139	24	85.7	53	4	US-10-424-599-201659	Sequence 201659,	212	24	85.7	232	4	US-10-425-114-69416	Sequence 69416, A
140	24	85.7	60	4	US-10-424-599-209472	Sequence 209472,	213	24	85.7	235	3	US-09-925-301-1293	Sequence 1293, Ap
141	24	85.7	61	4	US-10-437-963-145128	Sequence 145128,	214	24	85.7	235	3	US-09-925-301-1293	Sequence 1293, Ap
142	24	85.7	66	4	US-10-424-599-171097	Sequence 171097,	215	24	85.7	246	5	US-10-732-923-19005	Sequence 19005, A
143	24	85.7	71	4	US-10-437-963-173084	Sequence 173084,	216	24	85.7	247	4	US-10-425-115-272616	Sequence 272616,
144	24	85.7	73	4	US-10-424-599-152210	Sequence 152210,	217	24	85.7	250	4	US-10-424-599-255877	Sequence 255877,
145	24	85.7	73	4	US-10-425-115-359176	Sequence 359176,	218	24	85.7	257	4	US-10-482-706-47	Sequence 47, Appl
146	24	85.7	78	4	US-10-424-599-268657	Sequence 268657,	219	24	85.7	257	4	US-10-425-115-305827	Sequence 305827,
147	24	85.7	83	6	US-11-097-143-32895	Sequence 32895, A	220	24	85.7	264	4	US-10-156-761-9702	Sequence 9702, Ap
148	24	85.7	85	4	US-10-029-386-31119	Sequence 31119, A	221	24	85.7	264	4	US-10-156-761-9702	Sequence 9702, Ap
149	24	85.7	86	4	US-10-425-115-208923	Sequence 208923,	222	24	85.7	264	4	US-10-156-761-9702	Sequence 9702, Ap
150	24	85.7	87	4	US-10-425-114-52361	Sequence 52361, A	223	24	85.7	269	4	US-10-027-770-2	Sequence 2, Appl
151	24	85.7	87	4	US-10-425-115-333045	Sequence 333045,	224	24	85.7	269	4	US-10-027-770-2	Sequence 2, Appl
152	24	85.7	89	4	US-10-424-599-239942	Sequence 239942,	225	24	85.7	270	5	US-10-627-556-338	Sequence 338, App
153	24	85.7	89	4	US-10-437-963-153971	Sequence 153971,	226	24	85.7	270	5	US-10-627-556-342	Sequence 342, App
154	24	85.7	92	4	US-10-424-599-166358	Sequence 166358,	227	24	85.7	275	4	US-10-424-599-263712	Sequence 263712,
155	24	85.7	93	4	US-10-437-963-200139	Sequence 200139,	228	24	85.7	278	4	US-10-425-115-216984	Sequence 216984,
156	24	85.7	93	4	US-10-425-115-306378	Sequence 306378,	229	24	85.7	287	4	US-10-425-115-277508	Sequence 277508,
157	24	85.7	97	4	US-10-437-963-139267	Sequence 139267,	230	24	85.7	288	6	US-11-097-143-6153	Sequence 6153, Ap
158	24	85.7	101	4	US-10-437-963-198385	Sequence 198385,	231	24	85.7	292	4	US-10-369-493-10666	Sequence 10666, A
159	24	85.7	102	3	US-09-835-788A-20	Sequence 20, Appl	232	24	85.7	294	4	US-10-424-599-202074	Sequence 202074,
160	24	85.7	102	4	US-10-080-170-301	Sequence 301, App	233	24	85.7	294	4	US-10-425-115-272658	Sequence 272658,
161	24	85.7	102	4	US-10-175-042-20	Sequence 20, Appl	234	24	85.7	296	4	US-10-469-393-6	Sequence 6, Appl
162	24	85.7	102	4	US-10-080-170-301	Sequence 301, App	235	24	85.7	298	4	US-10-664-421-54	Sequence 54, Appl
163	24	85.7	102	4	US-10-468-356-301	Sequence 301, App	236	24	85.7	298	5	US-10-941-635-54	Sequence 54, Appl
164	24	85.7	107	4	US-10-425-115-308842	Sequence 308842,	237	24	85.7	299	4	US-10-425-115-272458	Sequence 272458,
165	24	85.7	108	4	US-10-104-047-3071	Sequence 3071, Ap	238	24	85.7	308	3	US-09-738-626-3592	Sequence 3592, Ap
166	24	85.7	113	4	US-10-424-599-148801	Sequence 148801,	239	24	85.7	310	4	US-10-282-122A-72174	Sequence 72174, A
167	24	85.7	114	4	US-10-437-963-168258	Sequence 168258,	240	24	85.7	312	4	US-10-425-114-61205	Sequence 61205, A
168	24	85.7	117	4	US-10-328-190-8	Sequence 8, Appl	241	24	85.7	314	4	US-10-217-574-20	Sequence 20, Appl
169	24	85.7	118	4	US-10-425-114-40094	Sequence 40094, A	242	24	85.7	316	4	US-10-217-555-20	Sequence 20, Appl
170	24	85.7	120	4	US-10-663-244-11	Sequence 11, Appl	243	24	85.7	316	5	US-10-491-467-31	Sequence 31, Appl
171	24	85.7	124	4	US-10-050-882-92	Sequence 92, Appl	244	24	85.7	317	5	US-10-723-850-984	Sequence 984, App
172	24	85.7	124	5	US-10-627-556-336	Sequence 336, App	245	24	85.7	317	5	US-10-756-149-4957	Sequence 4957, A
173	24	85.7	124	5	US-10-627-556-340	Sequence 340, App	246	24	85.7	318	4	US-10-282-122A-48550	Sequence 48550, A

247	24	85.7	319	4	US-10-437-963-156670	Sequence 156670, A	320	24	85.7	512	6	US-11-132-143-70	Sequence 70, Appl
248	24	85.7	321	5	US-10-631-467-1452	Sequence 1452, Ap	321	24	85.7	513	4	US-10-283-122A-49658	Sequence 49658, A
249	24	85.7	321	5	US-10-631-467-1483	Sequence 1483, Ap	322	24	85.7	513	4	US-10-168-583-2	Sequence 2, Appl1
250	24	85.7	324	4	US-10-282-122A-59900	Sequence 59900, A	323	24	85.7	517	4	US-10-679-620-68	Sequence 68, Appl
251	24	85.7	328	4	US-10-425-114-69321	Sequence 69321, A	324	24	85.7	517	6	US-11-132-143-68	Sequence 68, Appl
252	24	85.7	328	4	US-10-425-115-192938	Sequence 192938, A	325	24	85.7	519	4	US-10-679-620-66	Sequence 66, Appl
253	24	85.7	329	4	US-10-798-156-6	Sequence 6, Appl1	326	24	85.7	519	4	US-10-425-115-336576	Sequence 326576, A
254	24	85.7	334	4	US-10-295-927-712	Sequence 712, App	327	24	85.7	519	6	US-11-132-143-66	Sequence 66, Appl
255	24	85.7	334	4	US-10-469-393-4	Sequence 2, Appl1	328	24	85.7	521	4	US-10-369-493-23690	Sequence 22690, A
256	24	85.7	334	4	US-10-469-393-4	Sequence 4, Appl1	329	24	85.7	524	4	US-10-369-493-10180	Sequence 10180, A
257	24	85.7	339	4	US-10-425-115-272582	Sequence 172582, A	330	24	85.7	532	4	US-10-424-599-246107	Sequence 246107, A
258	24	85.7	341	4	US-10-437-963-174202	Sequence 174202, A	331	24	85.7	539	4	US-10-425-115-347540	Sequence 347540, A
259	24	85.7	341	4	US-10-425-115-284430	Sequence 284430, A	332	24	85.7	540	6	US-11-097-143-11778	Sequence 11778, A
260	24	85.7	341	5	US-10-965-313-4	Sequence 4, Appl1	333	24	85.7	543	4	US-10-092-900A-58	Sequence 58, Appl
261	24	85.7	341	6	US-11-092-809-4	Sequence 4, Appl1	334	24	85.7	548	4	US-10-369-493-540	Sequence 540, App
262	24	85.7	341	6	US-11-092-809-4	Sequence 4, Appl1	335	24	85.7	552	4	US-10-679-620-86	Sequence 86, Appl
263	24	85.7	343	5	US-10-732-923-10780	Sequence 10780, A	336	24	85.7	552	6	US-11-132-143-86	Sequence 86, Appl
264	24	85.7	349	4	US-10-264-049-2992	Sequence 2992, Ap	337	24	85.7	554	6	US-11-044-853-19	Sequence 19, Appl
265	24	85.7	350	5	US-10-732-923-10776	Sequence 10776, A	338	24	85.7	557	6	US-11-044-853-2	Sequence 2, Appl1
266	24	85.7	350	5	US-10-732-923-10778	Sequence 10778, A	339	24	85.7	559	4	US-10-282-122A-47860	Sequence 47860, A
267	24	85.7	351	3	US-09-771-161A-134	Sequence 194, App	340	24	85.7	561	3	US-09-922-138-8	Sequence 8, Appl1
268	24	85.7	351	4	US-10-296-115-1055	Sequence 1055, Ap	341	24	85.7	561	4	US-10-391-364-42	Sequence 42, Appl
269	24	85.7	343	5	US-10-732-923-10648	Sequence 10648, A	342	24	85.7	565	6	US-11-044-853-20	Sequence 20, Appl
270	24	85.7	351	5	US-10-732-923-10777	Sequence 10777, A	343	24	85.7	572	3	US-09-771-161A-120	Sequence 120, App
271	24	85.7	351	5	US-10-732-923-10781	Sequence 10781, A	344	24	85.7	572	4	US-10-282-122A-49068	Sequence 49068, A
272	24	85.7	355	4	US-10-425-114-39949	Sequence 39949, A	345	24	85.7	575	5	US-10-732-923-2608	Sequence 2608, Ap
273	24	85.7	357	4	US-10-282-122A-61260	Sequence 61260, A	346	24	85.7	575	5	US-10-732-923-2609	Sequence 2609, Ap
274	24	85.7	357	4	US-10-168-804B-15	Sequence 14, Appl	347	24	85.7	575	5	US-10-732-923-2610	Sequence 2610, Ap
275	24	85.7	360	4	US-10-168-804B-15	Sequence 15, Appl	348	24	85.7	575	6	US-11-097-143-13267	Sequence 1267, A
276	24	85.7	366	4	US-10-369-493-4137	Sequence 4137, Ap	349	24	85.7	583	4	US-10-369-493-549	Sequence 549, App
277	24	85.7	367	4	US-10-282-122A-61040	Sequence 61040, A	350	24	85.7	583	4	US-10-282-122A-77634	Sequence 77634, A
278	24	85.7	371	4	US-10-450-802-7	Sequence 7, Appl1	351	24	85.7	584	4	US-10-156-761-10934	Sequence 10934, A
279	24	85.7	372	3	US-09-881-752A-320	Sequence 320, App	352	24	85.7	594	5	US-10-761-983-59	Sequence 59, Appl
280	24	85.7	379	4	US-10-375-107-36	Sequence 36, Appl	353	24	85.7	595	4	US-10-072-036-69	Sequence 69, Appl
281	24	85.7	379	6	US-10-467-042-2	Sequence 2, Appl1	354	24	85.7	596	6	US-11-097-143-24870	Sequence 24870, A
282	24	85.7	379	6	US-11-046-868-2	Sequence 2, Appl1	355	24	85.7	604	6	US-11-097-143-3048	Sequence 3048, Ap
283	24	85.7	393	4	US-10-424-599-212484	Sequence 212484, A	356	24	85.7	604	6	US-11-097-143-3057	Sequence 3057, Ap
284	24	85.7	400	4	US-10-168-804B-13	Sequence 13, Appl	357	24	85.7	604	6	US-11-097-143-3060	Sequence 3060, Ap
285	24	85.7	408	4	US-10-425-115-363057	Sequence 363057, A	358	24	85.7	608	3	US-11-097-143-3360	Sequence 3360, Ap
286	24	85.7	409	4	US-10-369-493-19656	Sequence 19656, A	359	24	85.7	608	5	US-09-769-787-8	Sequence 8, Appl1
287	24	85.7	409	4	US-10-425-114-36980	Sequence 36980, A	360	24	85.7	611	6	US-10-472-928-4588	Sequence 4588, Ap
288	24	85.7	415	4	US-10-328-190-12	Sequence 12, Appl	361	24	85.7	615	4	US-11-097-143-33984	Sequence 33984, A
289	24	85.7	416	3	US-09-925-300-1395	Sequence 1395, Ap	362	24	85.7	615	4	US-10-369-493-18617	Sequence 18617, A
290	24	85.7	426	4	US-10-282-122A-46538	Sequence 46538, A	363	24	85.7	617	5	US-10-617-320-5096	Sequence 5096, Ap
291	24	85.7	442	6	US-11-097-143-17649	Sequence 17649, A	364	24	85.7	643	4	US-10-425-115-18781	Sequence 18781, A
292	24	85.7	442	6	US-11-097-143-17652	Sequence 17652, A	365	24	85.7	646	3	US-09-777-710A-1	Sequence 1, Appl1
293	24	85.7	447	5	US-10-842-929-2	Sequence 2, Appl1	366	24	85.7	648	4	US-10-425-115-66900	Sequence 66900, A
294	24	85.7	450	5	US-10-732-923-4317	Sequence 4317, Ap	367	24	85.7	654	4	US-10-425-115-310940	Sequence 310940, A
295	24	85.7	451	6	US-10-679-620-78	Sequence 78, Appl	368	24	85.7	654	4	US-10-437-963-135744	Sequence 135744, A
296	24	85.7	451	6	US-11-132-143-78	Sequence 78, Appl	369	24	85.7	667	6	US-11-097-143-20325	Sequence 20325, A
297	24	85.7	456	5	US-10-732-923-4311	Sequence 4311, Ap	370	24	85.7	670	3	US-09-777-710A-15	Sequence 15, Appl
298	24	85.7	456	5	US-10-732-923-4312	Sequence 4312, Ap	371	24	85.7	670	4	US-10-434-269-7	Sequence 7, Appl1
299	24	85.7	466	4	US-10-369-493-17472	Sequence 17472, A	372	24	85.7	685	4	US-10-424-599-265457	Sequence 265457, A
300	24	85.7	472	3	US-09-738-626-3610	Sequence 3610, Ap	373	24	85.7	689	4	US-10-332-288-4	Sequence 4, Appl1
301	24	85.7	476	4	US-10-108-260A-4812	Sequence 4812, Ap	374	24	85.7	692	4	US-10-437-963-161047	Sequence 161047, A
302	24	85.7	484	5	US-10-450-763-30435	Sequence 30435, A	375	24	85.7	693	4	US-10-408-785A-2229	Sequence 2229, Ap
303	24	85.7	493	5	US-10-732-923-1120	Sequence 1120, App	376	24	85.7	702	4	US-10-437-963-203823	Sequence 203823, A
304	24	85.7	502	5	US-10-627-556-344	Sequence 344, App	377	24	85.7	715	4	US-10-679-620-116	Sequence 116, App
305	24	85.7	502	5	US-10-627-556-346	Sequence 346, App	378	24	85.7	715	6	US-11-132-143-116	Sequence 116, App
306	24	85.7	503	4	US-10-092-900A-54	Sequence 54, Appl	379	24	85.7	713	4	US-10-679-620-64	Sequence 64, Appl
307	24	85.7	505	3	US-09-729-995-2	Sequence 2, Appl1	380	24	85.7	713	4	US-10-437-963-113424	Sequence 113424, A
308	24	85.7	505	3	US-09-729-995-4	Sequence 4, Appl1	381	24	85.7	713	6	US-11-132-143-64	Sequence 64, Appl
309	24	85.7	505	4	US-10-135-689-2	Sequence 2, Appl1	382	24	85.7	715	4	US-10-679-620-62	Sequence 62, Appl
310	24	85.7	505	4	US-10-135-689-4	Sequence 4, Appl1	383	24	85.7	715	6	US-11-132-143-62	Sequence 62, Appl
311	24	85.7	505	4	US-10-333-314-19	Sequence 19, Appl	384	24	85.7	715	6	US-10-425-115-272660	Sequence 272660, A
312	24	85.7	505	4	US-10-092-900A-56	Sequence 56, Appl	385	24	85.7	715	6	US-11-097-143-15942	Sequence 15942, A
313	24	85.7	505	4	US-10-690-617-2	Sequence 2, Appl1	386	24	85.7	727	4	US-10-033-174-11	Sequence 11, Appl
314	24	85.7	505	4	US-10-690-617-4	Sequence 4, Appl1	387	24	85.7	746	4	US-10-425-115-249856	Sequence 249856, A
315	24	85.7	505	5	US-10-981-461-2	Sequence 2, Appl1	388	24	85.7	748	5	US-10-501-282-6626	Sequence 6626, Ap
316	24	85.7	505	5	US-10-981-461-4	Sequence 4, Appl1	389	24	85.7	750	3	US-09-272-809-8	Sequence 8, Appl1
317	24	85.7	505	5	US-10-981-678-2	Sequence 2, Appl1	390	24	85.7	755	4	US-10-425-115-192940	Sequence 192940, A
318	24	85.7	505	5	US-10-981-678-4	Sequence 4, Appl1	391	24	85.7	756	4	US-10-287-274-436	Sequence 426, App
319	24	85.7	512	4	US-10-679-620-70	Sequence 70, Appl	392	24	85.7	756	4	US-10-369-493-23662	Sequence 23662, A

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394	24	85.7	757	4	US-10-369-493-21122	Sequence 21122, A	467	24	85.7	1335	4	US-10-425-115-272659	Sequence 272659, A
395	24	85.7	761	5	US-10-501-283-6628	Sequence 6628, Ap	468	24	85.7	1365	4	US-10-408-765A-2046	Sequence 2046, Ap
396	24	85.7	771	4	US-10-437-963-174200	Sequence 174200, A	469	24	85.7	1383	4	US-10-437-963-170846	Sequence 170846, A
397	24	85.7	773	4	US-10-437-963-138725	Sequence 138725, A	470	24	85.7	1392	4	US-10-437-963-148793	Sequence 148793, A
398	24	85.7	776	4	US-10-267-989-24	Sequence 24, Appl	471	24	85.7	1463	4	US-10-425-115-272527	Sequence 272527, A
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403	24	85.7	822	4	US-10-156-761-13338	Sequence 13338, A	476	24	85.7	1510	4	US-10-425-115-272470	Sequence 272470, A
404	24	85.7	827	4	US-10-425-115-272496	Sequence 272496, A	477	24	85.7	1511	4	US-10-425-115-272611	Sequence 272611, A
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409	24	85.7	848	4	US-10-425-115-272502	Sequence 272502, A	482	24	85.7	1596	4	US-10-437-963-190412	Sequence 190412, A
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441	24	85.7	1142	4	US-10-060-065-22	Sequence 22, Appl	514	24	85.7	5147	4	US-10-174-677-4	Sequence 4, Appl1
442	24	85.7	1142	4	US-10-059-585-43	Sequence 43, Appl	515	24	85.7	5147	6	US-11-097-143-6285	Sequence 6285, Ap
443	24	85.7	1142	4	US-10-394-322A-35	Sequence 35, Appl	516	23	82.1	34	4	US-10-437-963-151243	Sequence 151243, A
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542	23	82.1	127	4	US-10-425-115-315358	Sequence 315358,	615	23	82.1	536	3	US-09-866-050A-185	Sequence 185, App
543	23	82.1	139	4	US-10-282-122A-59819	Sequence 59819, A	616	23	82.1	538	4	US-10-398-097-13	Sequence 13, Appl
544	23	82.1	140	4	US-10-437-963-191382	Sequence 191382,	617	23	82.1	540	6	US-11-008-354-12	Sequence 12, Appl
545	23	82.1	146	4	US-10-062-831-47	Sequence 47, Appl	618	23	82.1	540	6	US-11-107-597-12	Sequence 12, Appl
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548	23	82.1	155	5	US-10-732-923-16994	Sequence 16994, A	621	23	82.1	593	4	US-10-369-493-736	Sequence 736, App
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550	23	82.1	183	3	US-09-729-674-120	Sequence 120, App	623	23	82.1	598	3	US-10-398-097-10	Sequence 10, Appl
551	23	82.1	183	4	US-10-264-237-2694	Sequence 2694, Ap	624	23	82.1	598	6	US-11-022-049-4	Sequence 4, Appl1
552	23	82.1	183	4	US-10-437-963-122132	Sequence 122132,	625	23	82.1	601	4	US-10-052-648A-56	Sequence 56, Appl
553	23	82.1	183	4	US-10-767-701-49157	Sequence 49157, A	626	23	82.1	601	5	US-10-756-149-5755	Sequence 5755, Ap
554	23	82.1	183	5	US-10-913-553-120	Sequence 120, App	627	23	82.1	609	6	US-11-097-143-405	Sequence 405, App
555	23	82.1	192	4	US-10-376-774-2695	Sequence 2695, Ap	628	23	82.1	641	4	US-10-093-463-42	Sequence 42, Appl
556	23	82.1	193	4	US-10-476-204-13	Sequence 13, Appl	629	23	82.1	642	4	US-10-437-963-204896	Sequence 204896,
557	23	82.1	193	4	US-10-767-701-41296	Sequence 41296, A	630	23	82.1	643	4	US-10-289-762-474	Sequence 474, App
558	23	82.1	200	5	US-10-450-763-49591	Sequence 49591, A	631	23	82.1	658	4	US-10-437-963-176041	Sequence 176041,
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566	23	82.1	221	4	US-10-424-599-168978	Sequence 168978,	639	23	82.1	801	4	US-10-174-677-20	Sequence 20, Appl
567	23	82.1	221	4	US-10-424-599-266753	Sequence 266753,	640	23	82.1	801	4	US-10-257-174-29	Sequence 29, Appl
568	23	82.1	230	4	US-10-425-115-277148	Sequence 277148,	641	23	82.1	801	4	US-10-408-765A-2471	Sequence 2471, Ap
569	23	82.1	243	4	US-10-476-204-14	Sequence 14, Appl	642	23	82.1	818	4	US-10-437-963-133520	Sequence 133520,
570	23	82.1	258	5	US-10-472-928-314	Sequence 314, App	643	23	82.1	836	4	US-10-437-963-137163	Sequence 137163,
571	23	82.1	259	5	US-10-732-923-16988	Sequence 16988, A	644	23	82.1	847	4	US-10-398-097-2	Sequence 2, Appl1
572	23	82.1	263	5	US-10-617-320-2968	Sequence 2968, Ap	645	23	82.1	847	4	US-10-476-204-3	Sequence 3, Appl1
573	23	82.1	267	4	US-10-335-977-7474	Sequence 7474, Ap	646	23	82.1	861	4	US-10-362-016-2	Sequence 2, Appl1
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575	23	82.1	277	4	US-10-437-963-137553	Sequence 137553,	648	23	82.1	890	4	US-10-764-425-155	Sequence 165, App
576	23	82.1	284	4	US-10-156-761-14333	Sequence 14333, A	649	23	82.1	894	4	US-10-497-963-119258	Sequence 119258,
577	23	82.1	286	4	US-10-029-386-32534	Sequence 32534, A	650	23	82.1	910	3	US-09-878-764-2	Sequence 2, Appl1
578	23	82.1	287	4	US-10-408-765A-2868	Sequence 2868, Ap	651	23	82.1	910	3	US-09-980-049-2	Sequence 2, Appl1
579	23	82.1	291	3	US-09-788-626-18	Sequence 18, Appl	652	23	82.1	910	4	US-10-012-140-17	Sequence 17, Appl
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581	23	82.1	316	4	US-10-425-114-62512	Sequence 62512, A	654	23	82.1	910	4	US-10-295-027-175	Sequence 175, App
582	23	82.1	320	4	US-10-437-963-119256	Sequence 119256,	655	23	82.1	910	4	US-10-295-027-1208	Sequence 1208, Ap
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584	23	82.1	334	4	US-10-425-114-45688	Sequence 45688, A	657	23	82.1	910	4	US-10-188-832-49	Sequence 49, Appl
585	23	82.1	337	4	US-10-424-599-202025	Sequence 202025,	658	23	82.1	910	6	US-11-051-454-121	Sequence 121, App
586	23	82.1	342	4	US-10-282-122A-73377	Sequence 73377, A	659	23	82.1	910	6	US-11-022-049-2	Sequence 2, Appl1
587	23	82.1	344	4	US-10-282-122A-75212	Sequence 75212, A	660	23	82.1	922	4	US-10-425-115-213712	Sequence 213712,
588	23	82.1	345	4	US-10-282-122A-75608	Sequence 75608, A	661	23	82.1	928	4	US-10-312-273-95	Sequence 95, Appl
589	23	82.1	345	4	US-10-289-763-89	Sequence 89, Appl	662	23	82.1	947	4	US-10-437-963-130973	Sequence 130973,
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593	23	82.1	369	4	US-10-205-194-13	Sequence 13, Appl	666	23	82.1	988	3	US-09-438-486-69	Sequence 69, Appl
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601	23	82.1	411	5	US-10-756-149-5620	Sequence 5620, Ap	674	23	82.1	988	5	US-10-877-124-112	Sequence 112, App
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872	22	78.6	200	5	US-10-450-763-53503	Sequence 53503, A	945	22	78.6	246	3	US-09-880-748-2075	Sequence 2075, Ap
873	22	78.6	203	4	US-10-424-599-229885	Sequence 229885,	946	22	78.6	246	4	US-10-293-418-2075	Sequence 2075, Ap
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877	22	78.6	208	5	US-10-225-066A-358	Sequence 358, App	950	22	78.6	249	4	US-10-369-493-16671	Sequence 16671, A
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880	22	78.6	209	4	US-10-424-599-277430	Sequence 277430,	953	22	78.6	251	4	US-10-369-493-14944	Sequence 14944, A
881	22	78.6	211	4	US-10-424-599-157929	Sequence 157929,	954	22	78.6	252	4	US-10-369-493-4532	Sequence 4532, Ap
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889	22	78.6	218	4	US-10-424-599-143075	Sequence 143075,	962	22	78.6	257	4	US-10-369-493-9154	Sequence 9154, Ap
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892	22	78.6	220	3	US-10-425-115-288431	Sequence 288431,	965	22	78.6	259	3	US-09-893-913A-338	Sequence 338, App
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899	22	78.6	227	3	US-08-592-711-6	Sequence 6, Appl	972	22	78.6	261	4	US-10-004-115A-36	Sequence 36, Appl
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990 22 78.6 261 4 US-10-782-258-124 Sequence 124, App  
991 22 78.6 261 4 US-10-782-258-126 Sequence 126, App  
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997 22 78.6 261 5 US-10-915-927-10 Sequence 10, Appl  
998 22 78.6 261 5 US-10-915-927-12 Sequence 12, Appl  
999 22 78.6 261 5 US-10-915-927-14 Sequence 14, Appl  
1000 22 78.6 261 5 US-10-915-927-16 Sequence 16, Appl

## ALIGNMENTS

RESULT 1  
US-09-771-383-5  
; Sequence 5, Application US/09771383  
; Patent No. US20020094562A1  
; GENERAL INFORMATION:  
; APPLICANT: Parrie, Kevin  
; APPLICANT: Somers, William  
; APPLICANT: Tam, Amy  
; APPLICANT: Lin, Laura  
; APPLICANT: Stahl, Mark  
; TITLE OF INVENTION: CRYSTAL STRUCTURE OF ACYL CARRIER PROTEIN SYNTHASE  
; FILE REFERENCE: 2369/12  
; CURRENT APPLICATION NUMBER: US/09/771,383  
; PRIOR FILING DATE: 2001-01-25  
; PRIOR APPLICATION NUMBER: US 60/178,639  
; PRIOR FILING DATE: 2000-01-28  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 5  
; LENGTH: 119  
; TYPE: PRT  
; ORGANISM: Staphylococcus  
US-09-771-383-5

Query Match 100.0%; Score 28; DB 3; Length 119;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 HYAMS 5  
Db 106 HYAMS 110

RESULT 2  
US-09-770-834-6  
; Sequence 6, Application US/09770834  
; Publication No. US20030211588A1  
; GENERAL INFORMATION:  
; APPLICANT: Parrie, Kevin  
; APPLICANT: Somers, William  
; APPLICANT: Tam, Amy  
; APPLICANT: Lin, Laura  
; APPLICANT: Stahl, Mark

; APPLICANT: Powers, Robert  
; APPLICANT: Xu, Guan-Yi  
; TITLE OF INVENTION: CRYSTAL STRUCTURE OF ACPS/ACP COMPLEX, SOLUTION STRUCTURE  
; TITLE OF INVENTION: OF B. SUBTILIS ACP, AND USES THEREOF  
; FILE REFERENCE: 2368/14  
; CURRENT APPLICATION NUMBER: US/09/770,834  
; PRIOR FILING DATE: 2001-10-12  
; PRIOR APPLICATION NUMBER: US 60/202,466  
; PRIOR FILING DATE: 2000-05-08  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 6  
; LENGTH: 119  
; TYPE: PRT  
; ORGANISM: Staphylococcus sp.  
US-09-770-834-6

Query Match 100.0%; Score 28; DB 3; Length 119;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5  
Db 106 HYAMS 110

RESULT 3  
US-10-282-122A-44196  
; Sequence 44196, Application US/10282122A  
; Publication No. US20040029129A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Liangsu  
; APPLICANT: Zamudio, Carlos  
; APPLICANT: Malone, Cheryl  
; APPLICANT: Haselbeck, Robert  
; APPLICANT: Ohlsen, Kari  
; APPLICANT: Zyskind, Judith  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John  
; APPLICANT: Carr, Grant  
; APPLICANT: Yamamoto, Robert  
; APPLICANT: Forsyth, R.  
; APPLICANT: Xu, H.  
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms  
; FILE REFERENCE: ELITRA.034A  
; CURRENT APPLICATION NUMBER: US/10/282,122A  
; CURRENT FILING DATE: 2003-02-20  
; PRIOR APPLICATION NUMBER: 60/191,078  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: 60/206,848  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR APPLICATION NUMBER: 60/207,727  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 60/230,335  
; PRIOR FILING DATE: 2000-09-06  
; PRIOR APPLICATION NUMBER: 60/230,347  
; PRIOR FILING DATE: 2000-09-09  
; PRIOR APPLICATION NUMBER: 60/242,578  
; PRIOR FILING DATE: 2000-10-23  
; PRIOR APPLICATION NUMBER: 60/253,625  
; PRIOR FILING DATE: 2000-11-27  
; PRIOR APPLICATION NUMBER: 60/257,931  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: 60/267,636  
; PRIOR FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: 60/269,308  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 78614  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 44196  
; LENGTH: 119  
; TYPE: PRT

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; ORGANISM: Staphylococcus aureus
US-10-282-122A-44196

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Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 HYAMS 5
DB      106 HYAMS 110

RESULT 4
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; Sequence 71569, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 71569
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Staphylococcus haemolyticus
US-10-282-122A-71569

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Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 HYAMS 5
DB      107 HYAMS 111

RESULT 5
US-10-717-138-6

; Sequence 6, Application US/10717138
; Publication No. US20040078147A1
; GENERAL INFORMATION:
; APPLICANT: Parris, Kevin
; APPLICANT: Somers, William
; APPLICANT: Tam, Amy
; APPLICANT: Lin, Laura
; APPLICANT: Stahl, Mark
; APPLICANT: Powers, Robert
; APPLICANT: Xu, Guan-Yi
; TITLE OF INVENTION: CRYSTAL STRUCTURE OF ACPs/ACP COMPLEX, SOLUTION STRUCTURE
; FILE REFERENCE: 2368/14
; CURRENT APPLICATION NUMBER: US/10/717,138
; CURRENT FILING DATE: 2003-11-19
; PRIOR APPLICATION NUMBER: US/09/770,834
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 60/202,466
; PRIOR FILING DATE: 2000-05-08
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Staphylococcus sp.
US-10-717-138-6

Query Match          100.0%; Score 28; DB 4; Length 119;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 HYAMS 5
DB      106 HYAMS 110

RESULT 6
US-10-857-625-722
; Sequence 722, Application US/10857625
; Publication No. US20050026189A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; TITLE OF INVENTION: MICROBIAL OPERONS
; FILE REFERENCE: ELITRA.036A
; CURRENT APPLICATION NUMBER: US/10/857,625
; CURRENT FILING DATE: 2004-05-28
; PRIOR APPLICATION NUMBER: 60/474768
; PRIOR FILING DATE: 2003-05-29
; NUMBER OF SEQ ID NOS: 833
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 722
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-857-625-722

Query Match          100.0%; Score 28; DB 5; Length 119;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 HYAMS 5
DB      106 HYAMS 110

RESULT 7
US-09-764-304-8
; Sequence 8, Application US/09764304
; Patent No. US2002026036A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
```

APPLICANT: HASEGAWA, MAMORU  
APPLICANT: MIYAJI, YOSHIHISA  
APPLICANT: KUWANA, YOSHIHISA  
TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY  
FILE REFERENCE: 249-101  
CURRENT APPLICATION NUMBER: US/09/764,304  
EARLIER FILING DATE: 2001-01-19  
EARLIER APPLICATION NUMBER: 09/225,322  
EARLIER FILING DATE: 1999-01-05  
EARLIER APPLICATION NUMBER: US 08/454,680  
EARLIER FILING DATE: 1995-05-31  
EARLIER APPLICATION NUMBER: US 08/408,133  
EARLIER FILING DATE: 1995-03-21  
EARLIER APPLICATION NUMBER: US 08/292,178  
EARLIER FILING DATE: 1994-08-17  
EARLIER APPLICATION NUMBER: US07/947,674  
EARLIER FILING DATE: 1992-09-17  
EARLIER APPLICATION NUMBER: JP 3-238375  
EARLIER FILING DATE: 1991-09-18  
NUMBER OF SEQ ID NOS: 19  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 8  
LENGTH: 130  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: cDNA KM-641  
US-09-764-304-8

Query Match 100.0%; Score 28; DB 3; Length 130;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5  
Db 41 HYAMS 45

RESULT 8  
US-09-764-304-18  
Sequence 18, Application US/09764304  
Publication No. US20020026036A1  
GENERAL INFORMATION:  
APPLICANT: SHITARA, KENYA  
APPLICANT: HANAI, NOBUO  
APPLICANT: HASEGAWA, MAMORU  
APPLICANT: MIYAJI, HIROMASA  
APPLICANT: KUWANA, YOSHIHISA  
TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY  
FILE REFERENCE: 249-101  
CURRENT APPLICATION NUMBER: US/09/764,304  
EARLIER FILING DATE: 2001-01-19  
EARLIER APPLICATION NUMBER: 09/225,322  
EARLIER FILING DATE: 1999-01-05  
EARLIER APPLICATION NUMBER: US 08/454,680  
EARLIER FILING DATE: 1995-05-31  
EARLIER APPLICATION NUMBER: US 08/408,133  
EARLIER FILING DATE: 1995-03-21  
EARLIER APPLICATION NUMBER: US 08/292,178  
EARLIER FILING DATE: 1994-08-17  
EARLIER APPLICATION NUMBER: US07/947,674  
EARLIER FILING DATE: 1992-09-17  
EARLIER APPLICATION NUMBER: JP 3-238375  
EARLIER FILING DATE: 1991-09-18  
NUMBER OF SEQ ID NOS: 19  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 18  
LENGTH: 130  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: cDNA KM-641  
US-09-764-304-18

Query Match 100.0%; Score 28; DB 3; Length 130;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5  
Db 41 HYAMS 45

RESULT 9  
US-10-265-713-8  
Sequence 18, Application US/10265713  
Publication No. US20030095964A1  
GENERAL INFORMATION:  
APPLICANT: SHITARA, KENYA  
APPLICANT: HANAI, NOBUO  
APPLICANT: HASEGAWA, MAMORU  
APPLICANT: MIYAJI, HIROMASA  
APPLICANT: KUWANA, YOSHIHISA  
TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY  
FILE REFERENCE: 249-101  
CURRENT APPLICATION NUMBER: US/10/265,713  
EARLIER FILING DATE: 2002-10-08  
EARLIER APPLICATION NUMBER: US/09/225,322  
EARLIER FILING DATE: 1999-01-05  
EARLIER APPLICATION NUMBER: US 08/454,680  
EARLIER FILING DATE: 1995-05-31  
EARLIER APPLICATION NUMBER: US 08/408,133  
EARLIER FILING DATE: 1995-03-21  
EARLIER APPLICATION NUMBER: US 08/292,178  
EARLIER FILING DATE: 1994-08-17  
EARLIER APPLICATION NUMBER: US07/947,674  
EARLIER FILING DATE: 1992-09-17  
EARLIER APPLICATION NUMBER: JP 3-238375  
EARLIER FILING DATE: 1991-09-18  
NUMBER OF SEQ ID NOS: 19  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 8  
LENGTH: 130  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: cDNA KM-641  
US-10-265-713-8

Query Match 100.0%; Score 28; DB 4; Length 130;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5  
Db 41 HYAMS 45

RESULT 10  
US-10-265-713-18  
Sequence 18, Application US/10265713  
Publication No. US20030095964A1  
GENERAL INFORMATION:  
APPLICANT: SHITARA, KENYA  
APPLICANT: HANAI, NOBUO  
APPLICANT: HASEGAWA, MAMORU  
APPLICANT: MIYAJI, HIROMASA  
APPLICANT: KUWANA, YOSHIHISA  
TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY  
FILE REFERENCE: 249-101  
CURRENT APPLICATION NUMBER: US/10/265,713  
EARLIER FILING DATE: 2002-10-08  
EARLIER APPLICATION NUMBER: US/09/225,322  
EARLIER FILING DATE: 1999-01-05  
EARLIER APPLICATION NUMBER: US 08/454,680  
EARLIER FILING DATE: 1995-05-31

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; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
; PRIOR APPLICATION NUMBER: US07/947,674
; PRIOR FILING DATE: 1992-09-17
; PRIOR APPLICATION NUMBER: JP 3-238375
; PRIOR FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:cdna KM-641
US-10-265-713-18

Query Match      100.0%; Score 28; DB 4; Length 130;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 HYAMS 5
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Db      41 HYAMS 45

RESULT 11
US-10-166-626-8
; Sequence 8, Application US/10166626
; Publication No. US20030166876A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUMANA, YOSHIHISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/10/166,626
; PRIOR FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: US/09/225,322B
; PRIOR FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: US 08/454,680
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
; PRIOR APPLICATION NUMBER: US07/947,674
; PRIOR FILING DATE: 1992-09-17
; PRIOR APPLICATION NUMBER: JP 3-238375
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: cdna KM-641
US-10-166-626-8

Query Match      100.0%; Score 28; DB 4; Length 130;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 HYAMS 5
       |||||
Db      41 HYAMS 45

RESULT 12
US-10-166-626-8
; Sequence 8, Application US/10166626
; Publication No. US20030166876A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUMANA, YOSHIHISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/10/166,626
; PRIOR FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: US/09/225,322B
; PRIOR FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: US 08/454,680
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
; PRIOR APPLICATION NUMBER: US07/947,674
; PRIOR FILING DATE: 1992-09-17
; PRIOR APPLICATION NUMBER: JP 3-238375
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: cdna KM-641
US-10-166-626-8

Query Match      100.0%; Score 28; DB 4; Length 130;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 HYAMS 5
       |||||
Db      41 HYAMS 45

RESULT 13
US-10-450-763-59338
; Sequence 59338, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 59338
; LENGTH: 156
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-450-763-59338

Query Match      100.0%; Score 28; DB 5; Length 156;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 HYAMS 5
       |||||
Db      41 HYAMS 45

US-10-166-626-18
; Sequence 18, Application US/10166626
; Publication No. US20030166876A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUMANA, YOSHIHISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/10/166,626
; CURRENT FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: US/09/225,322B
; PRIOR FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: US 08/454,680
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
; PRIOR APPLICATION NUMBER: US07/947,674
; PRIOR FILING DATE: 1992-09-17
; PRIOR APPLICATION NUMBER: JP 3-238375
; PRIOR FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:cdna KM-641
US-10-166-626-18

Query Match      100.0%; Score 28; DB 4; Length 130;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 HYAMS 5
       |||||
Db      41 HYAMS 45
```

Db           |||||  
          49 HVAMS 53

## RESULT 14

US-10-369-493-10250  
; Sequence 10250, Application US/10369493  
; Publication No. US20030233675A1

## GENERAL INFORMATION:

; APPLICANT: CAO, YONGWEI  
; APPLICANT: HINKLE, GREGORY J.  
; APPLICANT: SLATER, STEVEN C.  
; APPLICANT: GOLDMAN, BARRY S.  
; APPLICANT: CHEN, XIANFENG  
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES  
; FILE REFERENCE: 38-10(52052)B  
; CURRENT APPLICATION NUMBER: US/10/369,493  
; CURRENT FILING DATE: 2003-02-28  
; PRIOR APPLICATION NUMBER: US 60/360,039  
; PRIOR FILING DATE: 2002-02-21  
; NUMBER OF SEQ ID NOS: 47374  
; SEQ ID NO 10250  
; LENGTH: 412  
; TYPE: PRT  
; ORGANISM: Cytophaga hutchinsonii  
US-10-369-493-10250

Query Match           100.0%; Score 28; DB 4; Length 412;

Best Local Similarity 100.0%; Pred. No. 4.7e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY           1 HVAMS 5

Db           |||||  
          390 HVAMS 394

## RESULT 15

US-09-824-734-4  
; Sequence 4, Application US/09824734  
; Patent No. US20020083485A1

## GENERAL INFORMATION:

; APPLICANT: ZHU, JIAN-KANG  
; APPLICANT: SHI, HUAZHONG  
; APPLICANT: ISHITANI, MANABU  
; APPLICANT: STEVENSON, BECKY  
; TITLE OF INVENTION: PROTEINS AND DNA RELATED TO SALT TOLERANCE IN PLANTS  
; FILE REFERENCE: 205644US20  
; CURRENT APPLICATION NUMBER: US/09/824,734  
; CURRENT FILING DATE: 2001-04-04  
; PRIOR APPLICATION NUMBER: US 60/194,648  
; PRIOR FILING DATE: 2000-04-04  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 4  
; LENGTH: 424  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-824-734-4

Query Match           100.0%; Score 28; DB 3; Length 424;

Best Local Similarity 100.0%; Pred. No. 4.9e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY           1 HVAMS 5

Db           |||||  
          272 HVAMS 276

## RESULT 16

US-10-749-386-4  
; Sequence 4, Application US/10749386  
; Publication No. US20040186276A1

; GENERAL INFORMATION:  
; APPLICANT: ZHU, JIAN-KANG  
; APPLICANT: SHI, HUAZHONG  
; APPLICANT: ISHITANI, MANABU  
; APPLICANT: STEVENSON, BECKY  
; TITLE OF INVENTION: PROTEINS AND DNA RELATED TO SALT TOLERANCE IN PLANTS  
; FILE REFERENCE: 205644US20  
; CURRENT APPLICATION NUMBER: US/10/749,386  
; CURRENT FILING DATE: 2004-01-02  
; PRIOR APPLICATION NUMBER: US/09/824,734  
; PRIOR FILING DATE: 2001-04-04  
; PRIOR APPLICATION NUMBER: US 60/194,648  
; PRIOR FILING DATE: 2000-04-04  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 4  
; LENGTH: 424  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-10-749-386-4

Query Match           100.0%; Score 28; DB 4; Length 424;

Best Local Similarity 100.0%; Pred. No. 4.9e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY           1 HVAMS 5

Db           |||||  
          272 HVAMS 276

## RESULT 17

US-10-437-963-189155  
; Sequence 189155, Application US/10437963  
; Publication No. US20040123343A1

## GENERAL INFORMATION:

; APPLICANT: LA ROSA, THOMAS J.  
; APPLICANT: KOVALIC, DAVID K.  
; APPLICANT: ZHOU, YIHUA  
; APPLICANT: CAO, YONGWEI  
; APPLICANT: WU, WEI  
; APPLICANT: BOKHAROV, ANDREY A.  
; APPLICANT: BARBAZUK, BRAD  
; APPLICANT: LI, PING  
; TITLE OF INVENTION: RICE NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH  
; TITLE OF INVENTION: PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 189155  
; LENGTH: 1031  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_85691C.1.pep  
US-10-437-963-189155

Query Match           100.0%; Score 28; DB 4; Length 1031;

Best Local Similarity 100.0%; Pred. No. 1.2e+03;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY           1 HVAMS 5

Db           |||||  
          485 HVAMS 489

## RESULT 18

US-11-097-143-18732  
; Sequence 18732, Application US/11097143  
; Publication No. US2005020858A1

## GENERAL INFORMATION:

; APPLICANT: VENTER, J. CRAIG  
; APPLICANT: ET AL.



; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID  
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE  
; TITLE OF INVENTION: DROSOPHILA GENES.

; FILE REFERENCE: CL000728  
; CURRENT APPLICATION NUMBER: US/11/097,143  
; CURRENT FILING DATE: 2005-04-04  
; PRIOR APPLICATION NUMBER: 60/157,832  
; PRIOR FILING DATE: 1999-10-05  
; PRIOR APPLICATION NUMBER: 60/160,191  
; PRIOR FILING DATE: 1999-10-19  
; PRIOR APPLICATION NUMBER: 60/161,932  
; PRIOR FILING DATE: 1999-10-28  
; PRIOR APPLICATION NUMBER: 60/164,769  
; PRIOR FILING DATE: 1999-11-12  
; PRIOR APPLICATION NUMBER: 60/173,383  
; PRIOR FILING DATE: 1999-12-28  
; PRIOR APPLICATION NUMBER: 60/175,693  
; PRIOR FILING DATE: 2000-01-12  
; PRIOR APPLICATION NUMBER: 60/184,831  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: 60/191,637  
; PRIOR FILING DATE: 2000-03-23  
; NUMBER OF SEQ ID NOS: 43008  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 18732  
; LENGTH: 1669  
; TYPE: PRT  
; ORGANISM: DROSOPHILA  
US-11-097-143-18732

Query Match 100.0%; Score 28; DB 6; Length 1669;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03; Indels 0; Gaps 0;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5  
|||  
Db 566 HYAMS 570

RESULT 19  
US-10-424-599-240643  
; Sequence 240643, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa Thomas J  
; APPLICANT: Kovalic David K  
; APPLICANT: Zhou Yihua  
; APPLICANT: Cao Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 240643  
; LENGTH: 53  
; TYPE: PRT  
; ORGANISM: Glycine max  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)..(53)  
; OTHER INFORMATION: unsure at all Xaa locations  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_59328C.1.pep  
US-10-424-599-240643

Query Match 89.3%; Score 25; DB 4; Length 53;  
Best Local Similarity 80.0%; Pred. No. 3e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5  
|||  
Db 40 HYAMA 44

RESULT 20  
US-10-425-115-279811  
; Sequence 279811, Application US/10425115  
; Publication No. US20040214272A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants  
; FILE REFERENCE: 38-21(53222)B  
; CURRENT APPLICATION NUMBER: US/10/425,115  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 369326  
; SEQ ID NO 279811  
; LENGTH: 54  
; TYPE: PRT  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: MRT4577\_186768C.1.pep  
US-10-425-115-279811

Query Match 89.3%; Score 25; DB 4; Length 54;  
Best Local Similarity 80.0%; Pred. No. 3.1e+02; Indels 0; Gaps 0;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5  
|||  
Db 48 HYALS 52

RESULT 21  
US-10-424-599-181420  
; Sequence 181420, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa Thomas J  
; APPLICANT: Kovalic David K  
; APPLICANT: Zhou Yihua  
; APPLICANT: Cao Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 181420  
; LENGTH: 57  
; TYPE: PRT  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_134837C.1.pep  
US-10-424-599-181420

Query Match 89.3%; Score 25; DB 4; Length 57;  
Best Local Similarity 80.0%; Pred. No. 3.2e+02; Indels 0; Gaps 0;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5  
|||  
Db 48 HYAMT 52

RESULT 22  
US-10-425-115-249920  
; Sequence 249920, Application US/10425115  
; Publication No. US20040214272A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.

```

; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 249920
; LENGTH: 57
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_159510C.1.pap
US-10-425-115-249920

Query Match      89.3%; Score 25; DB 4; Length 57;
Best Local Similarity 80.0%; Pred. No. 3.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 HYAMS 5
DB      52 HYAMN 56

RESULT 23
US-10-424-599-177790
; Sequence 177790, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 177790
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(58)
; OTHER INFORMATION: unsure at all Xaa locations
; OTHER INFORMATION: Clone ID: PAT_MRT3847_131560C.1.pap
US-10-424-599-177790

Query Match      89.3%; Score 25; DB 4; Length 58;
Best Local Similarity 80.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 HYAMS 5
DB      19 HYSMS 23

RESULT 24
US-10-335-977-8261
; Sequence 8261, Application US/10335977
; Publication No. US20040052799A1
; GENERAL INFORMATION:
; APPLICANT: DOUGLAS SMITH et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
; RELATING TO HELICOBACTER PYLORI FOR
; DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 10031
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD

```

```

; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: Windows NT 4.0
; SOFTWARE: UNIX
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/335,977
; FILING DATE: 30-Dec-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/993,002
; FILING DATE: 17-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: GTN-018
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 8261:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Helicobacter pylori
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...58
; SEQUENCE DESCRIPTION: SEQ ID NO: 8261:
US-10-335-977-8261

Query Match      89.3%; Score 25; DB 4; Length 58;
Best Local Similarity 80.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 HYAMS 5
DB      21 HVALS 25

RESULT 25
US-10-424-599-214263
; Sequence 214263, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 214263
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_35506C.1.pap
US-10-424-599-214263

Query Match      89.3%; Score 25; DB 4; Length 70;
Best Local Similarity 80.0%; Pred. No. 3.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 HYAMS 5  
|||:|  
Db 5 HYALS 9

## RESULT 26

US-10-424-599-199143  
; Sequence 199143, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa Thomas J  
; APPLICANT: Kovalic David K  
; APPLICANT: Zhou Yihua  
; APPLICANT: Cao Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 199143  
; LENGTH: 77  
; TYPE: PRT  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_21850C.1.pep  
US-10-424-599-199143

Query Match 89.3%; Score 25; DB 4; Length 77;  
Best Local Similarity 80.0%; Pred. No. 4.3e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5  
|||:|  
Db 60 HYSMS 64

## RESULT 27

US-10-425-115-313005  
; Sequence 313005, Application US/10425115  
; Publication No. US20040214272A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants  
; FILE REFERENCE: 38-21(53222)B  
; CURRENT APPLICATION NUMBER: US/10/425,115  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 369326  
; SEQ ID NO 313005  
; LENGTH: 84  
; TYPE: PRT  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: MRT4577\_48519C.1.pep  
US-10-425-115-313005

Query Match 89.3%; Score 25; DB 4; Length 84;  
Best Local Similarity 80.0%; Pred. No. 4.7e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5  
|||:|  
Db 46 HYAMT 50

## RESULT 28

US-10-424-599-275379  
; Sequence 275379, Application US/10424599

; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa Thomas J  
; APPLICANT: Kovalic David K  
; APPLICANT: Zhou Yihua  
; APPLICANT: Cao Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 275379  
; LENGTH: 85  
; TYPE: PRT  
; ORGANISM: Glycine max  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)..(85)  
; OTHER INFORMATION: unsure at all Xaa locations  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_90688C.1.pep  
US-10-424-599-275379

Query Match 89.3%; Score 25; DB 4; Length 85;  
Best Local Similarity 80.0%; Pred. No. 4.8e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5  
|||:|  
Db 41 HYALS 45

## RESULT 29

US-10-424-599-180930  
; Sequence 180930, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa Thomas J  
; APPLICANT: Kovalic David K  
; APPLICANT: Zhou Yihua  
; APPLICANT: Cao Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 180930  
; LENGTH: 86  
; TYPE: PRT  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_134394C.1.pep  
US-10-424-599-180930

Query Match 89.3%; Score 25; DB 4; Length 86;  
Best Local Similarity 80.0%; Pred. No. 4.8e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5  
|||:|  
Db 15 HYALS 19

## RESULT 30

US-10-424-599-231987  
; Sequence 231987, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa Thomas J  
; APPLICANT: Kovalic David K  
; APPLICANT: Zhou Yihua

; APPLICANT: Cao Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 231987  
; LENGTH: 86  
; TYPE: PRT  
; ORGANISM: Glycine max  
; NAME/KEY: unsure  
; LOCATION: (1)..(86)  
; OTHER INFORMATION: unsure at all Xaa locations  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_51506C.1.pep  
US-10-424-599-231987

Query Match 89.3%; Score 25; DB 4; Length 86;  
Best Local Similarity 80.0%; Pred. No. 4.8e+02; Indels 0; Gaps 0;  
Matches 4; Conservative 1; Mismatches 0;

QY 1 HYAMS 5  
|||:  
Db 26 HYALS 30

RESULT 31  
US-10-424-599-184650  
; Sequence 184650, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J  
; APPLICANT: Kovalic, David K  
; APPLICANT: Zhou Yihua  
; APPLICANT: Cao Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 184650  
; LENGTH: 89  
; TYPE: PRT  
; ORGANISM: Glycine max  
; NAME/KEY: unsure  
; LOCATION: (1)..(100)  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_137755C.1.pep  
US-10-424-599-184650

Query Match 89.3%; Score 25; DB 4; Length 89;  
Best Local Similarity 80.0%; Pred. No. 5e+02; Indels 0; Gaps 0;  
Matches 4; Conservative 1; Mismatches 0;

QY 1 HYAMS 5  
|||:  
Db 37 HYALS 41

RESULT 32  
US-10-425-115-270245  
; Sequence 270245, Application US/10425115  
; Publication No. US20040214272A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; FILE OF INVENTION: Plants  
; FILE REFERENCE: 38-21(53222)B  
; CURRENT APPLICATION NUMBER: US/10/425,115

; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 369326  
; SEQ ID NO 270245  
; LENGTH: 99  
; TYPE: PRT  
; ORGANISM: Zea mays  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)..(99)  
; OTHER INFORMATION: unsure at all Xaa locations  
; FEATURE:  
; OTHER INFORMATION: Clone ID: MRT4577\_17805C.1.pep  
US-10-425-115-270245

Query Match 89.3%; Score 25; DB 4; Length 99;  
Best Local Similarity 80.0%; Pred. No. 5.5e+02; Indels 0; Gaps 0;  
Matches 4; Conservative 1; Mismatches 0;

QY 1 HYAMS 5  
|||:  
Db 10 HYALS 14

RESULT 33  
US-10-437-963-172988  
; Sequence 172988, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 172988  
; LENGTH: 100  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
; NAME/KEY: unsure  
; LOCATION: (1)..(100)  
; OTHER INFORMATION: unsure at all Xaa locations  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_71070C.1.pep  
US-10-437-963-172988

Query Match 89.3%; Score 25; DB 4; Length 100;  
Best Local Similarity 80.0%; Pred. No. 5.6e+02; Indels 0; Gaps 0;  
Matches 4; Conservative 1; Mismatches 0;

QY 1 HYAMS 5  
|||:  
Db 84 HYSMS 88

RESULT 34  
US-10-437-963-165791  
; Sequence 165791, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei

```

; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 165791
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_64563C.1.pap
US-10-437-963-165791

Query Match      89.3%; Score 25; DB 4; Length 107;
Best Local Similarity 80.0%; Pred. No. 6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 HYAMS 5
Db      69 HYAMT 73

RESULT 35
US-10-501-282-1606
; Sequence 1606, Application US/10501282
; Publication No. US20050203280A1
; GENERAL INFORMATION:
; APPLICANT: MICHAEL, JOHN CALHOUN
; APPLICANT: ZAGURSKY, ROBERT JOHN
; APPLICANT: RUSSELL, DAVID PARRISH
; APPLICANT: FLETCHER, LEAH DIANE
; TITLE OF INVENTION: ALLOIOCCUS OTITIDIS OPEN READING FRAMES (ORFS) ENCODING
; FILE REFERENCE: AM100780 L2
; CURRENT APPLICATION NUMBER: US/10/501,282
; CURRENT FILING DATE: 2004-07-09
; PRIOR APPLICATION NUMBER: 60/333,777
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: 60/426,742
; PRIOR FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: PCT/US02/36123
; PRIOR FILING DATE: 2002-11-25
; NUMBER OF SEQ ID NOS: 6653
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1606
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Alloiococcus otitidis
US-10-501-282-1606

Query Match      89.3%; Score 25; DB 5; Length 113;
Best Local Similarity 80.0%; Pred. No. 6.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 HYAMS 5
Db      74 HYALS 78

RESULT 36
US-10-282-122A-77481
; Sequence 77481, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl

; APPLICANT: Zykkind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 77481
; LENGTH: 126
; TYPE: PRT
; ORGANISM: Vibrio cholerae
US-10-282-122A-77481

Query Match      89.3%; Score 25; DB 4; Length 126;
Best Local Similarity 80.0%; Pred. No. 7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 HYAMS 5
Db      115 HYAMA 119

RESULT 37
US-10-437-963-106924
; Sequence 106924, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 106924
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:

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; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_11324C.1.pep  
US-10-437-963-106924

Query Match 89.3%; Score 25; DB 4; Length 131;  
Best Local Similarity 80.0%; Pred. No. 7.3e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5  
|||:  
Db 51 HYALS 55

RESULT 38

US-10-425-115-360208  
; Sequence 360208, Application US/10425115  
; Publication No. US20040214272A1  
; GENERAL INFORMATION:  
; APPLICANT: MCMICHAEL, JOHN CALHOUN  
; APPLICANT: ZAGURSKY, ROBERT JOHN  
; APPLICANT: RUSSELL, DAVID PARRISH  
; APPLICANT: FLETCHER, LEAH DIANE  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53222)B  
; CURRENT APPLICATION NUMBER: US/10/425,115  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 369326  
; SEQ ID NO 360208  
; LENGTH: 131  
; TYPE: PRT  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: MRT4577\_91685C.1.pep  
US-10-425-115-360208

Query Match 89.3%; Score 25; DB 4; Length 131;  
Best Local Similarity 80.0%; Pred. No. 7.3e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5  
|||:  
Db 78 HYAMA 82

RESULT 39

US-10-501-282-1614  
; Sequence 1614, Application US/10501282  
; Publication No. US20050203280A1  
; GENERAL INFORMATION:  
; APPLICANT: MCMICHAEL, JOHN CALHOUN  
; APPLICANT: ZAGURSKY, ROBERT JOHN  
; APPLICANT: RUSSELL, DAVID PARRISH  
; APPLICANT: FLETCHER, LEAH DIANE  
; TITLE OF INVENTION: ALLOIOCOCCUS OTITIDIS OPEN READING FRAMES (ORFS) ENCODING  
; TITLE OF INVENTION: POLYPEPTIDE ANTIGENS, IMMUNOGENIC COMPOSITIONS AND USES THEREOF  
; FILE REFERENCE: AM100780 L2  
; CURRENT APPLICATION NUMBER: US/10/501,282  
; CURRENT FILING DATE: 2004-07-09  
; PRIOR APPLICATION NUMBER: 60/333,777  
; PRIOR FILING DATE: 2001-11-29  
; PRIOR APPLICATION NUMBER: 60/426,742  
; PRIOR FILING DATE: 2002-11-18  
; PRIOR APPLICATION NUMBER: PCT/US02/36123  
; PRIOR FILING DATE: 2002-11-25  
; NUMBER OF SEQ ID NOS: 6653  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 1614  
; LENGTH: 133  
; TYPE: PRT  
; ORGANISM: Alloiococcus otitidis  
US-10-501-282-1614

Query Match 89.3%; Score 25; DB 5; Length 133;

Best Local Similarity 80.0%; Pred. No. 7.4e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5  
|||:  
Db 74 HYALS 78

RESULT 40

US-10-501-282-1608  
; Sequence 1608, Application US/10501282  
; Publication No. US20050203280A1  
; GENERAL INFORMATION:  
; APPLICANT: MCMICHAEL, JOHN CALHOUN  
; APPLICANT: ZAGURSKY, ROBERT JOHN  
; APPLICANT: RUSSELL, DAVID PARRISH  
; APPLICANT: FLETCHER, LEAH DIANE  
; TITLE OF INVENTION: ALLOIOCOCCUS OTITIDIS OPEN READING FRAMES (ORFS) ENCODING  
; TITLE OF INVENTION: POLYPEPTIDE ANTIGENS, IMMUNOGENIC COMPOSITIONS AND USES THEREOF  
; FILE REFERENCE: AM100780 L2  
; CURRENT APPLICATION NUMBER: US/10/501,282  
; CURRENT FILING DATE: 2004-07-09  
; PRIOR APPLICATION NUMBER: 60/333,777  
; PRIOR FILING DATE: 2001-11-29  
; PRIOR APPLICATION NUMBER: 60/426,742  
; PRIOR FILING DATE: 2002-11-18  
; PRIOR APPLICATION NUMBER: PCT/US02/36123  
; PRIOR FILING DATE: 2002-11-25  
; NUMBER OF SEQ ID NOS: 6653  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 1608  
; LENGTH: 134  
; TYPE: PRT  
; ORGANISM: Alloiococcus otitidis  
US-10-501-282-1608

Query Match 89.3%; Score 25; DB 5; Length 134;  
Best Local Similarity 80.0%; Pred. No. 7.4e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5  
|||:  
Db 95 HYALS 99

RESULT 41

US-10-424-599-207366  
; Sequence 207366, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa Thomas J  
; APPLICANT: Kovalic David K  
; APPLICANT: Zhou Yihua  
; APPLICANT: Cao Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 207366  
; LENGTH: 135  
; TYPE: PRT  
; ORGANISM: Glycine max  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)..(135)  
; OTHER INFORMATION: unsure at all Xaa locations  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_29277C.1.pap  
US-10-424-599-207366

Query Match 89.3%; Score 25; DB 4; Length 135;

Best Local Similarity 80.0%; Pred. No. 7.5e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5  
Db 102 HYALS 106

RESULT 42  
US-10-424-599-177566  
; Sequence 177566, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa Thomas J  
; APPLICANT: Kovalic David K  
; APPLICANT: Zhou Yihua  
; APPLICANT: Cao Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 177566  
; LENGTH: 136  
; TYPE: PRT  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_131358C.1.pep  
US-10-424-599-177566

Query Match 89.3%; Score 25; DB 4; Length 136;  
Best Local Similarity 80.0%; Pred. No. 7.5e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5  
Db 66 HYAMA 70

RESULT 43  
US-10-424-599-188149  
; Sequence 188149, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa Thomas J  
; APPLICANT: Kovalic David K  
; APPLICANT: Zhou Yihua  
; APPLICANT: Cao Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 188149  
; LENGTH: 148  
; TYPE: PRT  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_140912C.1.pep  
US-10-424-599-188149

Query Match 89.3%; Score 25; DB 4; Length 148;  
Best Local Similarity 80.0%; Pred. No. 8.2e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5  
Db 70 HYAMS 74

RESULT 44

US-09-764-868-938  
; Sequence 938, Application US/09764868  
; Patent No. US20020189711A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PT232  
; CURRENT APPLICATION NUMBER: US/09/764,868  
; CURRENT FILING DATE: 2001-01-17  
; Prior application data removed - refer to PALM or file wrapper  
; NUMBER OF SEQ ID NOS: 1510  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 938  
; LENGTH: 150  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (71)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
; NAME/KEY: SITE  
; LOCATION: (105)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
; NAME/KEY: SITE  
; LOCATION: (109)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
US-09-764-868-938

Query Match 89.3%; Score 25; DB 3; Length 150;  
Best Local Similarity 80.0%; Pred. No. 8.3e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5  
Db 65 HYALS 69

RESULT 45  
US-10-450-763-52145  
; Sequence 52145, Application US/10450763  
; Publication No. US20050196754A1  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc  
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES  
; FILE REFERENCE: 790CIP3/US  
; CURRENT APPLICATION NUMBER: US/10/450,763  
; CURRENT FILING DATE: 2003-06-11  
; PRIOR APPLICATION NUMBER: PCT/US01/08631  
; PRIOR FILING DATE: 2001-03-30  
; PRIOR APPLICATION NUMBER: 09/540,217  
; PRIOR FILING DATE: 2000-03-31  
; PRIOR APPLICATION NUMBER: 09/649,167  
; PRIOR FILING DATE: 2000-08-23  
; NUMBER OF SEQ ID NOS: 60736  
; SOFTWARE: Custom  
; SEQ ID NO 52145  
; LENGTH: 164  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-450-763-52145

Query Match 89.3%; Score 25; DB 5; Length 164;  
Best Local Similarity 80.0%; Pred. No. 9e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5  
Db 18 HYALS 22

RESULT 46  
US-10-425-115-225898  
; Sequence 225898, Application US/10425115

; Publication No. US20040214272A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants  
; FILE REFERENCE: 38-21(53222)B  
; CURRENT APPLICATION NUMBER: US/10/425,115  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 369326  
; SEQ ID NO 225898  
; LENGTH: 174  
; TYPE: PRT  
; ORGANISM: Zea mays  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)..(174)  
; OTHER INFORMATION: unsure at all Xaa locations  
; FEATURE:  
; OTHER INFORMATION: Clone ID: MRT4577\_13760C.1.pep  
US-10-425-115-225898

Query Match 89.3%; Score 25; DB 4; Length 174;  
Best Local Similarity 80.0%; Pred. No. 9.6e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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; Publication No. US20040023864A1  
; GENERAL INFORMATION:  
; APPLICANT: Dubois-Stringfellow, Nathalie  
; APPLICANT: Steve, Rocznia  
; APPLICANT: Zolotarev, Alya  
; TITLE OF INVENTION: Method of Regulating Angiogenesis Using RYK Protein  
; FILE REFERENCE: MSB 7266  
; CURRENT APPLICATION NUMBER: US/10/275,589  
; CURRENT FILING DATE: 2002-11-06  
; PRIOR APPLICATION NUMBER: US 09/568,783  
; PRIOR FILING DATE: 2000-05-11  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: PatentIn version 3.2  
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US-10-275-589-3

Query Match 89.3%; Score 25; DB 4; Length 180;  
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; Sequence 2, Application US/10275589  
; Publication No. US20040023864A1  
; GENERAL INFORMATION:  
; APPLICANT: Dubois-Stringfellow, Nathalie  
; APPLICANT: Steve, Rocznia  
; APPLICANT: Zolotarev, Alya  
; TITLE OF INVENTION: Method of Regulating Angiogenesis Using RYK Protein

; FILE REFERENCE: MSB 7266  
; CURRENT APPLICATION NUMBER: US/10/275,589  
; CURRENT FILING DATE: 2002-11-06  
; PRIOR APPLICATION NUMBER: US 09/568,783  
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; APPLICANT: Dubois-Stringfellow, Nathalie  
; APPLICANT: Steve, Rocznia  
; APPLICANT: Zolotarev, Alya  
; TITLE OF INVENTION: Method of Regulating Angiogenesis Using RYK Protein  
; FILE REFERENCE: MSB 7266  
; CURRENT APPLICATION NUMBER: US/10/275,589  
; CURRENT FILING DATE: 2002-11-06  
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; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants  
; FILE REFERENCE: 38-21(53222)B  
; CURRENT APPLICATION NUMBER: US/10/425,115  
; CURRENT FILING DATE: 2003-04-28  
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153	22	78.6	429	6	US-11-087-099-9500	Sequence 9500, Ap	226	21	75.0	120	7	US-11-005-726-2	Sequence 2, Appl
154	22	78.6	438	6	US-10-467-657-3188	Sequence 3188, Ap	227	21	75.0	120	7	US-11-005-726-3	Sequence 3, Appl
155	22	78.6	445	7	US-11-098-686-11367	Sequence 11367, A	228	21	75.0	120	7	US-11-005-726-9	Sequence 9, Appl
156	22	78.6	455	7	US-11-098-686-10297	Sequence 10297, A	229	21	75.0	121	6	US-10-648-816-16	Sequence 16, Appl
157	22	78.6	464	7	US-11-127-817-19	Sequence 19, Appl	230	21	75.0	123	7	US-11-102-512-69	Sequence 69, Appl
158	22	78.6	464	7	US-11-180-044-2	Sequence 2, Appl	231	21	75.0	123	7	US-11-218-813-69	Sequence 69, Appl
159	22	78.6	467	7	US-11-087-099-4656	Sequence 4656, Ap	232	21	75.0	123	7	US-11-218-813-70	Sequence 70, Appl
160	22	78.6	470	7	US-11-096-568A-23669	Sequence 23669, A	233	21	75.0	123	6	US-11-208-422-12	Sequence 12, Appl
161	22	78.6	471	7	US-11-077-619-58	Sequence 58, Appl	234	21	75.0	124	6	US-10-771-257-19	Sequence 19, Appl
162	22	78.6	501	6	US-10-485-517-381	Sequence 381, App	235	21	75.0	124	7	US-11-127-677-19	Sequence 19, Appl
163	22	78.6	504	7	US-11-096-568A-23668	Sequence 23668, A	236	21	75.0	125	7	US-11-049-536-646	Sequence 646, App
164	22	78.6	535	7	US-11-096-568A-30933	Sequence 30933, A	237	21	75.0	125	7	US-11-193-739-646	Sequence 646, App
165	22	78.6	548	6	US-10-858-730-68	Sequence 68, Appl	238	21	75.0	128	6	US-10-993-543-108	Sequence 108, App
166	22	78.6	550	7	US-11-096-568A-30932	Sequence 30932, A	239	21	75.0	131	7	US-11-096-568A-14461	Sequence 14461, A
167	22	78.6	582	7	US-11-172-740-2180	Sequence 2180, Ap	240	21	75.0	132	7	US-11-005-726-11	Sequence 11, Appl
168	22	78.6	601	7	US-11-103-957-3	Sequence 3, Appl	241	21	75.0	132	7	US-11-072-512-3557	Sequence 3557, Ap
169	22	78.6	601	7	US-11-018-868-119	Sequence 119, App	242	21	75.0	133	7	US-11-218-813-54	Sequence 54, Appl
170	22	78.6	605	7	US-11-127-877-71	Sequence 71, Appl	243	21	75.0	138	7	US-11-072-512-3612	Sequence 3612, Ap
171	22	78.6	623	7	US-11-087-099-5188	Sequence 5188, Ap	244	21	75.0	142	7	US-11-052-554A-334	Sequence 334, App

245	21	75.0	143	7	US-11-049-536-28	Sequence 28, Appl	318	21	75.0	306	7	US-11-087-099-9166	Sequence 9166, Ap
246	21	75.0	143	7	US-11-072-512-3542	Sequence 3542, Ap	319	21	75.0	308	7	US-11-096-568A-2109	Sequence 2109, Ap
247	21	75.0	143	7	US-11-199-739-28	Sequence 28, Appl	320	21	75.0	311	7	US-11-156-084-330	Sequence 330, App
248	21	75.0	148	7	US-11-096-568A-20503	Sequence 20503, A	321	21	75.0	312	7	US-11-087-099-3833	Sequence 3833, Ap
249	21	75.0	148	7	US-11-096-568A-10263	Sequence 10263, A	322	21	75.0	313	7	US-11-087-099-11346	Sequence 11346, A
250	21	75.0	160	7	US-11-096-686-10979	Sequence 10979, A	323	21	75.0	318	7	US-11-098-686-10960	Sequence 10960, A
251	21	75.0	162	7	US-11-096-568A-10262	Sequence 10262, A	324	21	75.0	321	7	US-11-087-099-12042	Sequence 12042, A
252	21	75.0	168	7	US-11-096-568A-14460	Sequence 14460, A	325	21	75.0	323	7	US-11-087-099-9424	Sequence 9424, Ap
253	21	75.0	169	7	US-11-098-686-66	Sequence 66, Appl	326	21	75.0	326	7	US-11-096-568A-25949	Sequence 25949, A
254	21	75.0	180	7	US-11-103-957-87	Sequence 87, Appl	327	21	75.0	327	7	US-11-113-424-40	Sequence 40, Appl
255	21	75.0	181	6	US-10-467-657-1918	Sequence 1918, Ap	328	21	75.0	329	7	US-11-096-568A-6040	Sequence 6040, Ap
256	21	75.0	183	7	US-11-096-568A-14459	Sequence 14459, A	329	21	75.0	329	7	US-11-087-099-9417	Sequence 9417, Ap
257	21	75.0	190	7	US-11-087-099-4627	Sequence 4627, Ap	330	21	75.0	332	7	US-11-087-099-4059	Sequence 4059, Ap
258	21	75.0	193	7	US-11-087-099-2566	Sequence 2566, Ap	331	21	75.0	335	7	US-11-087-099-8353	Sequence 8353, Ap
259	21	75.0	193	7	US-11-087-099-7094	Sequence 7094, Ap	332	21	75.0	335	7	US-11-087-099-9182	Sequence 9182, Ap
260	21	75.0	193	7	US-11-096-568A-19168	Sequence 19168, A	333	21	75.0	335	7	US-11-087-099-7137	Sequence 7137, Ap
261	21	75.0	193	7	US-11-096-568A-26321	Sequence 26321, A	334	21	75.0	337	7	US-10-467-657-2564	Sequence 2564, Ap
262	21	75.0	197	7	US-11-087-099-5815	Sequence 5815, Ap	335	21	75.0	343	6	US-10-506-454-1419	Sequence 1419, Ap
263	21	75.0	203	7	US-11-096-568A-10261	Sequence 10261, A	336	21	75.0	345	6	US-10-467-657-3446	Sequence 3446, Ap
264	21	75.0	207	6	US-10-878-556A-93	Sequence 93, Appl	337	21	75.0	358	6	US-11-096-568A-33635	Sequence 33635, A
265	21	75.0	210	7	US-11-096-568A-2776	Sequence 2776, Ap	338	21	75.0	359	7	US-11-098-686-10796	Sequence 10796, A
266	21	75.0	210	7	US-11-096-568A-33636	Sequence 33636, A	339	21	75.0	360	7	US-11-087-099-7199	Sequence 7199, Ap
267	21	75.0	216	7	US-11-096-568A-2775	Sequence 2775, Ap	340	21	75.0	363	6	US-10-793-626-3076	Sequence 3076, Ap
268	21	75.0	216	7	US-11-096-568A-2777	Sequence 2777, Ap	341	21	75.0	364	6	US-11-072-512-2763	Sequence 2763, Ap
269	21	75.0	220	7	US-11-087-099-9425	Sequence 9425, Ap	342	21	75.0	367	7	US-11-098-686-11074	Sequence 11074, A
270	21	75.0	226	7	US-11-183-205-42	Sequence 42, Appl	343	21	75.0	368	7	US-11-096-568A-32913	Sequence 32913, A
271	21	75.0	227	6	US-10-467-657-2352	Sequence 2352, Ap	344	21	75.0	369	7	US-11-096-568A-9495	Sequence 9495, Ap
272	21	75.0	227	6	US-10-467-657-3552	Sequence 3552, Ap	345	21	75.0	372	7	US-11-098-686-10103	Sequence 10103, A
273	21	75.0	228	7	US-11-096-568A-2774	Sequence 2774, Ap	346	21	75.0	376	7	US-11-096-568A-9494	Sequence 9494, Ap
274	21	75.0	228	7	US-11-096-568A-3625	Sequence 3625, Ap	347	21	75.0	378	7	US-11-087-099-12062	Sequence 12062, A
275	21	75.0	229	7	US-11-096-568A-3624	Sequence 3624, Ap	348	21	75.0	379	7	US-11-096-568A-9493	Sequence 9493, Ap
276	21	75.0	230	7	US-11-074-176-224	Sequence 224, Appl	349	21	75.0	383	7	US-11-087-099-7496	Sequence 7496, Ap
277	21	75.0	231	7	US-11-096-568A-39167	Sequence 39167, A	350	21	75.0	389	7	US-11-226-869-570	Sequence 570, App
278	21	75.0	232	7	US-11-096-568A-3623	Sequence 3623, Ap	351	21	75.0	399	7	US-10-793-626-1522	Sequence 1522, Ap
279	21	75.0	233	7	US-11-096-568A-25951	Sequence 25951, A	352	21	75.0	403	6	US-11-087-099-4442	Sequence 4442, Ap
280	21	75.0	236	7	US-11-224-071-16	Sequence 16, Appl	353	21	75.0	427	7	US-11-087-099-6197	Sequence 6197, Ap
281	21	75.0	240	7	US-11-054-515-2050	Sequence 2050, Ap	354	21	75.0	427	7	US-11-087-099-7136	Sequence 7136, Ap
282	21	75.0	240	7	US-11-266-444-2050	Sequence 2050, Ap	355	21	75.0	433	7	US-11-063-703-58	Sequence 58, Appl
283	21	75.0	242	7	US-11-096-568A-19830	Sequence 19830, A	356	21	75.0	433	7	US-11-102-240-58	Sequence 58, Appl
284	21	75.0	243	7	US-11-096-568A-23176	Sequence 23176, A	357	21	75.0	450	7	US-11-096-568A-14775	Sequence 14775, A
285	21	75.0	244	7	US-11-096-568A-2924	Sequence 2924, A	358	21	75.0	450	7	US-11-096-568A-22541	Sequence 22541, A
286	21	75.0	244	7	US-11-096-568A-2925	Sequence 2925, Ap	359	21	75.0	468	6	US-10-793-626-1618	Sequence 1618, Ap
287	21	75.0	245	7	US-11-109-831-48	Sequence 48, Appl	360	21	75.0	468	6	US-11-087-099-9108	Sequence 9108, Ap
288	21	75.0	245	7	US-11-096-568A-23175	Sequence 23175, A	361	21	75.0	469	6	US-11-087-099-10267	Sequence 10267, A
289	21	75.0	246	7	US-11-096-568A-22542	Sequence 22542, A	362	21	75.0	469	7	US-11-072-512-3516	Sequence 3516, Ap
290	21	75.0	247	7	US-11-226-869-571	Sequence 571, Appl	363	21	75.0	469	7	US-11-087-099-3380	Sequence 3380, Ap
291	21	75.0	248	7	US-11-054-515-848	Sequence 848, Ap	364	21	75.0	481	7	US-11-024-959-413	Sequence 413, App
292	21	75.0	248	7	US-11-054-515-1785	Sequence 1785, Ap	365	21	75.0	483	7	US-11-024-959-414	Sequence 414, App
293	21	75.0	248	7	US-11-266-444-848	Sequence 848, Appl	366	21	75.0	483	7	US-11-087-099-7042	Sequence 7042, Ap
294	21	75.0	248	7	US-11-266-444-1785	Sequence 1785, Ap	367	21	75.0	500	7	US-11-087-099-9108	Sequence 9108, Ap
295	21	75.0	250	7	US-11-054-515-7	Sequence 7, Appl	368	21	75.0	500	7	US-11-087-099-10267	Sequence 10267, A
296	21	75.0	250	7	US-11-266-444-7	Sequence 7, Appl	369	21	75.0	500	7	US-11-072-512-3516	Sequence 3516, Ap
297	21	75.0	254	7	US-11-054-515-1195	Sequence 1195, Ap	370	21	75.0	509	6	US-10-506-454-1303	Sequence 1303, Ap
298	21	75.0	254	7	US-11-266-444-1195	Sequence 1195, Ap	371	21	75.0	513	7	US-11-087-099-8135	Sequence 8135, Ap
299	21	75.0	259	7	US-11-118-855-1	Sequence 1, Appl	372	21	75.0	522	7	US-11-080-991-104	Sequence 104, App
300	21	75.0	266	7	US-11-156-084-187	Sequence 187, Appl	373	21	75.0	525	6	US-10-763-712A-108	Sequence 108, App
301	21	75.0	272	6	US-10-467-657-9017	Sequence 9017, Ap	374	21	75.0	540	7	US-11-096-568A-6039	Sequence 6039, Ap
302	21	75.0	272	7	US-11-082-389-76	Sequence 76, Appl	375	21	75.0	541	7	US-11-118-855-26	Sequence 26, Appl
303	21	75.0	273	7	US-11-113-424-16	Sequence 16, Appl	376	21	75.0	549	7	US-11-072-512-3479	Sequence 3479, Ap
304	21	75.0	273	7	US-11-113-424-18	Sequence 18, Appl	377	21	75.0	551	7	US-11-096-568A-30361	Sequence 30361, A
305	21	75.0	273	7	US-11-096-568A-2110	Sequence 2110, Ap	378	21	75.0	557	7	US-11-098-686-10483	Sequence 10483, A
306	21	75.0	275	7	US-11-110-977-2	Sequence 2, Appl	379	21	75.0	559	6	US-10-521-162-4	Sequence 4, Appl
307	21	75.0	277	7	US-11-156-084-180	Sequence 180, Appl	380	21	75.0	561	7	US-11-096-568A-9122	Sequence 9122, Ap
308	21	75.0	284	6	US-10-467-657-2768	Sequence 2768, A	381	21	75.0	568	6	US-10-055-877-300	Sequence 300, App
309	21	75.0	287	6	US-10-467-657-2768	Sequence 2768, A	382	21	75.0				
310	21	75.0	289	7	US-11-096-568A-16569	Sequence 16569, A	383	21	75.0				
311	21	75.0	289	7	US-11-096-568A-16568	Sequence 16568, A	384	21	75.0				
312	21	75.0	290	7	US-11-096-568A-16567	Sequence 16567, A	385	21	75.0				
313	21	75.0	292	7	US-11-098-686-10822	Sequence 10822, A	386	21	75.0				
314	21	75.0	292	7	US-11-096-568A-2922	Sequence 2922, Ap	387	21	75.0				
315	21	75.0	296	6	US-10-793-626-1674	Sequence 1674, Ap	388	21	75.0				
316	21	75.0	299	7	US-11-113-424-8	Sequence 8, Appl	389	21	75.0				
317	21	75.0	304	7	US-11-152-569-11	Sequence 11, Appl	390	21	75.0				

391	21	75.0	569	6	US-10-821-234-864	Sequence 864, App	464	20	71.4	14	7	US-11-266-444-2685	Sequence 2685, Ap
392	21	75.0	582	7	US-11-096-568A-38656	Sequence 28656, A	465	20	71.4	15	7	US-11-116-144-86	Sequence 86, Appl
393	21	75.0	582	7	US-11-096-568A-30360	Sequence 30360, A	466	20	71.4	16	7	US-11-054-515-2891	Sequence 2891, Ap
394	21	75.0	585	6	US-10-506-454-1359	Sequence 1359, Ap	467	20	71.4	16	7	US-11-266-444-2891	Sequence 2891, Ap
395	21	75.0	585	7	US-11-241-347-15	Sequence 15, Appl	468	20	71.4	17	7	US-11-054-515-2774	Sequence 2774, Ap
396	21	75.0	585	7	US-11-096-568A-9121	Sequence 9121, Ap	469	20	71.4	17	7	US-11-054-515-2831	Sequence 2831, Ap
397	21	75.0	585	7	US-11-096-568A-9123	Sequence 9123, Ap	470	20	71.4	17	7	US-11-266-444-2774	Sequence 2774, Ap
398	21	75.0	586	6	US-10-623-155-152	Sequence 152, App	471	20	71.4	17	7	US-11-266-444-2831	Sequence 2831, Ap
399	21	75.0	586	6	US-10-623-155-338	Sequence 338, App	472	20	71.4	18	7	US-11-054-515-2964	Sequence 2964, Ap
400	21	75.0	586	7	US-11-109-831-16	Sequence 16, Appl	473	20	71.4	18	7	US-11-266-444-2964	Sequence 2964, Ap
401	21	75.0	586	7	US-11-109-831-22	Sequence 22, Appl	474	20	71.4	19	7	US-11-167-872-50	Sequence 50, Appl
402	21	75.0	587	7	US-11-096-568A-28655	Sequence 28655, A	475	20	71.4	20	7	US-11-054-515-2747	Sequence 2747, Ap
403	21	75.0	596	7	US-11-087-099-9309	Sequence 9309, Ap	476	20	71.4	20	7	US-11-266-444-2747	Sequence 2747, Ap
404	21	75.0	608	7	US-11-226-701-8	Sequence 8, Appl	477	20	71.4	22	7	US-11-149-943-20	Sequence 20, Appl
405	21	75.0	608	7	US-11-241-347-9	Sequence 9, Appl	478	20	71.4	22	7	US-11-149-943-27	Sequence 27, Appl
406	21	75.0	608	7	US-11-241-347-9	Sequence 9, Appl	479	20	71.4	34	6	US-10-895-064-787	Sequence 787, App
407	21	75.0	613	6	US-10-537-061-10	Sequence 10, Appl	480	20	71.4	34	7	US-11-123-741-787	Sequence 787, App
408	21	75.0	622	6	US-10-491-468-11	Sequence 11, Appl	481	20	71.4	34	7	US-11-123-741-787	Sequence 787, App
409	21	75.0	622	7	US-11-147-360-4	Sequence 4, Appl	482	20	71.4	34	7	US-11-143-077-12	Sequence 12, Appl
410	21	75.0	632	7	US-11-096-568A-9120	Sequence 9120, Ap	483	20	71.4	37	7	US-11-187-364-12	Sequence 12, Appl
411	21	75.0	641	6	US-10-623-155-339	Sequence 339, App	484	20	71.4	40	6	US-10-467-657-5996	Sequence 5996, Ap
412	21	75.0	641	7	US-11-109-831-13	Sequence 13, Appl	485	20	71.4	53	7	US-11-033-105A-15	Sequence 15, Appl
413	21	75.0	642	7	US-11-096-568A-28654	Sequence 28654, A	486	20	71.4	53	7	US-11-004-339-2437	Sequence 2437, Ap
414	21	75.0	645	7	US-11-096-568A-19117	Sequence 19117, A	487	20	71.4	68	6	US-10-952-535A-23	Sequence 23, Appl
415	21	75.0	645	7	US-11-096-568A-19116	Sequence 19116, A	488	20	71.4	68	7	US-11-087-099-6917	Sequence 6917, Ap
416	21	75.0	680	6	US-10-623-155-342	Sequence 342, App	489	20	71.4	72	7	US-11-114-979-2	Sequence 2, Appl
417	21	75.0	680	7	US-11-109-831-19	Sequence 19, Appl	490	20	71.4	77	7	US-11-087-099-1780	Sequence 1780, Ap
418	21	75.0	694	6	US-10-649-591-17	Sequence 17, Appl	491	20	71.4	88	7	US-11-024-959-285	Sequence 285, App
419	21	75.0	711	7	US-11-096-568A-19115	Sequence 19115, A	492	20	71.4	88	7	US-11-024-959-285	Sequence 285, App
420	21	75.0	712	6	US-10-521-162-12	Sequence 12, Appl	493	20	71.4	92	6	US-10-467-657-3456	Sequence 3456, Ap
421	21	75.0	721	7	US-11-072-513-3212	Sequence 3212, Ap	494	20	71.4	93	7	US-11-024-959-404	Sequence 404, App
422	21	75.0	728	7	US-11-072-513-3359	Sequence 3359, Ap	495	20	71.4	93	7	US-11-024-959-407	Sequence 407, App
423	21	75.0	739	7	US-11-087-099-4827	Sequence 4827, Ap	496	20	71.4	96	6	US-10-993-543-287	Sequence 287, App
424	21	75.0	758	7	US-11-043-693-1	Sequence 1, Appl	497	20	71.4	97	7	US-11-093-274-34	Sequence 34, Appl
425	21	75.0	789	7	US-11-098-686-10148	Sequence 10148, A	498	20	71.4	97	6	US-10-783-273-10	Sequence 10, Appl
426	21	75.0	802	6	US-11-087-099-6978	Sequence 6978, Ap	499	20	71.4	98	7	US-11-144-248-32	Sequence 32, Appl
427	21	75.0	878	6	US-10-204-639-27	Sequence 27, Appl	500	20	71.4	98	7	US-11-054-669-22	Sequence 22, Appl
428	21	75.0	893	7	US-11-087-099-3696	Sequence 3696, Ap	501	20	71.4	98	7	US-11-084-554-33	Sequence 33, Appl
429	21	75.0	901	7	US-11-216-333-4	Sequence 4, Appl	502	20	71.4	98	7	US-11-084-554-36	Sequence 36, Appl
430	21	75.0	960	7	US-11-169-041-177	Sequence 177, App	503	20	71.4	98	7	US-11-144-232-32	Sequence 32, Appl
431	21	75.0	970	7	US-11-087-099-1181	Sequence 1181, Ap	504	20	71.4	98	7	US-11-004-590-20	Sequence 20, Appl
432	21	75.0	1001	7	US-11-072-513-2283	Sequence 2283, Ap	505	20	71.4	98	7	US-11-004-590-23	Sequence 23, Appl
433	21	75.0	1061	6	US-11-121-438-4	Sequence 4, Appl	506	20	71.4	98	7	US-11-136-250-33	Sequence 33, Appl
434	21	75.0	1092	6	US-10-821-234-999	Sequence 999, App	507	20	71.4	98	7	US-11-136-250-36	Sequence 36, Appl
435	21	75.0	1230	7	US-11-231-599-56	Sequence 56, Appl	508	20	71.4	98	7	US-11-183-543-32	Sequence 32, Appl
436	21	75.0	1338	6	US-10-821-234-1622	Sequence 1622, Ap	509	20	71.4	98	7	US-11-049-536-721	Sequence 721, App
437	21	75.0	1338	7	US-11-109-156-23	Sequence 23, Appl	510	20	71.4	100	7	US-11-084-554-40	Sequence 40, Appl
438	21	75.0	1338	7	US-11-075-047A-2	Sequence 2, Appl	511	20	71.4	100	7	US-11-004-590-31	Sequence 31, Appl
439	21	75.0	1341	7	US-11-226-869-565	Sequence 565, App	512	20	71.4	100	7	US-11-136-250-40	Sequence 40, Appl
440	21	75.0	1349	7	US-11-226-869-573	Sequence 573, App	513	20	71.4	101	7	US-11-096-568A-31173	Sequence 31173, A
441	21	75.0	1360	7	US-11-188-743-22	Sequence 22, Appl	514	20	71.4	105	7	US-11-024-959-405	Sequence 405, App
442	21	75.0	1360	7	US-11-183-294-26	Sequence 26, Appl	515	20	71.4	105	7	US-11-024-959-406	Sequence 406, App
443	21	75.0	1839	7	US-11-087-099-9631	Sequence 9631, Ap	516	20	71.4	109	6	US-10-941-717A-9	Sequence 9, Appl
444	21	75.0	2602	6	US-10-937-658-5	Sequence 5, Appl	517	20	71.4	110	6	US-10-771-257-1	Sequence 1, Appl
445	21	75.0	2647	6	US-10-821-234-1303	Sequence 1303, Ap	518	20	71.4	110	7	US-11-127-677-1	Sequence 1, Appl
446	21	75.0	2657	6	US-10-821-234-1262	Sequence 1262, Ap	519	20	71.4	111	7	US-11-072-512-2742	Sequence 2742, Ap
447	21	75.0	3300	7	US-11-052-554A-133	Sequence 133, App	520	20	71.4	113	6	US-10-665-658-6	Sequence 6, Appl
448	21	75.0	3353	6	US-11-037-243-64	Sequence 64, Appl	521	20	71.4	113	7	US-11-049-536-106	Sequence 106, App
449	21	71.4	5	6	US-10-982-440-80	Sequence 80, Appl	522	20	71.4	113	7	US-11-193-739-106	Sequence 106, App
450	20	71.4	5	7	US-11-127-677-119	Sequence 119, App	523	20	71.4	115	6	US-10-925-366A-225	Sequence 225, App
451	20	71.4	5	7	US-11-201-825-36	Sequence 36, Appl	524	20	71.4	115	6	US-10-925-366A-227	Sequence 227, App
452	20	71.4	6	7	US-11-149-309-22	Sequence 22, Appl	525	20	71.4	115	6	US-10-925-366A-229	Sequence 229, App
453	20	71.4	10	7	US-11-054-515-2161	Sequence 2161, Ap	526	20	71.4	116	6	US-10-925-366A-1	Sequence 1, Appl
454	20	71.4	10	7	US-11-171-567-142	Sequence 142, App	527	20	71.4	116	6	US-10-925-366A-223	Sequence 223, App
455	20	71.4	10	7	US-11-266-444-2161	Sequence 2161, Ap	528	20	71.4	116	6	US-10-925-366A-224	Sequence 224, App
456	20	71.4	14	7	US-11-054-515-2133	Sequence 2133, Ap	529	20	71.4	116	6	US-10-925-366A-228	Sequence 228, App
457	20	71.4	14	7	US-11-054-515-2149	Sequence 2149, Ap	530	20	71.4	116	6	US-10-925-366A-230	Sequence 230, App
458	20	71.4	14	7	US-11-054-515-2504	Sequence 2504, Ap	531	20	71.4	116	6	US-10-925-366A-231	Sequence 231, App
459	20	71.4	14	7	US-11-054-515-2685	Sequence 2685, Ap	532	20	71.4	116	7	US-11-125-837-35	Sequence 35, Appl
460	20	71.4	14	7	US-11-167-872-67	Sequence 67, Appl	533	20	71.4	116	7	US-11-125-837-38	Sequence 38, Appl
461	20	71.4	14	7	US-11-266-444-2133	Sequence 2133, Ap	534	20	71.4	116	7	US-11-127-677-51	Sequence 51, Appl
462	20	71.4	14	7	US-11-266-444-2149	Sequence 2149, Ap	535	20	71.4	116	7	US-11-127-932-4	Sequence 4, Appl
463	20	71.4	14	7	US-11-266-444-2504	Sequence 2504, Ap	536	20	71.4	116	7	US-11-127-903-4	Sequence 4, Appl

537	20	71.4	116	7	US-11-102-512-1	Sequence 1, Appli	610	20	71.4	123	7	US-11-112-304A-30	Sequence 30, Appli
538	20	71.4	117	6	US-10-771-257-53	Sequence 53, Appli	611	20	71.4	124	6	US-10-515-241-8	Sequence 8, Appli
539	20	71.4	117	6	US-10-981-356A-6	Sequence 6, Appli	612	20	71.4	124	6	US-10-720-603A-4	Sequence 4, Appli
540	20	71.4	117	6	US-11-096-046-6	Sequence 6, Appli	613	20	71.4	124	7	US-11-049-536-594	Sequence 594, Appl
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542	20	71.4	117	7	US-11-049-536-222	Sequence 222, Appl	615	20	71.4	124	7	US-11-096-568A-2221	Sequence 2221, Ap
543	20	71.4	117	7	US-11-049-536-226	Sequence 226, Appl	616	20	71.4	124	7	US-11-199-739-594	Sequence 594, App
544	20	71.4	117	7	US-11-049-536-634	Sequence 634, Appl	617	20	71.4	125	6	US-10-771-257-43	Sequence 43, Appl
545	20	71.4	117	7	US-11-199-739-178	Sequence 178, Appl	618	20	71.4	125	7	US-10-771-257-43	Sequence 43, Appl
546	20	71.4	117	7	US-11-199-739-222	Sequence 222, Appl	619	20	71.4	125	7	US-11-144-248-16	Sequence 16, Appl
547	20	71.4	117	7	US-11-199-739-226	Sequence 226, Appl	620	20	71.4	125	7	US-11-127-677-41	Sequence 41, Appl
548	20	71.4	117	7	US-11-199-739-226	Sequence 226, Appl	621	20	71.4	125	7	US-11-144-222-16	Sequence 16, Appl
549	20	71.4	118	7	US-11-112-240-22	Sequence 22, Appl	622	20	71.4	125	7	US-11-182-343-16	Sequence 16, Appl
550	20	71.4	118	7	US-11-112-304A-22	Sequence 22, Appl	623	20	71.4	126	6	US-11-096-568A-31171	Sequence 31171, A
551	20	71.4	118	7	US-11-049-536-338	Sequence 338, Appl	624	20	71.4	126	7	US-10-771-257-13	Sequence 13, Appl
552	20	71.4	118	7	US-11-049-536-350	Sequence 350, Appl	625	20	71.4	126	7	US-11-127-677-13	Sequence 13, Appl
553	20	71.4	118	7	US-11-199-739-338	Sequence 338, Appl	626	20	71.4	126	7	US-11-127-932-5	Sequence 5, Appli
554	20	71.4	118	7	US-11-199-739-350	Sequence 350, Appl	627	20	71.4	126	7	US-11-041-471-10	Sequence 10, Appl
555	20	71.4	118	7	US-11-149-309-13	Sequence 13, Appl	628	20	71.4	126	7	US-11-221-900-11	Sequence 11, Appl
556	20	71.4	118	7	US-11-149-309-14	Sequence 14, Appl	629	20	71.4	129	7	US-11-096-568A-4537	Sequence 4537, Ap
557	20	71.4	118	7	US-11-149-309-15	Sequence 15, Appl	630	20	71.4	130	7	US-11-108-264-51	Sequence 51, Appl
558	20	71.4	118	7	US-11-149-309-16	Sequence 16, Appl	631	20	71.4	130	7	US-11-109-264-52	Sequence 52, Appl
559	20	71.4	118	7	US-11-149-309-36	Sequence 36, Appl	632	20	71.4	130	7	US-11-109-264-53	Sequence 53, Appl
560	20	71.4	119	6	US-10-925-366A-347	Sequence 347, Appl	633	20	71.4	130	7	US-11-109-264-54	Sequence 54, Appl
561	20	71.4	119	6	US-10-771-257-10	Sequence 10, Appl	634	20	71.4	131	6	US-10-993-543-140	Sequence 140, App
562	20	71.4	119	7	US-11-120-338-9	Sequence 9, Appli	635	20	71.4	135	6	US-10-793-626-2676	Sequence 2676, Ap
563	20	71.4	119	7	US-11-127-677-10	Sequence 10, Appl	636	20	71.4	137	6	US-10-993-543-100	Sequence 100, App
564	20	71.4	119	7	US-11-106-820-9	Sequence 9, Appli	637	20	71.4	138	6	US-10-793-626-762	Sequence 762, App
565	20	71.4	119	7	US-11-154-337-6	Sequence 6, Appli	638	20	71.4	138	7	US-11-128-900-79	Sequence 79, Appl
566	20	71.4	119	7	US-11-182-908-6	Sequence 6, Appli	639	20	71.4	139	6	US-10-721-763-33	Sequence 33, Appl
567	20	71.4	119	7	US-11-049-536-394	Sequence 394, Appl	640	20	71.4	139	7	US-11-267-310-2	Sequence 2, Appli
568	20	71.4	119	7	US-11-049-536-538	Sequence 538, Appl	641	20	71.4	139	7	US-11-267-312-2	Sequence 2, Appli
569	20	71.4	119	7	US-11-049-536-570	Sequence 570, Appl	642	20	71.4	150	7	US-11-096-568A-4894	Sequence 4894, Ap
570	20	71.4	119	7	US-11-143-077-9	Sequence 9, Appli	643	20	71.4	151	6	US-10-131-826A-22	Sequence 22, Appl
571	20	71.4	119	7	US-11-190-364-9	Sequence 9, Appli	644	20	71.4	151	6	US-10-973-115B-22	Sequence 22, Appl
572	20	71.4	119	7	US-11-102-120-6	Sequence 6, Appli	645	20	71.4	156	6	US-10-821-234-1424	Sequence 1424, Ap
573	20	71.4	119	7	US-11-147-780-9	Sequence 9, Appli	646	20	71.4	157	7	US-11-049-536-110	Sequence 110, App
574	20	71.4	119	7	US-11-223-361-6	Sequence 6, Appli	647	20	71.4	157	7	US-11-199-739-110	Sequence 110, App
575	20	71.4	119	7	US-11-143-386-9	Sequence 9, Appli	648	20	71.4	159	7	US-11-000-463-333	Sequence 333, App
576	20	71.4	119	7	US-11-199-739-394	Sequence 394, Appl	649	20	71.4	162	7	US-11-069-642-6	Sequence 6, Appli
577	20	71.4	119	7	US-11-199-739-538	Sequence 538, Appl	650	20	71.4	171	7	US-11-096-568A-12623	Sequence 12623, A
578	20	71.4	119	7	US-11-199-739-570	Sequence 570, Appl	651	20	71.4	177	7	US-11-096-568A-33259	Sequence 33259, A
579	20	71.4	119	7	US-11-187-364-9	Sequence 9, Appli	652	20	71.4	182	7	US-11-096-568A-4536	Sequence 4536, Ap
580	20	71.4	119	7	US-11-217-919-162	Sequence 162, Appl	653	20	71.4	192	6	US-10-506-454-348	Sequence 348, App
581	20	71.4	120	6	US-10-925-366A-235	Sequence 235, Appl	654	20	71.4	192	6	US-10-506-454-348	Sequence 348, App
582	20	71.4	120	6	US-10-834-397-38	Sequence 38, Appl	655	20	71.4	197	6	US-10-500-941-8	Sequence 8, Appli
583	20	71.4	120	6	US-10-834-397-63	Sequence 63, Appl	656	20	71.4	203	6	US-10-981-873-45	Sequence 45, Appl
584	20	71.4	120	7	US-11-112-240-2	Sequence 2, Appli	657	20	71.4	203	6	US-10-980-388-79	Sequence 79, Appl
585	20	71.4	120	7	US-11-112-240-2	Sequence 2, Appli	658	20	71.4	203	6	US-10-980-388-102	Sequence 102, App
586	20	71.4	120	7	US-11-005-726-4	Sequence 4, Appli	659	20	71.4	204	6	US-10-980-388-102	Sequence 102, App
587	20	71.4	120	7	US-11-096-568A-4895	Sequence 4895, Ap	660	20	71.4	207	6	US-10-793-626-3028	Sequence 3028, Ap
588	20	71.4	121	7	US-11-041-471-2	Sequence 2, Appli	661	20	71.4	208	7	US-11-096-568A-18675	Sequence 18675, A
589	20	71.4	121	7	US-11-037-199-19	Sequence 19, Appl	662	20	71.4	212	6	US-10-498-026-110	Sequence 110, App
590	20	71.4	122	6	US-10-515-241-11	Sequence 11, Appl	663	20	71.4	213	7	US-11-096-568A-3517	Sequence 3517, Ap
591	20	71.4	122	7	US-11-144-248-24	Sequence 24, Appl	664	20	71.4	214	7	US-11-096-568A-20570	Sequence 20570, A
592	20	71.4	122	7	US-11-144-222-24	Sequence 24, Appl	665	20	71.4	217	7	US-11-096-568A-5014	Sequence 5014, Ap
593	20	71.4	122	7	US-11-112-240-6	Sequence 6, Appli	666	20	71.4	220	6	US-10-793-626-3058	Sequence 3058, Ap
594	20	71.4	122	7	US-11-112-304A-6	Sequence 6, Appli	667	20	71.4	220	7	US-11-096-568A-13023	Sequence 13023, A
595	20	71.4	122	7	US-11-182-343-24	Sequence 24, Appl	668	20	71.4	223	6	US-10-746-909-3	Sequence 3, Appli
596	20	71.4	122	7	US-11-049-536-278	Sequence 278, Appl	669	20	71.4	229	7	US-11-096-568A-15903	Sequence 15903, A
597	20	71.4	122	7	US-11-087-099-489	Sequence 489, Appl	670	20	71.4	235	6	US-10-453-372-406	Sequence 406, App
598	20	71.4	122	7	US-11-096-568A-25359	Sequence 25359, A	671	20	71.4	235	6	US-10-453-372-406	Sequence 406, App
599	20	71.4	122	7	US-11-199-739-278	Sequence 278, Appl	672	20	71.4	238	6	US-10-873-528-23	Sequence 23, Appl
600	20	71.4	123	6	US-10-771-257-59	Sequence 59, Appl	673	20	71.4	238	7	US-11-054-515-2067	Sequence 2067, Ap
601	20	71.4	123	6	US-10-771-257-84	Sequence 84, Appl	674	20	71.4	238	7	US-11-120-308-96	Sequence 96, Appl
602	20	71.4	123	6	US-10-771-257-88	Sequence 88, Appl	675	20	71.4	238	7	US-11-266-444-2067	Sequence 2067, Ap
603	20	71.4	123	6	US-10-771-257-90	Sequence 90, Appl	676	20	71.4	239	6	US-10-453-372-400	Sequence 400, App
604	20	71.4	123	6	US-10-771-257-95	Sequence 95, Appl	677	20	71.4	239	6	US-10-453-372-402	Sequence 402, App
605	20	71.4	123	6	US-10-982-440-23	Sequence 23, Appl	678	20	71.4	239	6	US-10-453-372-404	Sequence 404, App
606	20	71.4	123	6	US-10-982-440-59	Sequence 59, Appl	679	20	71.4	239	7	US-11-054-515-1922	Sequence 1922, Ap
607	20	71.4	123	7	US-11-127-677-57	Sequence 57, Appl	680	20	71.4	239	7	US-11-054-515-2018	Sequence 2018, Ap
608	20	71.4	123	7	US-11-112-240-30	Sequence 30, Appl	681	20	71.4	239	7	US-11-054-515-2035	Sequence 2035, Ap
609	20	71.4	123	7	US-11-127-903-40	Sequence 40, Appl	682	20	71.4	239	7	US-11-266-444-1922	Sequence 1922, Ap

683	20	71.4	239	7	US-11-266-444-2018	Sequence 2018, Ap	756	20	71.4	245	7	US-11-266-444-1757	Sequence 1757, Ap
684	20	71.4	239	7	US-11-266-444-2035	Sequence 2035, Ap	757	20	71.4	245	7	US-11-266-444-1794	Sequence 1794, Ap
685	20	71.4	240	6	US-10-925-366A-219	Sequence 219, App	758	20	71.4	245	7	US-11-266-444-1815	Sequence 1815, Ap
686	20	71.4	240	7	US-11-054-515-1886	Sequence 1886, Ap	759	20	71.4	245	7	US-11-266-444-1826	Sequence 1826, Ap
687	20	71.4	240	7	US-11-054-515-1918	Sequence 1918, Ap	760	20	71.4	246	7	US-11-054-515-928	Sequence 928, App
688	20	71.4	240	7	US-11-054-515-1930	Sequence 1930, Ap	761	20	71.4	246	7	US-11-054-515-1308	Sequence 1308, Ap
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691	20	71.4	240	7	US-11-054-515-2052	Sequence 2052, Ap	764	20	71.4	246	7	US-11-054-515-1426	Sequence 1426, Ap
692	20	71.4	240	7	US-11-054-515-2059	Sequence 2059, Ap	765	20	71.4	246	7	US-11-054-515-1781	Sequence 1781, Ap
693	20	71.4	240	7	US-11-054-515-2061	Sequence 2061, Ap	766	20	71.4	246	7	US-11-054-515-1818	Sequence 1818, Ap
694	20	71.4	240	7	US-11-098-686-10610	Sequence 10610, A	767	20	71.4	246	7	US-11-054-515-1975	Sequence 1975, Ap
695	20	71.4	240	7	US-11-266-444-1886	Sequence 1886, Ap	768	20	71.4	246	7	US-11-054-515-1980	Sequence 1980, Ap
696	20	71.4	240	7	US-11-266-444-1918	Sequence 1918, Ap	769	20	71.4	246	7	US-11-266-444-928	Sequence 928, App
697	20	71.4	240	7	US-11-266-444-1930	Sequence 1930, Ap	770	20	71.4	246	7	US-11-266-444-1308	Sequence 1308, App
698	20	71.4	240	7	US-11-266-444-2013	Sequence 2013, Ap	771	20	71.4	246	7	US-11-266-444-1314	Sequence 1314, Ap
699	20	71.4	240	7	US-11-266-444-2047	Sequence 2047, Ap	772	20	71.4	246	7	US-11-266-444-1324	Sequence 1324, Ap
700	20	71.4	240	7	US-11-266-444-2052	Sequence 2052, Ap	773	20	71.4	246	7	US-11-266-444-1426	Sequence 1426, Ap
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704	20	71.4	242	7	US-11-054-515-1761	Sequence 1761, Ap	777	20	71.4	246	7	US-11-266-444-1980	Sequence 1980, Ap
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706	20	71.4	242	7	US-11-054-515-1438	Sequence 1438, Ap	779	20	71.4	247	7	US-11-054-515-1400	Sequence 1400, Ap
707	20	71.4	242	7	US-11-054-515-1444	Sequence 1444, Ap	780	20	71.4	247	7	US-11-054-515-1652	Sequence 1652, Ap
708	20	71.4	242	7	US-11-054-515-1742	Sequence 1742, Ap	781	20	71.4	247	7	US-11-054-515-1766	Sequence 1766, Ap
709	20	71.4	242	7	US-11-054-515-1761	Sequence 1761, Ap	782	20	71.4	247	7	US-11-054-515-1923	Sequence 1923, Ap
710	20	71.4	242	7	US-11-054-515-1762	Sequence 1762, Ap	783	20	71.4	247	7	US-11-266-444-1193	Sequence 1193, Ap
711	20	71.4	242	7	US-11-266-444-1424	Sequence 1424, Ap	784	20	71.4	247	7	US-11-266-444-1400	Sequence 1400, Ap
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713	20	71.4	242	7	US-11-266-444-1438	Sequence 1438, Ap	786	20	71.4	247	7	US-11-266-444-1766	Sequence 1766, Ap
714	20	71.4	242	7	US-11-266-444-1444	Sequence 1444, Ap	787	20	71.4	247	7	US-11-266-444-1923	Sequence 1923, Ap
715	20	71.4	242	7	US-11-266-444-1678	Sequence 1678, Ap	788	20	71.4	248	7	US-11-080-628-23	Sequence 23, Appl
716	20	71.4	242	7	US-11-266-444-1742	Sequence 1742, Ap	789	20	71.4	248	7	US-11-054-515-921	Sequence 921, App
717	20	71.4	242	7	US-11-266-444-1761	Sequence 1761, Ap	790	20	71.4	248	7	US-11-054-515-959	Sequence 959, App
718	20	71.4	242	7	US-11-266-444-1762	Sequence 1762, Ap	791	20	71.4	248	7	US-11-054-515-1134	Sequence 1134, Ap
719	20	71.4	243	7	US-11-054-515-1929	Sequence 1929, Ap	792	20	71.4	248	7	US-11-054-515-1404	Sequence 1404, Ap
720	20	71.4	243	7	US-11-054-515-1942	Sequence 1942, Ap	793	20	71.4	248	7	US-11-054-515-1456	Sequence 1456, Ap
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722	20	71.4	243	7	US-11-054-515-1944	Sequence 1944, Ap	795	20	71.4	248	7	US-11-054-515-1653	Sequence 1653, Ap
723	20	71.4	243	7	US-11-054-515-2056	Sequence 2056, Ap	796	20	71.4	248	7	US-11-054-515-1782	Sequence 1782, Ap
724	20	71.4	243	7	US-11-087-099-3907	Sequence 3907, Ap	797	20	71.4	248	7	US-11-266-444-921	Sequence 921, App
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## ALIGNMENTS

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; Sequence 3, Application US/10473037
; Publication No. US20050260206A1
; GENERAL INFORMATION:
; APPLICANT: KYOWA HAKKO KOGYO CO., LTD.
; TITLE OF INVENTION: Agents for treatment of cancer using recombinant anti-GD3 antibody
; TITLE OF INVENTION: the antibody fragments
; FILE REFERENCE: 11374WO1
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: US/10/473,037
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 3
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-473-037-3
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Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; Publication No. US20050260206A1
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; TITLE OF INVENTION: Agents for treatment of cancer using recombinant anti-GD3 antibody
; TITLE OF INVENTION: the antibody fragments
; FILE REFERENCE: 11374WO1
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: US/10/473,037
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: JP2001-097483
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; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 9
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Artificial Sequence
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; OTHER INFORMATION: Description of Artificial Sequence:synthetic protein
US-10-473-037-9
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; TITLE OF INVENTION: Agents for treatment of cancer using recombinant anti-GD3 antibody
; TITLE OF INVENTION: the antibody fragments
; FILE REFERENCE: 11374WO1
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: US/10/473,037
; PRIOR FILING DATE: 2001-03-29
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; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUWANA, YOSHIHISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/11/228,293
; CURRENT FILING DATE: 2005-09-19
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; PRIOR FILING DATE: 1999-01-05
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; PRIOR FILING DATE: 1995-05-31
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; PRIOR FILING DATE: 1992-09-17
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; PRIOR FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: cDNA KM-641
US-11-228-293-8
Query Match          100.0%; Score 28; DB 7; Length 130;
Best Local Similarity 100.0%; Pred. No. 8.3;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 HYAMS 5
      |||||
Db      41 HYAMS 45

RESULT 5
US-11-228-293-18
; Sequence 18, Application US/11228293
; Publication No. US20060057139A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUMANA, YOSHIHISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/11/228,293
; PRIOR FILING DATE: 2005-09-19
; PRIOR APPLICATION NUMBER: US/09/225,322
; PRIOR FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: US 08/454,680
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
; PRIOR APPLICATION NUMBER: US07/947,674
; PRIOR FILING DATE: 1992-09-17
; PRIOR APPLICATION NUMBER: JP 3-238375
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: cDNA KM-641
US-11-228-293-18
Query Match          100.0%; Score 28; DB 7; Length 130;
Best Local Similarity 100.0%; Pred. No. 8.3;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 HYAMS 5
      |||||
Db      41 HYAMS 45

RESULT 6
US-11-228-319-8
; Sequence 8, Application US/11228319
; Publication No. US2006005812A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA

```

```

; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUMANA, YOSHIHISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/11/228,319
; CURRENT FILING DATE: 2005-09-19
; PRIOR APPLICATION NUMBER: US/09/225,322
; PRIOR FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: US 08/454,680
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
; PRIOR APPLICATION NUMBER: US07/947,674
; PRIOR FILING DATE: 1992-09-17
; PRIOR APPLICATION NUMBER: JP 3-238375
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: cDNA KM-641
US-11-228-319-8
Query Match          100.0%; Score 28; DB 7; Length 130;
Best Local Similarity 100.0%; Pred. No. 8.3;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 HYAMS 5
      |||||
Db      41 HYAMS 45

RESULT 7
US-11-228-319-18
; Sequence 18, Application US/11228319
; Publication No. US20060058512A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUMANA, YOSHIHISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/11/228,319
; CURRENT FILING DATE: 2005-09-19
; PRIOR APPLICATION NUMBER: US/09/225,322
; PRIOR FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: US 08/454,680
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
; PRIOR APPLICATION NUMBER: US07/947,674
; PRIOR FILING DATE: 1992-09-17
; PRIOR APPLICATION NUMBER: JP 3-238375
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: cDNA KM-641

```

## US-11-228-319-18

Query Match 100.0%; Score 28; DB 7; Length 130;  
Best Local Similarity 100.0%; Pred. No. 8.3;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5  
|||||  
Db 41 HYAMS 45

## RESULT 8

US-10-473-037-1  
; Sequence 1, Application US/10473037  
; Publication No. US20050260206A1  
; GENERAL INFORMATION:  
; APPLICANT: KYOWA HAKKO KOGYO CO., LTD.  
; TITLE OF INVENTION: Agents for treatment of cancer using recombinant anti-GD3 antibody  
; FILE REFERENCE: 11374W01  
; CURRENT APPLICATION NUMBER: US/10/473,037  
; CURRENT FILING DATE: 2003-09-26  
; PRIOR APPLICATION NUMBER: JP2001-097483  
; PRIOR FILING DATE: 2001-03-29  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 138  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-473-037-1

Query Match 100.0%; Score 28; DB 6; Length 138;  
Best Local Similarity 100.0%; Pred. No. 8.8;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5  
|||||  
Db 50 HYAMS 54

## RESULT 9

US-10-793-626-908  
; Sequence 908, Application US/10793626  
; Publication No. US20050255478A1  
; GENERAL INFORMATION:  
; APPLICANT: KIMMERLY, WILLIAM JOHN  
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS  
; FILE REFERENCE: PU3480US  
; CURRENT APPLICATION NUMBER: US/10/793,626  
; CURRENT FILING DATE: 2004-03-04  
; PRIOR APPLICATION NUMBER: 60/164,258  
; PRIOR FILING DATE: 1999-11-09  
; NUMBER OF SEQ ID NOS: 4472  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 908  
; LENGTH: 116  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: amino acid sequence  
US-10-793-626-908

Query Match 89.3%; Score 25; DB 6; Length 116;  
Best Local Similarity 80.0%; Pred. No. 38;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5  
|||||  
Db 34 HYAMT 38

## RESULT 10

US-11-087-099-8547  
; Sequence 8547, Application US/11087099  
; Publication No. US20060041961A1  
; GENERAL INFORMATION:  
; APPLICANT: Abad, Mark S. et al.  
; TITLE OF INVENTION: Genes and Uses for Plant Improvement  
; FILE REFERENCE: 38-21(53450)B EP  
; CURRENT APPLICATION NUMBER: US/11/087,099  
; CURRENT FILING DATE: 2005-03-22  
; NUMBER OF SEQ ID NOS: 12464  
; SEQ ID NO 8547  
; LENGTH: 203  
; TYPE: PRT  
; ORGANISM: Escherichia coli CFT073  
US-11-087-099-8547

Query Match 89.3%; Score 25; DB 7; Length 203;  
Best Local Similarity 80.0%; Pred. No. 67;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5  
|||||  
Db 116 HYAMN 120

## RESULT 11

US-11-096-568A-20951  
; Sequence 20951, Application US/11096568A  
; Publication No. US20060048240A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexandrov, Nickolai et al.  
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides  
; FILE REFERENCE: 2750-1592PUS2  
; CURRENT APPLICATION NUMBER: US/11/096,568A  
; CURRENT FILING DATE: 2005-04-01  
; NUMBER OF SEQ ID NOS: 34471  
; SEQ ID NO 20951  
; LENGTH: 218  
; TYPE: PRT  
; ORGANISM: Zea mays subsp. mays  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)-(218)  
; OTHER INFORMATION: Ceres Seq. ID no. 12391405  
US-11-096-568A-20951

Query Match 89.3%; Score 25; DB 7; Length 218;  
Best Local Similarity 80.0%; Pred. No. 71;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5  
|||||  
Db 118 HYALS 122

## RESULT 12

US-11-096-568A-20950  
; Sequence 20950, Application US/11096568A  
; Publication No. US20060048240A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexandrov, Nickolai et al.  
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides  
; FILE REFERENCE: 2750-1592PUS2  
; CURRENT APPLICATION NUMBER: US/11/096,568A  
; CURRENT FILING DATE: 2005-04-01  
; NUMBER OF SEQ ID NOS: 34471  
; SEQ ID NO 20950  
; LENGTH: 236  
; TYPE: PRT  
; ORGANISM: Zea mays subsp. mays

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; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(236)
; OTHER INFORMATION: Ceres Seq. ID no. 12391404
US-11-096-568A-20950

Query Match      89.3%; Score 25; DB 7; Length 236;
Best Local Similarity 80.0%; Pred. No. 77;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 HYAMS 5
Db      136 HYALS 140

RESULT 13
US-10-506-454-1384
; Sequence 1384, Application US/10506454
; Publication No. US2006068386A1
; GENERAL INFORMATION:
; APPLICANT: Slesarev, Alexi I
; APPLICANT: Mezheva, Katja V
; APPLICANT: Polushin, Nikolai N
; APPLICANT: Shcherbinina, Olga V
; APPLICANT: Shakhova, Vera V
; APPLICANT: Malykh, Andrei G
; APPLICANT: Kozyavkin, Sergei A
; TITLE OF INVENTION: The Complete Genome and Protein Sequences of the Hyperthermophile
; TITLE OF INVENTION: Methanopyrus kandleri AV19 and Monophyly of Archaeal Methanogens
; TITLE OF INVENTION: and Methods of Use Thereof
; FILE REFERENCE: FID001
; CURRENT APPLICATION NUMBER: US/10/506,454
; PRIOR FILING DATE: 2004-08-31
; PRIOR APPLICATION NUMBER: PCT/US03/06664
; PRIOR FILING DATE: 2003-03-04
; PRIOR APPLICATION NUMBER: 60/361,742
; PRIOR FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 1722
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 1384
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Methanopyrus kandleri
US-10-506-454-1384

Query Match      89.3%; Score 25; DB 6; Length 247;
Best Local Similarity 80.0%; Pred. No. 81;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 HYAMS 5
Db      243 HYALS 247

RESULT 14
US-10-793-626-1072
; Sequence 1072, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 1072
; LENGTH: 308
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
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; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-1072

Query Match      89.3%; Score 25; DB 6; Length 308;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 HYAMS 5
Db      209 HYALS 213

RESULT 15
US-10-793-626-2706
; Sequence 2706, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 2706
; LENGTH: 308
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-2706

Query Match      89.3%; Score 25; DB 6; Length 308;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 HYAMS 5
Db      209 HYALS 213

RESULT 16
US-11-087-099-2909
; Sequence 2909, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 2909
; LENGTH: 317
; TYPE: PRT
; ORGANISM: Oryza sativa (japonica cultivar-group)
US-11-087-099-2909

Query Match      89.3%; Score 25; DB 7; Length 317;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 HYAMS 5
Db      82 HYAMN 86

RESULT 17
US-11-087-099-7062
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; Sequence 7062, Application US/11087099  
; Publication No. US20060041961A1  
; GENERAL INFORMATION:  
; APPLICANT: Abad, Mark S. et al.  
; TITLE OF INVENTION: Genes and Uses for Plant Improvement  
; FILE REFERENCE: 38-21(53450)B EP  
; CURRENT APPLICATION NUMBER: US/11/087,099  
; CURRENT FILING DATE: 2005-03-22  
; NUMBER OF SEQ ID NOS: 12464  
; SEQ ID NO 7062  
; LENGTH: 317  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
US-11-087-099-7062

Query Match 89.3%; Score 25; DB 7; Length 317;  
Best Local Similarity 80.0%; Pred. No. 1.e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5  
|||:  
Db 82 HYAMN 86

## RESULT 18

US-11-087-099-2997  
; Sequence 2997, Application US/11087099  
; Publication No. US20060041961A1  
; GENERAL INFORMATION:  
; APPLICANT: Abad, Mark S. et al.  
; TITLE OF INVENTION: Genes and Uses for Plant Improvement  
; FILE REFERENCE: 38-21(53450)B EP  
; CURRENT APPLICATION NUMBER: US/11/087,099  
; CURRENT FILING DATE: 2005-03-22  
; NUMBER OF SEQ ID NOS: 12464  
; SEQ ID NO 2997  
; LENGTH: 350  
; TYPE: PRT  
; ORGANISM: Oryza sativa (indica cultivar-group)  
US-11-087-099-2997

Query Match 89.3%; Score 25; DB 7; Length 350;  
Best Local Similarity 80.0%; Pred. No. 1.2e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5  
|||:  
Db 290 HYALS 294

## RESULT 19

US-11-087-099-303  
; Sequence 303, Application US/11087099  
; Publication No. US20060041961A1  
; GENERAL INFORMATION:  
; APPLICANT: Abad, Mark S. et al.  
; TITLE OF INVENTION: Genes and Uses for Plant Improvement  
; FILE REFERENCE: 38-21(53450)B EP  
; CURRENT APPLICATION NUMBER: US/11/087,099  
; CURRENT FILING DATE: 2005-03-22  
; NUMBER OF SEQ ID NOS: 12464  
; SEQ ID NO 303  
; LENGTH: 488  
; TYPE: PRT  
; ORGANISM: Arabidopsis thaliana  
US-11-087-099-303

Query Match 89.3%; Score 25; DB 7; Length 488;  
Best Local Similarity 80.0%; Pred. No. 1.6e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5  
|||:

Db 16 HYALS 20

## RESULT 20

US-11-087-099-4045  
; Sequence 4045, Application US/11087099  
; Publication No. US20060041961A1  
; GENERAL INFORMATION:  
; APPLICANT: Abad, Mark S. et al.  
; TITLE OF INVENTION: Genes and Uses for Plant Improvement  
; FILE REFERENCE: 38-21(53450)B EP  
; CURRENT APPLICATION NUMBER: US/11/087,099  
; CURRENT FILING DATE: 2005-03-22  
; NUMBER OF SEQ ID NOS: 12464  
; SEQ ID NO 4045  
; LENGTH: 735  
; TYPE: PRT  
; ORGANISM: Gluconacetobacter xylinus  
US-11-087-099-4045

Query Match 89.3%; Score 25; DB 7; Length 735;  
Best Local Similarity 80.0%; Pred. No. 2.4e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5  
|||:  
Db 199 HYAMN 203

## RESULT 21

US-11-010-239-42  
; Sequence 42, Application US/11010239  
; Publication No. US20060015970A1  
; GENERAL INFORMATION:  
; APPLICANT: Roger PENNELL  
; APPLICANT: Jack OKAMURO  
; APPLICANT: Richard SCHNEEBERGER  
; APPLICANT: Yiwen FANG  
; APPLICANT: Shing KWOK  
; APPLICANT: Diane JOFUKU  
; APPLICANT: Edward A. KIEGLE  
; APPLICANT: Jonathan DONSON  
; APPLICANT: Nestor APUYA  
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AND POLYPEPTIDES ENCODED THEREBY USEFUL FOR  
; TITLE OF INVENTION: MODIFYING PLANT CHARACTERISTICS  
; FILE REFERENCE: 2750-1585PUS2  
; CURRENT APPLICATION NUMBER: US/11/010,239  
; CURRENT FILING DATE: 2004-12-09  
; PRIOR APPLICATION NUMBER: US 60/529,352  
; PRIOR FILING DATE: 2003-12-12  
; NUMBER OF SEQ ID NOS: 133  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 42  
; LENGTH: 946  
; TYPE: PRT  
; ORGANISM: Arabidopsis thaliana  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)..(946)  
; OTHER INFORMATION: 12661844\_protein\_ID\_12661845  
US-11-010-239-42

Query Match 89.3%; Score 25; DB 7; Length 946;  
Best Local Similarity 80.0%; Pred. No. 3.1e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5  
|||:  
Db 848 HYALS 852

RESULT 22  
US-11-171-567-191

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; Sequence 191, Application US/11171567
; Publication No. US20060057651A1
; GENERAL INFORMATION:
; APPLICANT: Bowdish, Katherine S.
; APPLICANT: McWhirter, John
; TITLE OF INVENTION: POLYPEPTIDES AND ANTIBODIES DERIVED FROM CHRONIC LYMPHOCYTIC LEUK
; FILE OF INVENTION: CELLS AND USES THEREOF
; FILE REFERENCE: ALEX-P06-060
; CURRENT APPLICATION NUMBER: US/11/171,567
; CURRENT FILING DATE: 2005-06-30
; PRIOR APPLICATION NUMBER: US 10/996,316
; PRIOR FILING DATE: 2004-11-23
; PRIOR APPLICATION NUMBER: US 10/894,672
; PRIOR FILING DATE: 2004-07-20
; PRIOR APPLICATION NUMBER: US 10/736,188
; PRIOR FILING DATE: 2003-12-15
; PRIOR APPLICATION NUMBER: US 10/379,151
; PRIOR FILING DATE: 2003-03-04
; PRIOR APPLICATION NUMBER: PCT/US01/47931
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/254,113
; PRIOR FILING DATE: 2000-12-08
; NUMBER OF SEQ ID NOS: 213
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 191
; LENGTH: 12
; TYPE: PRT
; ORGANISM: murine
; US-11-171-567-191

Query Match      85.7%; Score 24; DB 7; Length 12;
Best Local Similarity 100.0%; Pred. No. 6.6;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 HYAM 4
      ||||
DB      7 HYAM 10

RESULT 23
US-11-072-512-3071
; Sequence 3071, Application US/11072512
; Publication No. US20060029945A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHIKO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOKYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: 084335-0191
; CURRENT APPLICATION NUMBER: US/11/072,512
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/350,978
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: JP 2001-379298
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3071

Query Match      85.7%; Score 24; DB 7; Length 12;
Best Local Similarity 100.0%; Pred. No. 6.6;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 HYAM 4
      ||||
DB      7 HYAM 10

US-11-072-512-3071
; Sequence 3071, Application US/11072512
; Publication No. US20060029945A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHIKO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOKYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: 084335-0191
; CURRENT APPLICATION NUMBER: US/11/072,512
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/350,978
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: JP 2001-379298
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3071

; Sequence 191, Application US/11171567
; Publication No. US20060057651A1
; GENERAL INFORMATION:
; APPLICANT: Bowdish, Katherine S.
; APPLICANT: McWhirter, John
; TITLE OF INVENTION: POLYPEPTIDES AND ANTIBODIES DERIVED FROM CHRONIC LYMPHOCYTIC LEUK
; FILE OF INVENTION: CELLS AND USES THEREOF
; FILE REFERENCE: ALEX-P06-060
; CURRENT APPLICATION NUMBER: US/11/171,567
; CURRENT FILING DATE: 2005-06-30
; PRIOR APPLICATION NUMBER: US 10/996,316
; PRIOR FILING DATE: 2004-11-23
; PRIOR APPLICATION NUMBER: US 10/894,672
; PRIOR FILING DATE: 2004-07-20
; PRIOR APPLICATION NUMBER: US 10/736,188
; PRIOR FILING DATE: 2003-12-15
; PRIOR APPLICATION NUMBER: US 10/379,151
; PRIOR FILING DATE: 2003-03-04
; PRIOR APPLICATION NUMBER: PCT/US01/47931
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/254,113
; PRIOR FILING DATE: 2000-12-08
; NUMBER OF SEQ ID NOS: 213
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 191
; LENGTH: 12
; TYPE: PRT
; ORGANISM: murine
; US-11-171-567-191

Query Match      85.7%; Score 24; DB 7; Length 12;
Best Local Similarity 100.0%; Pred. No. 6.6;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 HYAM 4
      ||||
DB      7 HYAM 10

US-11-072-512-3071
; Sequence 3071, Application US/11072512
; Publication No. US20060029945A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHIKO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOKYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: 084335-0191
; CURRENT APPLICATION NUMBER: US/11/072,512
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/350,978
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: JP 2001-379298
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3071
```

```
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-072-512-3071

Query Match      85.7%; Score 24; DB 7; Length 108;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 HYAM 4
      ||||
DB      54 HYAM 57

RESULT 24
US-11-049-536-678
; Sequence 678, Application US/11049536
; Publication No. US20060024297A1
; GENERAL INFORMATION:
; APPLICANT: Wood, Clive R.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Pieters, Henk
; APPLICANT: Hoet, Rene
; APPLICANT: Hufton, Simon E.
; TITLE OF INVENTION: TIE COMPLEX BINDING PROTEINS
; FILE REFERENCE: 10280-128001
; CURRENT APPLICATION NUMBER: US/11/049,536
; CURRENT FILING DATE: 2005-02-02
; PRIOR APPLICATION NUMBER: US 10/916,840
; PRIOR FILING DATE: 2004-08-12
; PRIOR APPLICATION NUMBER: US 60/494,713
; PRIOR FILING DATE: 2003-08-12
; NUMBER OF SEQ ID NOS: 721
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 678
; LENGTH: 118
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: Antibody
; US-11-049-536-678

Query Match      85.7%; Score 24; DB 7; Length 118;
Best Local Similarity 80.0%; Pred. No. 86;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 HYAMS 5
      ||||
DB      31 HYVMS 35

RESULT 25
US-11-199-739-678
; Sequence 678, Application US/11199739
; Publication No. US20060057138A1
; GENERAL INFORMATION:
; APPLICANT: Wood, Clive R.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Pieters, Henk
; APPLICANT: Hoet, Rene
; APPLICANT: Hufton, Simon E.
; TITLE OF INVENTION: TIE COMPLEX BINDING PROTEINS
; FILE REFERENCE: 10280-135001
; CURRENT APPLICATION NUMBER: US/11/199,739
; CURRENT FILING DATE: 2005-08-09
; PRIOR APPLICATION NUMBER: US 11/049,536
; PRIOR FILING DATE: 2005-02-02
; PRIOR APPLICATION NUMBER: US 10/916,840
; PRIOR FILING DATE: 2004-08-12
; PRIOR APPLICATION NUMBER: US 60/494,713
; PRIOR FILING DATE: 2003-08-12
; NUMBER OF SEQ ID NOS: 726
; SOFTWARE: FastSeq for Windows Version 4.0
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; SEQ ID NO 678  
; LENGTH: 118  
; TYPE: PRT  
; ORGANISM: ARTIFICIAL  
; FEATURE:  
; OTHER INFORMATION: Antibody  
US-11-199-739-678

Query Match 85.7%; Score 24; DB 7; Length 118;  
Best Local Similarity 80.0%; Pred. No. 66;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HYAMS 5  
|||  
Db 31 HYMS 35

RESULT 26  
US-11-072-512-3241  
; Sequence 3241, Application US/11072512  
; Publication No. US20060029945A1  
; GENERAL INFORMATION:  
; APPLICANT: ISOGAI, TAKAO  
; APPLICANT: SUGIYAMA, TOMOYASU  
; APPLICANT: OTSUKI, TETSUJI  
; APPLICANT: WAKAMATSU, AI  
; APPLICANT: SATO, HIROYUKI  
; APPLICANT: ISHII, SHIZUKO  
; APPLICANT: YAMAMOTO, JUN-ICHI  
; APPLICANT: ISONO, YUUKO  
; APPLICANT: HIO, YURI  
; APPLICANT: OTSUKA, KAORU  
; APPLICANT: NAGAI, KEIICHI  
; APPLICANT: IRIE, RYOTARO  
; APPLICANT: TAMECHIKA, ICHIRO  
; APPLICANT: SEKI, NAOHICO  
; APPLICANT: YOSHIKAWA, TSUTOMU  
; APPLICANT: OTSUKA, MOTOTYUKI  
; APPLICANT: NAGAHARI, KENJI  
; APPLICANT: MASUHO, YASUHIKO  
; TITLE OF INVENTION: Novel full length cDNA  
; FILE REFERENCE: 084335-0191  
; CURRENT APPLICATION NUMBER: US/11/072,512  
; CURRENT FILING DATE: 2005-03-07  
; PRIOR APPLICATION NUMBER: US 60/350,978  
; PRIOR FILING DATE: 2002-01-25  
; PRIOR APPLICATION NUMBER: JP 2001-379298  
; PRIOR FILING DATE: 2001-11-05  
; NUMBER OF SEQ ID NOS: 4096  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3241  
; LENGTH: 137  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-072-512-3241

Query Match 85.7%; Score 24; DB 7; Length 137;  
Best Local Similarity 100.0%; Pred. No. 77;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAM 4  
||||  
Db 83 HYAM 86

RESULT 27  
US-10-329-258-29  
; Sequence 29, Application US/10329258  
; Publication No. US2006004233A1  
; GENERAL INFORMATION:  
; APPLICANT: MUELLER, SABINE  
; APPLICANT: GONZALEZ-ZULUETA, MIRELLA  
; APPLICANT: FOEHR, ERIK

; APPLICANT: CHIN, DANIEL J.  
; TITLE OF INVENTION: USE OF BIOMOLECULAR TARGETS IN THE TREATMENT AND VISUALIZATION OF  
; FILE REFERENCE: AGY-008US2  
; CURRENT APPLICATION NUMBER: US/10/329,258  
; CURRENT FILING DATE: 2002-12-23  
; PRIOR APPLICATION NUMBER: 60/343,422  
; PRIOR FILING DATE: 2001-12-27  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 29  
; LENGTH: 317  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-329-258-29

Query Match 85.7%; Score 24; DB 6; Length 317;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAM 4  
||||  
Db 96 HYAM 99

RESULT 28  
US-11-074-176-368  
; Sequence 368, Application US/11074176  
; Publication No. US20050250135A1  
; GENERAL INFORMATION:  
; APPLICANT: Klaenhammer, Todd R.  
; APPLICANT: Russell, William M.  
; APPLICANT: Altermann, Eric  
; APPLICANT: McAuliffe, Olivia  
; APPLICANT: Peril, Andrea Azcarate  
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding  
; FILE REFERENCE: 5051-694  
; CURRENT APPLICATION NUMBER: US/11/074,176  
; CURRENT FILING DATE: 2005-03-07  
; PRIOR APPLICATION NUMBER: 60/551,161  
; PRIOR FILING DATE: 2004-03-08  
; NUMBER OF SEQ ID NOS: 381  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 368  
; LENGTH: 325  
; TYPE: PRT  
; ORGANISM: Lactobacillus acidophilus  
US-11-074-176-368

Query Match 85.7%; Score 24; DB 7; Length 325;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAM 4  
||||  
Db 48 HYAM 51

RESULT 29  
US-11-096-568A-3897  
; Sequence 3897, Application US/11096568A  
; Publication No. US20060048240A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexandrov, Nikolai et al.  
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides  
; FILE REFERENCE: 2750-1592PUS2  
; CURRENT APPLICATION NUMBER: US/11/096,568A  
; CURRENT FILING DATE: 2005-04-01  
; NUMBER OF SEQ ID NOS: 34471  
; SEQ ID NO 3897  
; LENGTH: 328  
; TYPE: PRT



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; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(328)
; OTHER INFORMATION: Ceres Seq. ID no. 13594131
US-11-096-568A-3897

Query Match      85.7%; Score 24; DB 7; Length 328;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 HYAM 4
Db      161 HYAM 164
|||||

RESULT 30
US-11-096-568A-3896
; Sequence 3896, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 3896
; LENGTH: 334
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(334)
; OTHER INFORMATION: Ceres Seq. ID no. 13594130
US-11-096-568A-3896

Query Match      85.7%; Score 24; DB 7; Length 334;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 HYAM 4
Db      167 HYAM 170
|||||

RESULT 31
US-11-172-740-45
; Sequence 45, Application US/11172740
; Publication No. US20060057724A1
; GENERAL INFORMATION:
; APPLICANT: MASCIA, Peter
; APPLICANT: ALEXANDROV, Nikolai
; APPLICANT: BROVER, Vyacheslav
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AND POLYPEPTIDES ENCODED THEREBY USEFUL FOR
; TITLE OF INVENTION: PLANT CHARACTERISTICS AND PHENOTYPES
; FILE REFERENCE: 2750-1602PUS2
; CURRENT APPLICATION NUMBER: US/11/172,740
; CURRENT FILING DATE: 2005-06-30
; PRIOR APPLICATION NUMBER: 60/583,621
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: 60/584,829
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: 60/584,800
; PRIOR FILING DATE: 2004-06-30
; NUMBER OF SEQ ID NOS: 2523
; SEQ ID NO 45
; LENGTH: 334
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: misc_feature
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; LOCATION: (1)..(334)
; OTHER INFORMATION: Ceres CLONE ID no. 554851
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: Utility: Useful for accelerating flowering time
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: Utility: Useful for increasing chlorophyll and photosynthetic ca
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: Utility: Useful for making ornamental plants with modified flowe
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: Utility: Useful for making smaller plants
US-11-172-740-45

Query Match      85.7%; Score 24; DB 7; Length 334;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 HYAM 4
Db      167 HYAM 170
|||||

RESULT 32
US-11-092-168-4
; Sequence 4, Application US/11092168
; Publication No. US20050277658A1
; GENERAL INFORMATION:
; APPLICANT: Arizona Board of Regents on behalf of The University of Arizona
; APPLICANT: Montigen Pharmaceuticals, Inc.
; APPLICANT: Hurley, Laurence H.
; APPLICANT: Mahadevan, Daruka
; APPLICANT: Han, Hailyong
; APPLICANT: Bearss, David J.
; APPLICANT: Vankayalapati, Hariprasad
; APPLICANT: Bashyam, Sridevi
; APPLICANT: Munoz, Ruben M.
; APPLICANT: Warner, Steven L.
; APPLICANT: Della Croce, Kimiko
; APPLICANT: Von Hoff, Daniel D.
; APPLICANT: Grand, Cory L.
; TITLE OF INVENTION: PROTEIN KINASE INHIBITORS
; FILE REFERENCE: 920214.00003CONT3
; CURRENT APPLICATION NUMBER: US/11/092,168
; CURRENT FILING DATE: 2005-03-29
; PRIOR APPLICATION NUMBER: US 10/965,313
; US 60/608,529
; US 60/511,486
; US 60/511,489
; PRIOR FILING DATE: 2004-10-14
; 2004-09-09
; 2003-10-14
; 2003-10-14
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-092-168-4

Query Match      85.7%; Score 24; DB 7; Length 341;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 HYAM 4
|||||
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Db 59 HYAM 62

RESULT 33  
US-10-497-767-4  
; Sequence 4, Application US/10497767  
; Publication No. US20050261836A1  
; GENERAL INFORMATION:  
; APPLICANT: VERTEX PHARMACEUTICALS INCORPORATED  
; APPLICANT: MENG, WUYI  
; APPLICANT: SWENSON, LOVORKA  
; TITLE OF INVENTION: CRYSTAL STRUCTURE OF MITOGEN-ACTIVATED PROTEIN  
; TITLE OF INVENTION: KINASE-ACTIVATED PROTEIN KINASE 2 AND BINDING POCKETS  
; TITLE OF INVENTION: THEREOF  
; FILE REFERENCE: VP1/01-13 PCT  
; CURRENT APPLICATION NUMBER: US/10/497,767  
; CURRENT FILING DATE: 2004-06-04  
; PRIOR APPLICATION NUMBER: 60/337,513  
; PRIOR FILING DATE: 2001-12-05  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 350  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; NAME/KEY: MOD RES  
; FEATURE:  
; LOCATION: (110)  
; OTHER INFORMATION: Variable amino acid  
; FEATURE:  
; NAME/KEY: MOD RES  
; LOCATION: (338)  
; OTHER INFORMATION: Variable amino acid  
US-10-497-767-4

Query Match 85.7%; Score 24; DB 6; Length 350;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAM 4  
|||

Db 68 HYAM 71

RESULT 34  
US-11-132-142-14  
; Sequence 14, Application US/11132142  
; Publication No. US20050276818A1  
; GENERAL INFORMATION:  
; APPLICANT: The Burnham Institute  
; APPLICANT: Sikora, Sergey  
; APPLICANT: Godzik, Adam  
; TITLE OF INVENTION: UNCHARACTERIZED ORF3 IN SARS-CORONAVIRUS IS A  
; TITLE OF INVENTION: CYCLIC-AMP-DEPENDENT KINASE AND A TARGET FOR SARS THERAPY  
; FILE REFERENCE: 8014-011-US  
; CURRENT APPLICATION NUMBER: US/11/132,142  
; CURRENT FILING DATE: 2005-05-17  
; PRIOR APPLICATION NUMBER: 60/571,698  
; PRIOR FILING DATE: 2004-05-17  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 14  
; LENGTH: 351  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-132-142-14

Query Match 85.7%; Score 24; DB 7; Length 351;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAM 4  
|||

Db 69 HYAM 72

RESULT 35  
US-11-055-822-972  
; Sequence 972, Application US/11055822  
; Publication No. US20050260707A1  
; GENERAL INFORMATION:  
; APPLICANT: Pompejus, Markus  
; APPLICANT: Kroger, Burkhard  
; APPLICANT: Schroder, Hartwig  
; APPLICANT: Zelder, Oskar  
; APPLICANT: Haberhauer, Gregor  
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING  
; TITLE OF INVENTION: METABOLIC PATHWAY PROTEINS  
; FILE REFERENCE: BGI-121PCPN  
; CURRENT APPLICATION NUMBER: US/11/055,822  
; CURRENT FILING DATE: 2005-02-11  
; PRIOR APPLICATION NUMBER: 09/606,740  
; PRIOR FILING DATE: 2000-06-23  
; PRIOR APPLICATION NUMBER: 60/141,031  
; PRIOR FILING DATE: 1999-06-25  
; PRIOR APPLICATION NUMBER: 60/142,101  
; PRIOR FILING DATE: 1999-07-02  
; PRIOR APPLICATION NUMBER: 60/148,613  
; PRIOR FILING DATE: 1999-08-12  
; PRIOR APPLICATION NUMBER: 60/187,970  
; PRIOR FILING DATE: 2000-03-09  
; PRIOR APPLICATION NUMBER: DE 19930476.9  
; PRIOR FILING DATE: 1999-07-01  
; PRIOR APPLICATION NUMBER: DE 19931415.2  
; PRIOR FILING DATE: 1999-07-08  
; PRIOR APPLICATION NUMBER: DE 19931418.7  
; PRIOR FILING DATE: 1999-07-08  
; PRIOR APPLICATION NUMBER: DE 19931419.5  
; PRIOR FILING DATE: 1999-07-08  
; PRIOR APPLICATION NUMBER: DE 19931420.9  
; PRIOR FILING DATE: 1999-07-08  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 1158  
; SEQ ID NO 972  
; LENGTH: 356  
; TYPE: PRT  
; ORGANISM: Corynebacterium glutamicum  
US-11-055-822-972

Query Match 85.7%; Score 24; DB 7; Length 356;  
Best Local Similarity 80.0%; Pred. No. 2e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAMS 5  
|:|

Db 210 HPAMS 214

RESULT 36  
US-11-055-822-1052  
; Sequence 1052, Application US/11055822  
; Publication No. US20050260707A1  
; GENERAL INFORMATION:  
; APPLICANT: Pompejus, Markus  
; APPLICANT: Kroger, Burkhard  
; APPLICANT: Schroder, Hartwig  
; APPLICANT: Zelder, Oskar  
; APPLICANT: Haberhauer, Gregor  
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING  
; TITLE OF INVENTION: METABOLIC PATHWAY PROTEINS  
; FILE REFERENCE: BGI-121PCPN  
; CURRENT APPLICATION NUMBER: US/11/055,822  
; CURRENT FILING DATE: 2005-02-11  
; PRIOR APPLICATION NUMBER: 09/606,740  
; PRIOR FILING DATE: 2000-06-23  
; PRIOR APPLICATION NUMBER: 60/141,031

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; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 60/142,101
; PRIOR FILING DATE: 1999-07-02
; PRIOR APPLICATION NUMBER: 60/148,613
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 60/187,970
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: DE 19930476.9
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931415.2
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931418.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931419.5
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931420.9
; PRIOR FILING DATE: 1999-07-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1158
; SEQ ID NO 1052
; LENGTH: 356
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-11-055-822-1052

Query Match      85.7%; Score 24; DB 7; Length 356;
Best Local Similarity 80.0%; Pred. No. 2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 HYAMS 5
      |||||
Db      210 HFAMS 214

RESULT 37
US-10-501-035-298
; Sequence 298, Application US/10501035
; Publication No. US20060046249A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: IDENTIFICATION OF POLYNUCLEOTIDES AND POLYPEPTIDE FOR PREDICTING
; TITLE OF INVENTION: ACTIVITY OF COMPOUNDS THAT INTERACT WITH PROTEIN TYROSINE KINASE
; TITLE OF INVENTION: AND/OR PROTEIN TYROSINE KINASE PATHWAYS
; FILE REFERENCE: D0185 PCT
; CURRENT APPLICATION NUMBER: US/10/501,035
; CURRENT FILING DATE: 2004-07-09
; PRIOR APPLICATION NUMBER: US 60/350,061
; PRIOR FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 795
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 298
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-501-035-298

Query Match      85.7%; Score 24; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 HYAM 4
      |||||
Db      78 HYAM 81

RESULT 38
US-11-096-568A-3895
; Sequence 3895, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: Therby
```

```
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 3895
; LENGTH: 388
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(388)
; OTHER INFORMATION: Ceres Seq. ID no. 13594129
US-11-096-568A-3895

Query Match      85.7%; Score 24; DB 7; Length 388;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 HYAM 4
      |||||
Db      221 HYAM 224

RESULT 39
US-11-087-099-11733
; Sequence 11733, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 11733
; LENGTH: 404
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(404)
; OTHER INFORMATION: unsure at all Xaa locations
US-11-087-099-11733

Query Match      85.7%; Score 24; DB 7; Length 404;
Best Local Similarity 80.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 HYAMS 5
      |||||
Db      199 HYAIS 203

RESULT 40
US-10-467-657-3034
; Sequence 3034, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: Seqwin99, version 1.04
; SEQ ID NO 3034
; LENGTH: 439
```

; TYPE: PRT  
; ORGANISM: Neisseria gonorrhoeae  
US-10-467-657-3034

Query Match 85.7%; Score 24; DB 6; Length 439;  
Best Local Similarity 80.0%; Pred. No. 2.5e+02;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HYAMS 5  
|| ||  
Db 207 HYMS 211

## RESULT 41

US-11-096-568A-31074  
; Sequence 31074, Application US/11096568A  
; Publication No. US20060048240A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexandrov, Nikolai et al.  
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides  
; FILE REFERENCE: 2750-1592PUS2  
; CURRENT APPLICATION NUMBER: US/11/096,568A  
; CURRENT FILING DATE: 2005-04-01  
; NUMBER OF SEQ ID NOS: 34471  
; SEQ ID NO 31074  
; LENGTH: 454  
; TYPE: PRT  
; ORGANISM: Arabidopsis thaliana  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)..(454)  
; OTHER INFORMATION: Ceres Seq. ID no. 4986641  
US-11-096-568A-31074

Query Match 85.7%; Score 24; DB 7; Length 454;  
Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAM 4  
||||  
Db 333 HYAM 336

## RESULT 42

US-11-096-568A-28682  
; Sequence 28682, Application US/11096568A  
; Publication No. US20060048240A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexandrov, Nikolai et al.  
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides  
; FILE REFERENCE: 2750-1592PUS2  
; CURRENT APPLICATION NUMBER: US/11/096,568A  
; CURRENT FILING DATE: 2005-04-01  
; NUMBER OF SEQ ID NOS: 34471  
; SEQ ID NO 28682  
; LENGTH: 473  
; TYPE: PRT  
; ORGANISM: Arabidopsis thaliana  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)..(473)  
; OTHER INFORMATION: Ceres Seq. ID no. 3034894  
US-11-096-568A-28682

Query Match 85.7%; Score 24; DB 7; Length 473;  
Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAM 4  
||||  
Db 352 HYAM 355

## RESULT 43

US-11-096-568A-31073  
; Sequence 31073, Application US/11096568A  
; Publication No. US20060048240A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexandrov, Nikolai et al.  
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides  
; FILE REFERENCE: 2750-1592PUS2  
; CURRENT APPLICATION NUMBER: US/11/096,568A  
; CURRENT FILING DATE: 2005-04-01  
; NUMBER OF SEQ ID NOS: 34471  
; SEQ ID NO 31073  
; LENGTH: 473  
; TYPE: PRT  
; ORGANISM: Arabidopsis thaliana  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)..(473)  
; OTHER INFORMATION: Ceres Seq. ID no. 4986640  
US-11-096-568A-31073

Query Match 85.7%; Score 24; DB 7; Length 473;  
Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYAM 4  
||||  
Db 352 HYAM 355

## RESULT 44

US-11-055-822-970  
; Sequence 970, Application US/11055822  
; Publication No. US20050260707A1  
; GENERAL INFORMATION:  
; APPLICANT: Pompeius, Markus  
; APPLICANT: Kroger, Burkhard  
; APPLICANT: Schroder, Hartwig  
; APPLICANT: Zelder, Oskar  
; APPLICANT: Haberhauer, Gregor  
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING  
; TITLE OF INVENTION: METABOLIC PATHWAY PROTEINS  
; FILE REFERENCE: BGI-121CPCN  
; CURRENT APPLICATION NUMBER: US/11/055,822  
; CURRENT FILING DATE: 2005-02-11  
; PRIOR APPLICATION NUMBER: 09/606,740  
; PRIOR FILING DATE: 2000-06-23  
; PRIOR APPLICATION NUMBER: 60/141,031  
; PRIOR FILING DATE: 1999-06-25  
; PRIOR APPLICATION NUMBER: 60/142,101  
; PRIOR FILING DATE: 1999-07-02  
; PRIOR APPLICATION NUMBER: 60/148,613  
; PRIOR FILING DATE: 1999-08-12  
; PRIOR APPLICATION NUMBER: 60/187,970  
; PRIOR FILING DATE: 2000-03-09  
; PRIOR APPLICATION NUMBER: DE 19930476.9  
; PRIOR FILING DATE: 1999-07-01  
; PRIOR APPLICATION NUMBER: DE 19931415.2  
; PRIOR FILING DATE: 1999-07-08  
; PRIOR APPLICATION NUMBER: DE 19931418.7  
; PRIOR FILING DATE: 1999-07-08  
; PRIOR APPLICATION NUMBER: DE 19931419.5  
; PRIOR FILING DATE: 1999-07-08  
; PRIOR APPLICATION NUMBER: DE 19931420.9  
; PRIOR FILING DATE: 1999-07-08  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 1158  
; SEQ ID NO 970  
; LENGTH: 477  
; TYPE: PRT

```
; ORGANISM: Corynebacterium glutamicum
US-11-055-822-970

Query Match      85.7%; Score 24; DB 7; Length 477;
Best Local Similarity 80.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 HVAMS 5
DB      210 HFAMS 214

RESULT 45
US-11-055-822-1050
; Sequence 1050, Application US/11055822
; Publication No. US20050260707A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
; FILE REFERENCE: BGI-121CPCN
; CURRENT APPLICATION NUMBER: US/11/055,822
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: 09/606,740
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/141,031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 60/142,101
; PRIOR FILING DATE: 1999-07-02
; PRIOR APPLICATION NUMBER: 60/148,613
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 60/187,970
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: DE 19930476.9
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931415.2
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931418.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931419.5
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931420.9
; PRIOR FILING DATE: 1999-07-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1158
; SEQ ID NO 1050
; LENGTH: 477
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-11-055-822-1050

Query Match      85.7%; Score 24; DB 7; Length 477;
Best Local Similarity 80.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 HVAMS 5
DB      210 HFAMS 214

RESULT 46
US-11-087-099-4915
; Sequence 4915, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
```

```
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 4915
; LENGTH: 483
; TYPE: PRT
; ORGANISM: Rickettsia prowazekii
US-11-087-099-4915

Query Match      85.7%; Score 24; DB 7; Length 483;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 HYAM 4
DB      256 HYAM 259

RESULT 47
US-11-087-099-5880
; Sequence 5880, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 5880
; LENGTH: 483
; TYPE: PRT
; ORGANISM: Rickettsia sibirica
US-11-087-099-5880

Query Match      85.7%; Score 24; DB 7; Length 483;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 HYAM 4
DB      256 HYAM 259

RESULT 48
US-11-096-568A-31316
; Sequence 31316, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 31316
; LENGTH: 512
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(512)
; OTHER INFORMATION: Ceres Seq. ID no. 15222682
US-11-096-568A-31316

Query Match      85.7%; Score 24; DB 7; Length 512;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 HYAM 4
DB      179 HYAM 182
```

Db 187 HYAM 190

Search completed: April 6, 2006, 09:22:51  
Job time : 12.0847 secs

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RESULT 49
US-10-979-095-2
; Sequence 2, Application US/10979095
; Publication No. US20060068481A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: YANG, Junming
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: BURFORD, Neil
; APPLICANT: AU-YOUNG, Janice
; APPLICANT: LU, Dyung Aina M.
; APPLICANT: REDDY, Roopa
; APPLICANT: YUE, Henry
; APPLICANT: YAO, Monique G.
; APPLICANT: LAL, Preeti
; APPLICANT: KAHN, Farrah A.
; TITLE OF INVENTION: HUMAN KINASES
; FILE REFERENCE: PI-0002 PCT
; CURRENT APPLICATION NUMBER: US/10/979,095
; CURRENT FILING DATE: 2004-11-02
; PRIOR APPLICATION NUMBER: US/10/168,582
; PRIOR FILING DATE: 2002-06-20
; PRIOR APPLICATION NUMBER: 60/176,066; 60/176,107; 60/176,107; 60/177,731
; PRIOR FILING DATE: 1999-12-23; 2000-01-14; 2000-01-14; 2000-01-21
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PERL Program
; SEQ ID NO 2
; LENGTH: 513
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 2041716CD1
US-10-979-095-2

Query Match      85.7%; Score 24; DB 6; Length 513;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 HYAM 4
      ||||
Db      162 HYAM 165

RESULT 50
US-11-096-568A-31315
; Sequence 31315, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 31315
; LENGTH: 520
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(520)
; OTHER INFORMATION: Ceres Seq. ID no. 15222681
US-11-096-568A-31315

Query Match      85.7%; Score 24; DB 7; Length 520;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 HYAM 4
      ||||
```

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: April 6, 2006, 08:54:46 ; Search time 126.203 Seconds  
(without alignments)  
59.186 Million cell updates/sec

Title: US-10-089-500-4

Perfect score: 89

Sequence: 1 YISSGGSTYYSDSVK 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

A\_Geneseq\_21.\*  
1: Genesep1980s.\*  
2: Genesep1990s.\*  
3: Genesep2000s.\*  
4: Genesep2001s.\*  
5: Genesep2002s.\*  
6: Genesep2003as.\*  
7: Genesep2003bs.\*  
8: Genesep2004s.\*  
9: Genesep2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query %	Match	Length	DB	ID	Description
1	89	100.0	17	4	AAB81980		Aab81980 Gangliosid
2	89	100.0	17	4	ABU11005		Abu11005 Modified
3	89	100.0	17	9	AD257811		Ad257811 Gangliosid
4	89	100.0	119	4	AAB81985		Aab81985 Gangliosid
5	89	100.0	119	4	AAB81989		Aab81989 Gangliosid
6	89	100.0	119	6	ABU11012		Abu11012 Modified
7	89	100.0	119	6	ABU11010		Abu11010 Modified
8	89	100.0	119	9	AD257816		Ad257816 Gangliosid
9	89	100.0	119	9	AD257818		Ad257818 Gangliosid
10	89	100.0	119	9	AD257821		Ad257821 Gangliosid
11	89	100.0	130	2	AAR33256		Aar33256 Rat immun
12	89	100.0	130	2	AAR53341		Aar53341 RM641 L c
13	89	100.0	130	2	AA0128369		AAy28369 pRM641 HA
14	89	100.0	130	3	AAB01627		Aab01627 Murine im
15	89	100.0	138	4	AAB81977		Aab81977 Gangliosid
16	89	100.0	138	6	ABU11002		Abu11002 Modified
17	89	100.0	582	4	AAB81987		Aab81987 Gangliosid
18	89	100.0	582	4	AAB81991		Aab81991 Gangliosid
19	77	86.5	119	2	AAW11919		AAw11919 Humanised
20	77	86.5	247	2	AAW11917		AAw11917 Murine MA
21	75	84.3	118	2	AAR41233		Aar41233 Monoclonal
22	74	83.1	17	7	ADJ95630		Adj95630 Rat insul
23	74	83.1	17	9	ADZ08153		Adz08153 Rat IGF-s
24	74	83.1	118	7	ADJ95639		Adj95639 Insulin-1

25	74	83.1	118	9	ADZ08201		Adz08201 IGF-epect
26	74	83.1	118	9	ADZ08173		Adz08173 IGF-epect
27	74	83.1	118	9	ADZ08158		Adz08158 IGF-epect
28	74	83.1	137	7	ADJ95626		Adj95626 Rat insul
29	74	83.1	137	9	ADZ08159		Adz08159 IGF-epect
30	74	83.1	137	9	ADZ08220		Adz08220 IGF-epect
31	74	83.1	137	9	ADZ08149		Adz08149 Rat IGF-s
32	74	83.1	137	9	ADZ08221		Adz08221 IGF-epect
33	74	83.1	240	8	ADZ08261		Adz08261 Human c-M
34	74	83.1	468	9	ADW44417		Adw44417 Dog immun
35	73	82.0	117	8	ADG25805		Adg25805 Anti-CD30
36	73	82.0	120	7	ADZ4437		Adz4437 TMEFP2#10
37	72	80.9	17	9	ADZ45351		Adz45351 Murine fa
38	72	80.9	17	9	ADZ51264		Adz51264 Amino aci
39	72	80.9	17	9	ADZ42138		Adz42138 Mouse ant
40	72	80.9	121	9	ADZ45349		Adz45349 Murine fa
41	72	80.9	121	9	ADZ51262		Adz51262 Amino aci
42	72	80.9	121	9	ADZ42136		Adz42136 Mouse ant
43	72	80.9	237	5	ABP46028		Abp46028 Human Bly
44	72	80.9	237	5	ABP45895		Abp45895 Human Bly
45	72	80.9	237	7	ADG96722		Adg96722 Single ch
46	72	80.9	237	7	ADG96855		Adg96855 Single ch
47	72	80.9	240	5	ABP45894		Abp45894 Human Bly
48	72	80.9	240	7	ADG96721		Adg96721 Single ch
49	72	80.9	246	7	ADG30412		Adg30412 Human GMB
50	71	79.8	136	2	AAR06251		Aar06251 Variable
51	71	79.8	247	1	AAFP80156		Aap80156 Biosynthe
52	71	79.8	249	4	AAAB20436		Aab20436 Anti-FIX/
53	71	79.8	249	4	AAAB20435		Aab20435 Anti-FIX/
54	71	79.8	294	4	AAAB20442		Aab20442 Anti-FIX/
55	71	79.8	325	4	AAAB20438		Aab20438 Anti-FIX/
56	71	79.8	732	4	AAAB20437		Aab20437 Anti-FIX/
57	70	78.7	119	2	AAAR82986		Aar82986 LK26 huma
58	70	78.7	119	2	AAAR82980		Aar82980 LK26 huma
59	70	78.7	119	2	AAAR82981		Aar82981 LK26 huma
60	70	78.7	119	2	AAAR82982		Aar82982 LK26 huma
61	70	78.7	119	2	AAAR82979		Aar82979 LK26 huma
62	70	78.7	119	2	AAAR82977		Aar82977 LK26 heav
63	70	78.7	121	3	AAAY96063		Aay96063 Human ant
64	69	77.5	21	2	AAAW99565		Aaw99565 Immunoglo
65	69	77.5	30	2	AAAW99570		Aaw99570 Immunoglo
66	69	77.5	30	3	AAAY78332		Aay78332 Anti-DNA
67	69	77.5	30	4	AAAB36921		Aab36921 Peptide P
68	69	77.5	30	4	AAAB36914		Aab36914 Peptide #
69	69	77.5	30	5	AAAE23169		Aae23169 Monoclonal
70	69	77.5	30	5	AAAE16153		Aae16153 Anti-DNA
71	69	77.5	30	7	ADG28020		Adg28020 Synthetic
72	69	77.5	30	7	ADL88656		Adl88656 P3 membra
73	69	77.5	30	8	ADF70131		Adf70131 Anti-idio
74	69	77.5	30	8	ADR50633		Adr50633 Membrane
75	69	77.5	30	9	ADW71221		Adw71221 Heavy cha
76	69	77.5	30	9	ADY38705		Ady38705 Novel pro
77	69	77.5	30	9	ASB28497		Aeb28497 P3 transd
78	69	77.5	31	2	AAW99572		Aaw99572 Immunoglo
79	69	77.5	33	2	AAW99571		Aaw99571 Immunoglo
80	69	77.5	49	2	AAW99573		Aaw99573 Immunoglo
81	69	77.5	120	7	ADMA1878		Adm1878 Human ant
82	69	77.5	120	7	ADMA1836		Adm1836 Human ant
83	69	77.5	123	2	AAW66099		Aaw66099 anti-CD22
84	69	77.5	123	6	AAO27193		Aao27193 Chimeric
85	69	77.5	123	6	AAO27198		Aao27198 Murine an
86	69	77.5	123	6	AAO27200		Aao27200 Chimeric
87	69	77.5	123	6	AAO27200		Aao27200 Chimeric
88	69	77.5	123	8	ADH50839		Adh50839 Mouse ant
89	69	77.5	123	8	ADH50841		Adh50841 Human VH#
90	69	77.5	123	8	ADT02529		Adt02529 Anti-CD22
91	69	77.5	123	8	ADW75671		Adw75671 Novel mod
92	69	77.5	123	8	ADW75669		Adw75669 Novel mod
93	69	77.5	123	9	AEA50164		Aea50164 Anti-CD22
94	69	77.5	123	9	AEA50147		Aea50147 Anti-CD22
95	69	77.5	140	6	ABG74241		Abg74241 Mouse ant
96	69	77.5	246	8	ADH50844		Adh50844 SGLII RPB
97	69	77.5	246	8	ADH50847		Adh50847 SGLI RFB4

98	69	77.5	246	8	ADH50843	Adh50843 RFB4 spec	171	68	76.4	121	8	ADM78071	Adm78071 Human SKB
99	69	77.5	246	8	ADH50845	Adh50845 SG11 var	172	68	76.4	123	8	ADR38656	Adr38656 Mouse hea
100	69	77.5	246	8	ADH50846	Adh50846 SGIV RPB4	173	68	76.4	124	4	AA97193	Aa97193 Murine an
101	69	77.5	262	8	ADP02523	Adt02523 Anti-CD22	174	68	76.4	134	6	ABP60555	Abp60555 Murine an
102	68	76.4	17	5	AAU72804	Aau72804 TRA-8 hea	175	68	76.4	137	2	AAW57592	Aaw57592 Chimeric
103	68	76.4	17	6	AAU728072	Aao29872 Mouse ant	176	68	76.4	137	2	AAW57603	Aaw57603 Chimeric
104	68	76.4	17	6	ABP60560	Abp60560 Murine an	177	68	76.4	137	2	AAW89635	Aaw89635 Human ant
105	68	76.4	17	7	ADJ79790	Adj79790 TRA-8 hea	178	68	76.4	137	2	AAW89625	Aaw89625 Mouse hum
106	68	76.4	17	8	ADM78127	Adm78127 Human SJB	179	68	76.4	137	3	AAW77513	Aay77513 Mouse ant
107	68	76.4	17	8	ADM78121	Adm78121 Human SJB	180	68	76.4	137	3	AAW77514	Aay77514 Peptide e
108	68	76.4	17	9	AEC20781	Aec20781 M-CSF spe	181	68	76.4	137	4	AAW67112	Aag67112 Amino aci
109	68	76.4	66	4	ABU56859	Abu56859 Bont/A Hc	182	68	76.4	137	4	AAW67102	Aag67102 Amino aci
110	68	76.4	87	4	AAU60990	Aao60990 Mouse ger	183	68	76.4	137	4	AAW64775	Aag64775 Mouse ant
111	68	76.4	87	9	ADQ89275	Adq89275 Mouse imm	184	68	76.4	137	4	AAW64776	Aag64776 Humanised
112	68	76.4	87	9	AE809548	Aeb09548 Murine ge	185	68	76.4	137	4	AAW63393	Aag63393 Amino aci
113	68	76.4	89	4	AAU606986	Aao606986 Mouse ger	186	68	76.4	137	4	AAW63394	Aag63394 Amino aci
114	68	76.4	89	8	ADQ89271	Adq89271 Mouse imm	187	68	76.4	137	5	ABW95208	Abw95208 Mouse joi
115	68	76.4	89	9	AE809544	Aeb09544 Murine ge	188	68	76.4	137	5	ABW95209	Abw95209 Human joi
116	68	76.4	98	4	AAU60976	Aao60976 Mouse ger	189	68	76.4	137	6	ABJ36667	Abj36667 Angiogene
117	68	76.4	98	4	AAU60978	Aao60978 Mouse ger	190	68	76.4	137	8	ADO33884	Ado33884 Human par
118	68	76.4	98	4	AAU60975	Aao60975 Mouse ger	191	68	76.4	137	8	ADO33883	Ado33883 Murine pa
119	68	76.4	98	8	ADQ89263	Adq89263 Mouse imm	192	68	76.4	138	6	ABJ36668	Abj36668 Angiogene
120	68	76.4	98	8	ADQ89261	Adq89261 Mouse imm	193	68	76.4	142	3	AAJ43868	Aay43868 Heavy cha
121	68	76.4	98	8	ADQ89260	Adq89260 Mouse ger	194	68	76.4	143	3	AAJ43867	Aay43867 Heavy cha
122	68	76.4	98	9	AE809534	Aeb09534 Murine ge	195	68	76.4	145	3	AAJ43870	Aay43870 Heavy cha
123	68	76.4	98	9	AE809536	Aeb09536 Murine ge	196	68	76.4	237	7	AAE38657	Aae38657 Mouse G1
124	68	76.4	98	9	AE809533	Aeb09533 Murine ge	197	68	76.4	293	9	ADZ51608	Adz51608 High-func
125	68	76.4	108	2	AAU95283	Aay95283 Anti-proe	198	68	76.4	293	9	ADZ51616	Adz51616 High-func
126	68	76.4	108	2	AAU91364	Aay91364 Anti-proe	199	68	76.4	293	9	ADZ51612	Adz51612 High-func
127	68	76.4	108	8	ADM78067	Adm78067 Human SKB	200	68	76.4	293	9	ADZ51606	Adz51606 High-func
128	68	76.4	116	2	AAU79245	Aar79245 Heavy cha	201	68	76.4	293	9	ADZ51610	Adz51610 High-func
129	68	76.4	116	2	AAU79246	Aar79246 Heavy cha	202	68	76.4	293	9	ADZ51614	Adz51614 High-func
130	68	76.4	117	8	ADI26500	Adi26500 Human ECL	203	68	76.4	447	5	ADI30289	Adi30289 Human par
131	68	76.4	117	8	ADI26492	Adi26492 Human ECL	204	68	76.4	449	5	AEC20773	Aec20773 M-CSF spe
132	68	76.4	118	2	AAW57591	Aaw57591 Chimeric	205	68	76.4	462	6	AAO29869	Aao29869 Mouse ant
133	68	76.4	118	2	AAW57576	Aaw57576 Chimeric	206	68	76.4	462	6	AAU79787	Aaj79787 TRA-8 hea
134	68	76.4	118	2	AAW89627	Aaw89627 Mouse hum	207	68	76.4	464	5	AAU72801	Aaj72801 Pgp-regie
135	68	76.4	118	2	AAW89636	Aaw89636 Human ant	208	67.5	75.8	125	8	ADM39241	Adm39241 Canine im
136	68	76.4	118	3	AAU77512	Aay77512 Peptide s	209	67	75.3	17	7	ADM07773	Adm07773 Canine im
137	68	76.4	118	3	AAU77502	Aay77502 Peptide s	210	67	75.3	17	8	ADR47400	Adr47400 Heavy cha
138	68	76.4	118	4	AAU76918	Aab76918 Human PTH	211	67	75.3	98	4	AAE06981	Aae06981 Mouse ger
139	68	76.4	118	4	AAU76928	Aab76928 Human ant	212	67	75.3	98	8	ADQ89266	Adq89266 Mouse imm
140	68	76.4	118	4	AAU76890	Aab76890 Human PTH	213	67	75.3	98	9	ABW95339	Abw95339 Murine ge
141	68	76.4	118	4	AAU76890	Aab76890 Human ant	214	67	75.3	116	7	ADM33438	Adm33438 Naid60 VH
142	68	76.4	118	4	AAU64764	Aag64764 Mouse ant	215	67	75.3	117	2	AAW48865	Aaw48865 Murine mo
143	68	76.4	118	4	AAU64774	Aag64774 Humanised	216	67	75.3	117	2	AAW48866	Aaw48866 Chimeric
144	68	76.4	118	4	AAU63382	Aag63382 Amino aci	217	67	75.3	117	2	AAW86141	Aaw86141 Protein s
145	68	76.4	118	4	AAU63392	Aag63392 Amino aci	218	67	75.3	117	2	AAW86135	Aaw86135 Protein s
146	68	76.4	118	4	AAU76909	Aab76909 Human ant	219	67	75.3	117	2	AAW86139	Aaw86139 Protein s
147	68	76.4	118	4	AAU76899	Aab76899 Human PTH	220	67	75.3	117	2	AAW86137	Aaw86137 Protein s
148	68	76.4	118	5	ABW95207	Abw95207 Human joi	221	67	75.3	119	2	AAW69322	Aaw69322 15D3 anti
149	68	76.4	118	5	ABW95197	Abw95197 Mouse joi	222	67	75.3	119	2	AAW73503	Aaw73503 Antibody
150	68	76.4	118	6	ABJ36659	Abj36659 Angiogene	223	67	75.3	119	2	AAJ32832	Aaj32832 15D3 VH c
151	68	76.4	118	6	ABJ36649	Abj36649 Angiogene	224	67	75.3	119	8	ADR47407	Adr47407 Heavy cha
152	68	76.4	118	6	ABJ36649	Abj36649 Murine pa	225	67	75.3	119	8	ADR47405	Adr47405 Heavy cha
153	68	76.4	118	8	ADO33843	Ado33843 Murine pa	226	67	75.3	119	8	ADR47405	Adr47405 IC8 VH do
154	68	76.4	118	8	ADO33853	Ado33853 Human par	227	67	75.3	119	8	ADR47408	Adr47408 Heavy cha
155	68	76.4	119	5	AAU72813	Aau72813 Humanised	228	67	75.3	124	9	ABE12557	Aeb12557 Humanised
156	68	76.4	119	5	AAU72809	Aau72809 Heavy cha	229	67	75.3	124	9	ABE12542	Aeb12542 Antibody
157	68	76.4	119	5	AAU72812	Aau72812 Humanised	230	67	75.3	124	9	ABE12542	Aeb12542 Antibody
158	68	76.4	119	5	AAU72811	Aau72811 Humanised	231	67	75.3	125	4	AAW48937	Aaw48937 Anti-1-TrkA
159	68	76.4	119	5	AAU72814	Aau72814 Humanised	232	67	75.3	136	2	AAW56962	Aaw56962 MAb A33 h
160	68	76.4	119	6	AAO29879	Aao29879 Humanised	233	67	75.3	138	2	AAW20064	Aar20064 MRK16-H c
161	68	76.4	119	6	AAO29877	Aao29877 Humanised	234	67	75.3	138	8	ADR47397	Adr47397 Heavy cha
162	68	76.4	119	6	AAO29882	Aao29882 M type fu	235	67	75.3	140	5	AAU76132	Aau76132 Mouse mAb
163	68	76.4	119	6	AAO29881	Aao29881 Humanised	236	67	75.3	140	5	AAU76133	Aau76133 Mouse mon
164	68	76.4	119	7	ADJ79824	Adj79824 H4-type h	237	67	75.3	140	5	AAU76122	Aau76122 Mouse mon
165	68	76.4	119	7	ADJ79825	Adj79825 H4-type hu	238	67	75.3	144	8	ADR47417	Adr47417 Heavy cha
166	68	76.4	119	7	ADJ79820	Adj79820 H1-type h	239	67	75.3	237	3	AAW95440	Aaw95440 A33/212 s
167	68	76.4	119	7	ADJ79795	Adj79795 Humanised	240	67	75.3	241	2	AAW95441	Aaw95441 A33/218 s
168	68	76.4	119	7	ADJ79823	Adj79823 H2-type h	241	67	75.3	241	3	AAW954837	Aaw954837 Linked fu
169	68	76.4	120	2	AAW00240	Aaw00240 EGF recep	242	67	75.3	245	2	AAW97891	Aaw97891 A33/218 s
170	68	76.4	121	6	ABR41818	AbR41818 Heavy cha	243	67	75.3	246	5	ABP45303	Abp45303 Human Bly



244	67	75.3	246	7	ADG96130	Single ch	317	66	74.2	237	5	ABP46107	Human Bly
245	67	75.3	251	8	ADR47465	g133 encod	318	66	74.2	237	5	ABP45995	Human Bly
246	67	75.3	264	5	Aaw73049	Humanised	319	66	74.2	237	5	ABP46033	Human Bly
247	67	75.3	265	5	AAU75159		320	66	74.2	237	5	ABP46100	Human Bly
248	67	75.3	265	6	ABG73147	A33/218 s	321	66	74.2	237	5	ABP45992	Human Bly
249	67	75.3	265	6	ABG73867	A33/218 s	322	66	74.2	237	5	ABP46008	Human Bly
250	67	75.3	295	4	AA848934	Anti-TrkA	323	66	74.2	237	5	ABP46025	Human Bly
251	67	75.3	532	2	Aaw73051	533dCH2, z	324	66	74.2	237	5	ABP46103	Human Bly
252	67	75.3	643	2	Aaw73050	233g2G237	325	66	74.2	237	5	ABP46104	Human Bly
253	67	75.3	643	2	AAW73048	A33 chime	326	66	74.2	237	5	ABP46106	Human Bly
254	66	74.2	17	5	AAU82550	Llama CDR	327	66	74.2	237	5	ABP45994	Human Bly
255	66	74.2	17	8	ADP47182	Human pho	328	66	74.2	237	5	ABP46006	Human Bly
256	66	74.2	17	8	ADP47164	Human pho	329	66	74.2	237	5	ABP46009	Human Bly
257	66	74.2	17	8	ADR38775	Mouse hea	330	66	74.2	237	5	ABP46029	Human Bly
258	66	74.2	17	9	ADX98328	Human ant	331	66	74.2	237	5	ABP46099	Human Bly
259	66	74.2	22	2	AAU06694		332	66	74.2	237	7	ADG96931	Single ch
260	66	74.2	22	8	ADQ39676	Human S85	333	66	74.2	237	7	ADG96926	Single ch
261	66	74.2	96	8	ADU04240	Human imm	334	66	74.2	237	7	ADG96852	Single ch
262	66	74.2	96	8	ADU04237	Human imm	335	66	74.2	237	7	ADG96856	Single ch
263	66	74.2	98	2	AAW59614	Anti-RSV	336	66	74.2	237	7	ADG96822	Single ch
264	66	74.2	98	3	AA840075	Anti-hi11	337	66	74.2	237	7	ADG96927	Single ch
265	66	74.2	98	3	AA840113		338	66	74.2	237	7	ADG96835	Single ch
266	66	74.2	98	4	AA848022		339	66	74.2	237	7	ADG96859	Single ch
267	66	74.2	98	5	ABG78188	Human Fv	340	66	74.2	237	7	ADG96934	Single ch
268	66	74.2	98	5	ABG78204	Human Fv	341	66	74.2	237	7	ADG96928	Single ch
269	66	74.2	98	5	ABG77149	Germline	342	66	74.2	237	7	ADG96836	Single ch
270	66	74.2	98	5	ABG91879	Human ant	343	66	74.2	237	7	ADG96920	Single ch
271	66	74.2	98	5	ABG91895	Human ant	344	66	74.2	237	7	ADG96819	Single ch
272	66	74.2	98	6	ABO27084	Human ger	345	66	74.2	237	7	ADG96844	Single ch
273	66	74.2	98	7	ADD28042	Lymphoma	346	66	74.2	237	7	ADG96930	Single ch
274	66	74.2	98	7	ADD28076	Lymphoma	347	66	74.2	237	7	ADG96833	Single ch
275	66	74.2	98	7	ADP10121	Antibody	348	66	74.2	237	7	ADG96843	Single ch
276	66	74.2	98	7	ADP10019	Antibody	349	66	74.2	237	7	ADG96821	Single ch
277	66	74.2	98	7	ADP09911	Antibody	350	66	74.2	238	5	ABP46013	Human Bly
278	66	74.2	98	8	ADJ80297	VH gene 1	351	66	74.2	238	5	ADG96840	Single ch
279	66	74.2	98	8	ADJ28564	Human ant	352	66	74.2	239	5	ABP46023	Human Bly
280	66	74.2	98	9	ADV75302	Protein e	353	66	74.2	240	5	ADG96850	Single ch
281	66	74.2	98	9	AE880218	Germline	354	66	74.2	240	5	ABP46005	Human Bly
282	66	74.2	109	7	ADC60996	Human ant	355	66	74.2	240	5	ABP46033	Human Bly
283	66	74.2	109	8	ADP22382	Human ant	356	66	74.2	240	5	ABP46094	Human Bly
284	66	74.2	109	8	ADR47406	Human sub	357	66	74.2	240	5	ABP46037	Human Bly
285	66	74.2	114	6	AAE34873	BIWA8 ant	358	66	74.2	240	5	ABP46014	Human Bly
286	66	74.2	114	9	AEA41085	Germline	359	66	74.2	240	5	ABP46019	Human Bly
287	66	74.2	115	9	AEA41086	Germline	360	66	74.2	240	5	ABP46097	Human Bly
288	66	74.2	115	9	AEA41078	Germline	361	66	74.2	240	5	ABP46018	Human Bly
289	66	74.2	117	9	AAE66305	Human imm	362	66	74.2	240	5	ABP45996	Human Bly
290	66	74.2	117	5	AAO15187	Anti	363	66	74.2	240	5	ABP46034	Human Bly
291	66	74.2	117	9	AEA41076	Germline	364	66	74.2	240	5	ABP46106	Human Bly
292	66	74.2	117	9	AE812760	Antibody	365	66	74.2	240	5	ABP46030	Human Bly
293	66	74.2	120	9	ADR98413	Human ant	366	66	74.2	240	5	ABP46102	Human Bly
294	66	74.2	122	6	ABR55779	Heavy cha	367	66	74.2	240	7	ADG96864	Single ch
295	66	74.2	122	6	ABR55821	Heavy cha	368	66	74.2	240	7	ADG96929	Single ch
296	66	74.2	122	6	ABR55775	Heavy cha	369	66	74.2	240	7	ADG96921	Single ch
297	66	74.2	122	9	ADW88758	Hepatitis	370	66	74.2	240	7	ADG96933	Single ch
298	66	74.2	122	9	AE812762	Antibody	371	66	74.2	240	7	ADG96841	Single ch
299	66	74.2	123	2	AAW08582	Human ant	372	66	74.2	240	7	ADG96857	Single ch
300	66	74.2	123	8	ADQ25848	Camelidae	373	66	74.2	240	7	ADG96823	Single ch
301	66	74.2	124	5	AAO18439	Anti-GD2	374	66	74.2	240	7	ADG96860	Single ch
302	66	74.2	124	5	AAO18440	Anti-GD2	375	66	74.2	240	7	ADG96924	Single ch
303	66	74.2	131	4	AAQ65566	Amino aci	376	66	74.2	240	7	ADG96846	Single ch
304	66	74.2	131	5	AAO15843	Human imm	377	66	74.2	240	7	ADG96845	Single ch
305	66	74.2	131	8	ABG75396	Rearrange	378	66	74.2	240	7	ADG96857	Single ch
306	66	74.2	131	8	ADQ36120	Human VH3	379	66	74.2	240	7	ADG96861	Single ch
307	66	74.2	133	8	ADP09928	Anti-huma	380	66	74.2	245	2	AAO06714	Antibody
308	66	74.2	141	9	ADX98253	Human ant	381	66	74.2	245	8	ADO39733	Human c-m
309	66	74.2	196	3	AAV56862	Human imm	382	66	74.2	248	5	ABP45963	Human Bly
310	66	74.2	234	2	AAE64819	OMVU10 SC	383	66	74.2	248	5	ABP45954	Human Bly
311	66	74.2	236	4	AA846055	Human TF	384	66	74.2	248	5	ADG96790	Single ch
312	66	74.2	236	5	ADP45999	Human Bly	385	66	74.2	248	7	ADG96781	Single ch
313	66	74.2	236	7	ADG96826	Single ch	386	66	74.2	250	5	ABP45168	Human Bly
314	66	74.2	237	5	ABP46101	Human Bly	387	66	74.2	250	7	ADG95995	Single ch
315	66	74.2	237	5	ABP46017	Human Bly	388	66	74.2	444	6	AAE35327	Humanleed
316	66	74.2	237	5	ABP46032	Human Bly	389	66	74.2	444	6	AAE34876	BIWA4/8 a

390	66	74.2	444	8	ADL15443	Adl15443 Humanised	463	65	73.0	122	2	AAR54301	Aar54301 Anti-HIV
391	66	74.2	444	8	ADO00851	Ado00851 Humanised	464	65	73.0	122	2	AAW01259	Aaw01259 VH region
392	66	74.2	444	8	AEB29789	Aeb29789 Humanised	465	65	73.0	122	2	AAy98220	Aay98220 Anti-gp12
393	66	74.2	444	9	AEB29780	Aeb29780 Humanised	466	65	73.0	122	3	AAy95111	Aay95111 Anti-gp12
394	66	74.2	460	9	AEA41063	Aea41063 Human ant	467	65	73.0	127	2	AAW05715	Aaw05715 AlphaTT2
395	66	74.2	460	9	AEA41028	Aea41028 Human ant	468	65	73.0	129	8	ADO36395	Ado36395 Intracell
396	66	74.2	460	9	AEA41035	Aea41035 Human ant	469	65	73.0	138	3	AAy32404	Aay32404 Mouse ant
397	66	74.2	460	9	AEA41043	Aea41043 Human ant	470	65	73.0	138	3	AAy32406	Aay32406 Mouse ant
398	66	74.2	461	9	AEA41064	Aea41064 Human ant	471	65	73.0	143	6	ADA43059	Ada43059 Human ant
399	66	74.2	461	9	AEA41062	Aea41062 Human ant	472	65	73.0	144	5	ABB79730	Abb79730 Anti-Stre
400	66	74.2	461	9	AEA41047	Aea41047 Human ant	473	65	73.0	155	6	ABP72295	Abp72295 Chimeric
401	66	74.2	461	9	AEA41056	Aea41056 Human ant	474	65	73.0	155	6	ADQ15508	Adq15508 Chimeric
402	66	74.2	461	9	AEA41061	Aea41061 Human ant	475	65	73.0	165	6	ABP72294	Abp72294 Chimeric
403	66	74.2	461	9	AEA41065	Aea41065 Human ant	476	65	73.0	165	8	ADQ15506	Adq15506 Histatin
404	66	74.2	462	9	AEA41054	Aea41054 Human ant	477	65	73.0	217	8	ADR16818	Adr16818 Human bre
405	66	74.2	462	9	AEA41066	Aea41066 Human ant	478	65	73.0	228	8	ADL70776	Adl70776 Anti-TNFA
406	66	74.2	462	9	AEA41051	Aea41051 Human ant	479	65	73.0	247	5	ABP45641	Abp45641 Human Bly
407	66	74.2	464	9	AEA41072	Aea41072 Human ant	480	65	73.0	247	7	ADG96468	Adg96468 Single ch
408	66	74.2	473	5	ABG77162	Abg77162 Germline	481	65	73.0	249	4	AAAB20434	Aaab20434 Anti-FIX/
409	66	74.2	473	8	ADR28584	Adr28584 Human ant	482	65	73.0	256	5	ABP46108	Abp46108 Human Bly
410	66	74.2	473	9	ADX57904	Adx57904 Human ger	483	65	73.0	256	7	ADG96935	Adg96935 Single ch
411	66	74.2	604	9	AEA49909	Aea49909 Anti-cryp	484	65	73.0	384	4	AAU14462	Aau14462 Human nov
412	65	73.0	17	5	ABF52347	Abf52347 Fv region	485	65	73.0	384	4	AAU14463	Aau14463 Human nov
413	65	73.0	17	7	ADM07765	Adm07765 Canine im	486	65	73.0	384	4	AAU14461	Aau14461 Human nov
414	65	73.0	17	7	ADM07758	Adm07758 Canine im	487	65	73.0	384	4	AAU14464	Aau14464 Human nov
415	65	73.0	17	8	ADH89411	Adh89411 Human Eph	488	65	73.0	384	8	ADH80782	Adh80782 Human pol
416	65	73.0	17	8	ADH89411	Adh89411 Human tra	489	65	73.0	384	8	ADH80779	Adh80779 Human pol
417	65	73.0	17	8	ADL23073	Adl23073 Human Eph	490	65	73.0	385	8	ADH80781	Adh80781 Human pol
418	65	73.0	17	8	ADT75118	Adt75118 Murine he	491	65	73.0	385	8	ADH80780	Adh80780 Human pol
419	65	73.0	17	8	ADT75049	Adt75049 Murine he	492	65	73.0	702	9	ASEC08432	Asec08432 Amino aci
420	65	73.0	17	8	ADT75115	Adt75115 Murine he	493	65	73.0	702	9	ASEC08433	Asec08433 Amino aci
421	65	73.0	17	8	ADY32307	Ady32307 Human Eph	494	65	73.0	731	9	AECC08431	Aecc08431 ScFV-2-1G
422	65	73.0	17	9	AEA34930	Aea34930 Human ant	495	65	73.0	734	9	AECC08430	Aecc08430 ScFV-1-1F
423	65	73.0	17	9	AEB17171	Aeb17171 Epha2-spe	496	64	71.9	17	2	AAy05053	Aay05053 Tumour an
424	65	73.0	17	9	AEA42971	Aea42971 Epha2 ant	497	64	71.9	17	7	ADC83824	Adc83824 CDR regio
425	65	73.0	98	5	ABP52308	Abp52308 Fv region	498	64	71.9	17	8	ADR38751	Adr38751 Mouse hea
426	65	73.0	113	8	ADT75036	Adt75036 Heavy cha	499	64	71.9	17	8	ADR38743	Adr38743 Mouse hea
427	65	73.0	115	8	ADH85733	Adh85733 Human Eph	500	64	71.9	17	8	ADR38739	Adr38739 Mouse hea
428	65	73.0	115	8	ADL23071	Adl23071 Human Eph	501	64	71.9	17	8	ADR38747	Adr38747 Mouse hea
429	65	73.0	115	8	ADT74989	Adt74989 Heavy cha	502	64	71.9	17	8	ADR38755	Adr38755 Mouse hea
430	65	73.0	115	8	ADT74982	Adt74982 Heavy cha	503	64	71.9	17	8	ADT75044	Adt75044 Murine he
431	65	73.0	115	9	ADY32227	Ady32227 Human Eph	504	64	71.9	17	9	AEA45423	Aea45423 Murine fa
432	65	73.0	115	9	AEA34928	Aea34928 Human ant	505	64	71.9	17	9	AEA45760	Aea45760 Apolipop
433	65	73.0	115	9	AEB17169	Aeb17169 Epha2-spe	506	64	71.9	40	6	ABJ25307	Abj25307 SAC isola
434	65	73.0	115	9	AEA42969	Aea42969 Epha2 ant	507	64	71.9	66	6	ABU56860	Abu56860 BoNT/A Hc
435	65	73.0	116	4	AAU02631	Aau02631 Anti-adip	508	64	71.9	66	6	ABU56861	Abu56861 BoNT/A Hc
436	65	73.0	118	8	ADO36351	Ado36351 Intracell	509	64	71.9	98	4	AAE06982	Aae06982 Mouse ger
437	65	73.0	118	8	ADQ75224	Adq75224 Immunoglo	510	64	71.9	98	8	ADQ89267	Adq89267 Mouse germ
438	65	73.0	119	8	ADT75108	Adt75108 Heavy cha	511	64	71.9	98	9	AEBO9540	Aebo9540 Murine ge
439	65	73.0	119	8	ADT75087	Adt75087 Heavy cha	512	64	71.9	110	2	AAW06207	Aaw06207 Rat antib
440	65	73.0	119	8	ADT75088	Adt75088 Heavy cha	513	64	71.9	115	3	AAAB12460	Aaab12460 IGG monoc
441	65	73.0	119	8	ADT75101	Adt75101 Heavy cha	514	64	71.9	117	6	ABR55328	Abbr55328 Amino aci
442	65	73.0	119	8	ADT75102	Adt75102 Heavy cha	515	64	71.9	117	6	ABR55324	Abrr55324 Amino aci
443	65	73.0	119	8	ADT75105	Adt75105 Heavy cha	516	64	71.9	118	2	AAW06208	Aaw06208 Xenograft
444	65	73.0	119	8	ADT75093	Adt75093 Heavy cha	517	64	71.9	118	8	ADR38657	Adr38657 Mouse hea
445	65	73.0	119	8	ADT75094	Adt75094 Heavy cha	518	64	71.9	118	8	ADR38658	Adr38658 Mouse hea
446	65	73.0	119	8	ADT75100	Adt75100 Heavy cha	519	64	71.9	118	8	ADT75023	Adt75023 Heavy cha
447	65	73.0	119	8	ADT75091	Adt75091 Heavy cha	520	64	71.9	120	2	AAW54930	Aaw54930 Fc recept
448	65	73.0	119	8	ADT75106	Adt75106 Heavy cha	521	64	71.9	120	2	AAW54929	Aaw54929 Fc recept
449	65	73.0	120	7	AAU02610	Aau02610 Anti-adip	522	64	71.9	120	2	AAW54931	Aaw54931 Fc recept
450	65	73.0	120	7	ADL91324	Adl91324 VH chain	523	64	71.9	120	5	AAO18391	Aao18391 Murine CB
451	65	73.0	121	2	AAW22951	Aaw22951 Monoclon	524	64	71.9	120	5	AAO18395	Aao18395 Humanised
452	65	73.0	121	2	AAW86118	Aaw86118 Murine 34	525	64	71.9	120	5	AAO18398	Aao18398 Humanised
453	65	73.0	121	2	AAW86120	Aaw86120 Protein s	526	64	71.9	120	5	AAO18396	Aao18396 Humanised
454	65	73.0	121	2	AAW86125	Aaw86125 Protein s	527	64	71.9	123	2	AAW45187	Aaw45187 Heavy cha
455	65	73.0	121	2	AAW86124	Aaw86124 Protein s	528	64	71.9	123	3	AAW51266	Aaw51266 Monoclon
456	65	73.0	121	2	AAW86122	Aaw86122 Protein s	529	64	71.9	123	3	ADX02123	Adx02123 SARS coro
457	65	73.0	121	5	AAE15709	Aae15709 Mouse mon	530	64	71.9	124	9	ADZ45421	Adz45421 Murine fa
458	65	73.0	121	5	AAE15706	Aae15706 Mouse mon	531	64	71.9	139	2	AAW21652	Aaw21652 Humanised
459	65	73.0	121	5	AAE15707	Aae15707 Mouse mon	532	64	71.9	139	2	AAW21656	Aaw21656 Chimeric
460	65	73.0	121	5	AAE15703	Aae15703 Mouse mon	533	64	71.9	140	2	AAW21654	Aaw21654 Mouse MAb
461	65	73.0	121	5	AAE15708	Aae15708 Mouse mon	534	64	71.9	140	2	AAW06205	Aaw06205 Xenograft
462	65	73.0	121	7	ADP03960	Adp03960 Murine-ex	535	64	71.9	140	2		



682	62	69.7	17	5	AAU82546	Aau82546	Llama CDR	755	61	68.5	115	8	ADP66611	Adp66611	Anti-RAS
683	62	69.7	17	5	AAE16431	Aae16431	Llama CDR	756	61	68.5	115	8	ADP66610	Adp66610	Anti-RAS
684	62	69.7	17	5	ABP58266	Abp58266	Mouse ant	757	61	68.5	115	8	ADP66605	Adp66605	Anti-RAS
685	62	69.7	17	6	ABR55313	AbR55313	Complemen	758	61	68.5	115	8	ADP96608	Adp96608	Anti-RAS
686	62	69.7	17	8	ADP471137	Adp471137	Human pho	759	61	68.5	115	8	ADP96610	Adp96610	Anti-RAS
687	62	69.7	17	9	AEA45670	Aea45670	Apolipoppr	760	61	68.5	115	8	ADP96607	Adp96607	Anti-RAS
688	62	69.7	17	9	AEA46296	Aea46296	Apolipoppr	761	61	68.5	115	8	ADP96611	Adp96611	Anti-RAS
689	62	69.7	40	6	ABJ25342	Abj25342	SAC isola	762	61	68.5	115	8	ADP96603	Adp96603	Anti-RAS
690	62	69.7	43	8	ADP96639	Adp96639	Anti-RAS	763	61	68.5	115	8	ADP96604	Adp96604	Anti-RAS
691	62	69.7	45	8	ADP96637	Adp96637	Anti-RAS	764	61	68.5	115	8	ADP96609	Adp96609	Anti-RAS
692	62	69.7	108	2	AAK95285	Aak95285	Anti-proe	765	61	68.5	115	8	ADP96604	Adp96604	Anti-RAS
693	62	69.7	112	8	ADO36339	Ado36339	Intracell	766	61	68.5	115	8	ADO79334	Ado79334	Anti-RAS
694	62	69.7	112	8	ADP66604	Adp66604	Anti-RAS	767	61	68.5	115	8	ADO79336	Ado79336	Anti-RAS
695	62	69.7	112	8	ADP96602	Adp96602	Anti-RAS	768	61	68.5	115	8	ADO79330	Ado79330	Anti-RAS
696	62	69.7	112	8	ADP96602	Adp96602	Anti-RAS	769	61	68.5	115	8	ADO79329	Ado79329	Anti-RAS
697	62	69.7	112	8	ADP96602	Adp96602	Anti-RAS	770	61	68.5	115	8	ADO79333	Ado79333	Anti-RAS
698	62	69.7	114	7	ADL91312	Adl91312	Consenus	771	61	68.5	115	8	ADO79337	Ado79337	Anti-RAS
699	62	69.7	117	6	ABR55318	AbR55318	Variable	772	61	68.5	115	8	ADO79335	Ado79335	Anti-RAS
700	62	69.7	117	6	ABR55326	AbR55326	Amino aci	773	61	68.5	115	8	ADT74976	Adt74976	Heavy cha
701	62	69.7	117	6	ABR55327	AbR55327	Amino aci	774	61	68.5	115	8	ADT74980	Adt74980	Heavy cha
702	62	69.7	119	2	AAW29996	Aaw29996	Humanised	775	61	68.5	115	9	AEb08750	Aeb08750	Anti-NOGO
703	62	69.7	119	2	AAW29994	Aaw29994	Humanised	776	61	68.5	116	8	ADP22178	Adp22178	Human ant
704	62	69.7	119	6	ABP58271	Abp58271	Humanised	777	61	68.5	116	8	ADP22242	Adp22242	Human ant
705	62	69.7	120	5	ABJ04944	Abj04944	Human IGG	778	61	68.5	116	8	ADP22234	Adp22234	Human ant
706	62	69.7	120	5	ABJ04944	Abj04944	Human IGG	779	61	68.5	116	8	ADT74977	Adt74977	Heavy cha
707	62	69.7	121	5	AAE16426	Aae16426	Mouse ant	780	61	68.5	117	8	ADT74983	Adt74983	Heavy cha
708	62	69.7	124	6	ABR54879	AbR54879	IGG kappa	781	61	68.5	117	8	ADT74987	Adt74987	Heavy cha
709	62	69.7	124	6	ABR54878	AbR54878	IGG kappa	782	61	68.5	119	2	AAK32240	Aak32240	Humanised
710	62	69.7	124	9	ABE119255	AbE119255	IGG heavy	783	61	68.5	119	2	AAK32244	Aak32244	Humanised
711	62	69.7	124	9	ABE119254	AbE119254	IGG heavy	784	61	68.5	119	2	AAK32243	Aak32243	Humanised
712	62	69.7	128	2	AAK69085	Aak69085	Anti-HIV	785	61	68.5	119	3	AAW27144	Aaw27144	Mature he
713	62	69.7	128	2	AAK69086	Aak69086	Anti-HIV	786	61	68.5	119	3	AAW87570	Aaw87570	Humanised
714	62	69.7	128	2	AAW08734	Aaw08734	Human ant	787	61	68.5	119	8	ADT75104	Adt75104	Heavy cha
715	62	69.7	128	2	AAW08735	Aaw08735	Human ant	788	61	68.5	119	8	ADT75096	Adt75096	Heavy cha
716	62	69.7	133	6	ABG74243	Abg74243	Mouse ant	789	61	68.5	119	8	ADT75103	Adt75103	Heavy cha
717	62	69.7	138	5	ABG76928	Abg76928	Humanised	790	61	68.5	121	7	ADB78580	AdB78580	Rat F997-
718	62	69.7	138	5	ABG76928	Abg76928	Humanised	791	61	68.5	123	8	ADR38655	Adr38655	Mouse hea
719	62	69.7	138	5	ABG76932	Abg76932	Humanised	792	61	68.5	124	7	ADG70095	Adg70095	Diversifi
720	62	69.7	138	8	ADR88412	AdR88412	Humanised	793	61	68.5	124	7	ADM41876	Adm41876	Human ant
721	62	69.7	138	8	ADR88408	AdR88408	Murine 3D	794	61	68.5	125	6	ABR54935	AbR54935	IGG lambd
722	62	69.7	138	8	ADR88416	AdR88416	Humanised	795	61	68.5	125	9	ABE19311	Abe19311	IGG heavy
723	62	69.7	142	6	ABR55332	AbR55332	Amino aci	796	61	68.5	126	2	AAW08984	Aaw08984	Llama ant
724	62	69.7	256	5	ABP45593	Abp45593	Human Bly	797	61	68.5	126	8	ADO25818	Ado25818	Camelidae
725	62	69.7	256	5	ADG96420	Adg96420	Single ch	798	61	68.5	127	8	ADO25834	Ado25834	Camelidae
726	62	69.7	367	4	AAU14556	Aau14556	Human nov	799	61	68.5	130	7	ABR82062	AbR82062	Camel ant
727	62	69.7	367	8	ADH80874	Adh80874	Human pol	800	61	68.5	130	7	AEa53304	Aea53304	Novel hum
728	62	69.7	449	6	ABP58273	Abp58273	Humanised	801	61	68.5	137	2	AAK32246	Aak32246	BR55-2 mu
729	62	69.7	461	9	AEA41017	Aea41017	Human ant	802	61	68.5	138	2	AAK32242	Aak32242	Chimeric
730	62	69.7	468	6	ABP58275	Abp58275	Humanised	803	61	68.5	139	2	AAK31588	Aak31588	BR55-2 he
731	61.5	69.1	117	9	AEBA46921	Aeba46921	Human var	804	61	68.5	147	2	AAW08986	Aaw08986	Llama pro
732	61.5	69.1	240	9	AEBA46921	Aeba46921	Human CDI	805	61	68.5	242	8	ADQ75289	Adq75289	Immunoglo
733	61.5	69.1	447	9	AEBA46921	Aeba46921	CDL spec	806	61	68.5	244	8	ADQ75290	Adq75290	Immunoglo
734	61	68.5	16	5	AAU82601	Aau82601	Llama CDR	807	61	68.5	251	4	AAU00211	Aau00211	Monoclonal
735	61	68.5	17	5	AAU82539	Aau82539	Llama CDR	808	61	68.5	409	2	AAW08989	Aaw08989	Llama pro
736	61	68.5	17	7	ADB78557	AdB78557	Rat F997-	809	61	68.5	472	5	ADL17260	Adl17260	Human NOV
737	61	68.5	17	8	ADP471155	Adp471155	Human pho	810	61	68.5	638	8	ADL27332	Adl27332	Human aci
738	61	68.5	17	8	ADT75121	Adt75121	Murine he	811	61	68.5	638	8	ADL27333	Adl27333	Amino aci
739	61	68.5	17	9	AEa53653	Aea53653	Novel hum	812	60.5	68.0	16	8	ADP25798	Adp25798	Anti-alph
740	61	68.5	17	9	AEa5783	Aea5783	Apolipoppr	813	60.5	68.0	88	4	AAE06988	Aae06988	Mouse ger
741	61	68.5	17	9	AEA46034	Aea46034	Apolipoppr	814	60.5	68.0	88	8	AQD89273	Aqd89273	Mouse lmm
742	61	68.5	17	9	AEA45684	Aea45684	Apolipoppr	815	60.5	68.0	88	9	AEb09546	Aeb09546	Murine ge
743	61	68.5	17	9	AEb21689	Aeb21689	Anti-NOGO	816	60.5	68.0	119	8	ADT88872	Adt88872	Human IGF
744	61	68.5	17	9	AEb08724	Aeb08724	antibody	817	60.5	68.0	119	8	ADT88864	Adt88864	Human IGF
745	61	68.5	40	6	ABJ25314	Abj25314	SAC isola	818	60.5	68.0	119	8	ADT88866	Adt88866	Human IGF
746	61	68.5	66	9	ABU56836	AbU56836	BoNT/A Hc	819	60.5	68.0	119	8	ADT88862	Adt88862	Human IGF
747	61	68.5	96	9	AEA54104	Aea54104	Novel hum	820	60.5	68.0	119	8	ADT88873	Adt88873	Human IGF
748	61	68.5	115	4	ABG2760	Abg2760	Human HIV	821	60.5	68.0	122	8	ADP25816	Adp25816	Anti-alph
749	61	68.5	115	7	ADL91350	Adl91350	VH chain	822	60.5	68.0	122	8	ADR30760	Adr30760	Mouse B2G
750	61	68.5	115	7	ADL91351	Adl91351	VH chain	823	60	67.4	17	5	AAU82537	Aau82537	Llama CDR
751	61	68.5	115	8	ADP66612	Adp66612	Anti-RAS	824	60	67.4	17	8	ADL61984	Adl61984	Human TS-
752	61	68.5	115	8	ADP66613	Adp66613	Anti-RAS	825	60	67.4	17	8	ADP66613	Adp66613	Anti-IL-2
753	61	68.5	115	8	ADP66606	Adp66606	Anti-RAS	826	60	67.4	17	8	ADW046637	Adw046637	Peptide d
754	61	68.5	115	8	ADP66609	Adp66609	Anti-RAS	827	60	67.4	17	9	ADW04687	Adw04687	PAPP-A im

828	60	67.4	17	9	ADW04775	Adw04775 PAPP-A im	901	60	67.4	243	7	ADG96918	Adg96918 Single ch
829	60	67.4	17	9	ADZ45427	Adz45427 Murine fa	902	60	67.4	244	9	ADW95690	Adw95690 Anti-IL-6
830	60	67.4	17	9	ADZ45415	Adz45415 Murine fa	903	60	67.4	244	9	ADX15695	Adx15695 Mouse ant
831	60	67.4	17	9	AEA45996	Aea45996 Apolipop	904	60	67.4	247	1	AAP80155	Aap80155 FRS and C
832	60	67.4	43	8	ADP96638	Adp96638 Anti-RAS	905	60	67.4	247	5	ABP45942	Abp45942 Human Bly
833	60	67.4	43	8	ADP96636	Adp96636 Anti-RAS	906	60	67.4	247	5	ABP45942	Abp45942 Human Bly
834	60	67.4	66	6	ABU56862	Abu56862 BONT/A Hc	907	60	67.4	247	8	ADS82681	Ads82681 Anti-IL-2
835	60	67.4	66	6	ABU56865	Abu56865 BONT/A Hc	908	60	67.4	247	8	ADS82681	Ads82681 Anti-IL-2
836	60	67.4	66	6	ABU56864	Abu56864 BONT/A Hc	909	60	67.4	250	8	ADI61980	Adi61980 Human gsf
837	60	67.4	66	6	ABU56863	Abu56863 BONT/A Hc	910	60	67.4	254	2	AAW49693	Aaw49693 Human Scf
838	60	67.4	66	6	ABU56864	Abu56863 BONT/A Hc	910	60	67.4	262	2	ADH44200	Adh44200 gfv antiB
839	60	67.4	98	2	AAR34279	Aar34279 Human TNF	911	60	67.4	295	8	ADN07004	Adn07004 Human EFG
840	60	67.4	98	3	AAB40130	Aab40130 Anti-hiL1	912	60	67.4	448	9	ABE46956	Abe46956 CD1a spec
841	60	67.4	98	3	AAB40134	Aab40134 Anti-hiL1	913	59.5	66.9	312	4	AAU14227	Aau14227 Human nov
842	60	67.4	98	5	ABG78207	Abg78207 Human Fv	914	59	66.3	17	2	AAW16651	Aaw16651 Anti-canc
843	60	67.4	98	5	ABG91898	Abg91898 Human ant	915	59	66.3	17	2	AAW05047	Aay05047 Tumour an
844	60	67.4	98	6	ABO27095	AbO27095 Human ger	916	59	66.3	17	2	AAW05047	Aay05047 Tumour an
845	60	67.4	98	7	ADD28062	Add28062 Lymphoma	917	59	66.3	17	4	AAW95213	Ant1-95213 Anti-plat
846	60	67.4	98	7	ADF10034	Adf10034 VEGF anti	918	59	66.3	17	4	AAW95213	Ant1-95213 Anti-plat
847	60	67.4	98	7	ADP09926	Adp09926 Antibody	919	59	66.3	17	4	ABE61400	AbE61400 Enhanced
848	60	67.4	98	7	ADF10136	Adf10136 Antibody	920	59	66.3	17	6	ABR01548	AbR01548 Human ant
849	60	67.4	98	7	ADJ80308	Adj80308 VH gene 1	921	59	66.3	17	6	ADA90032	Ada90032 Anti-Abet
850	60	67.4	98	9	ADY75313	Ady75313 Protein e	922	59	66.3	17	6	ADA90594	Ada90594 MS-Roche
851	60	67.4	109	2	AAR95286	Aar95286 Anti-proe	923	59	66.3	17	6	ADA90100	Ada90100 Anti-Abet
852	60	67.4	109	8	ADP22390	Adp22390 Human ant	924	59	66.3	17	6	ADA90421	Ada90421 MS-Roche
853	60	67.4	111	2	AAR34280	Aar34280 Human hea	925	59	66.3	17	6	ADA90575	Ada90575 MS-Roche
854	60	67.4	114	7	ADP03975	Adp03975 Murine-ex	926	59	66.3	17	6	ADA90587	Ada90587 MS-Roche
855	60	67.4	114	8	ADJ16562	Adj16562 Human ant	927	59	66.3	17	6	ADA90591	Ada90591 MS-Roche
856	60	67.4	115	8	ADI61978	Adi61978 Human TS-	928	59	66.3	17	6	ADA91306	Ada91306 MS-R Fab/
857	60	67.4	116	4	AAU02604	Aau02604 Anti-adip	929	59	66.3	17	6	ADA90574	Ada90574 MS-Roche
858	60	67.4	116	9	AEA41083	Aea41083 Germline	930	59	66.3	17	6	ADA90576	Ada90576 MS-Roche
859	60	67.4	116	2	AAR52065	Aar52065 Heavy cha	931	59	66.3	17	6	ADA90714	Ada90714 MS-Roche
860	60	67.4	117	2	AAR77305	Aar77305 Variable	932	59	66.3	17	6	ADA90716	Ada90716 MS-Roche
861	60	67.4	117	2	AAR66336	Aar66336 Human imm	933	59	66.3	17	6	ADA90718	Ada90718 MS-Roche
862	60	67.4	117	9	ABE12759	Abe12759 Antibody	934	59	66.3	17	6	ADA90419	Ada90419 MS-Roche
863	60	67.4	118	8	ADR38661	Adr38661 Mouse hea	935	59	66.3	17	6	ADA90705	Ada90705 MS-Roche
864	60	67.4	118	8	ADR38662	Adr38662 Mouse hea	936	59	66.3	17	6	ADA90907	Ada90907 MS-Roche
865	60	67.4	118	8	ADR38662	Adr38662 Mouse hea	937	59	66.3	17	6	ADA91315	Ada91315 MS-R Fab/
866	60	67.4	118	8	ADR38659	Adr38659 Mouse hea	938	59	66.3	17	6	ADA90715	Ada90715 MS-Roche
867	60	67.4	118	9	ABE46913	Abe46913 Human var	939	59	66.3	17	6	ADA90966	Ada90966 MS-R Fab/
868	60	67.4	119	7	ADG60993	Adg60993 Human ant	940	59	66.3	17	6	ADA91074	Ada91074 MS-R Fab/
869	60	67.4	119	7	ADP03976	Adp03976 Murine-ex	941	59	66.3	17	6	ADA91185	Ada91185 MS-R Fab/
870	60	67.4	120	2	AAR54802	Aar54802 SpA-react	942	59	66.3	17	6	ADA90416	Ada90416 MS-Roche
871	60	67.4	120	2	AAR54804	Aar54804 SpA-react	943	59	66.3	17	6	ADA90417	Ada90417 MS-Roche
872	60	67.4	120	2	AAR54808	Aar54808 SpA-react	944	59	66.3	17	6	ADA90588	Ada90588 MS-Roche
873	60	67.4	120	2	AAR54805	Aar54805 SpA-react	945	59	66.3	17	6	ADA90906	Ada90906 MS-Roche
874	60	67.4	120	2	AAR54807	Aar54807 SpA-react	946	59	66.3	17	6	ADA90589	Ada90589 MS-Roche
875	60	67.4	120	2	AAR54806	Aar54806 SpA-react	947	59	66.3	17	6	ADA90592	Ada90592 MS-Roche
876	60	67.4	120	2	AAR54809	Aar54809 SpA-react	948	59	66.3	17	6	ADA90597	Ada90597 MS-Roche
877	60	67.4	120	2	AAR54803	Aar54803 SpA-react	949	59	66.3	17	6	ADA91182	Ada91182 MS-R Fab/
878	60	67.4	120	2	AAR54812	Aar54812 SpA-react	950	59	66.3	17	6	ADA91197	Ada91197 MS-R Fab/
879	60	67.4	121	8	ADW95724	Adw95724 Mouse ant	951	59	66.3	17	6	ADA91303	Ada91303 MS-R Fab/
880	60	67.4	121	9	ADX15729	Adx15729 Mouse ant	952	59	66.3	17	6	ADA91384	Ada91384 MS-R Fab/
881	60	67.4	121	9	ADW95724	Adw95724 Mouse ant	953	59	66.3	17	6	ADA89985	Ada89985 Anti-Abet
882	60	67.4	123	8	ADO36393	Ado36393 Intracell	954	59	66.3	17	6	ADA90908	Ada90908 MS-Roche
883	60	67.4	124	7	ADJ80429	Adj80429 Hybrid hu	955	59	66.3	17	6	ADA91191	Ada91191 MS-R Fab/
884	60	67.4	124	9	ADW45425	Adw45425 Murine fa	956	59	66.3	17	6	ADA90590	Ada90590 MS-Roche
885	60	67.4	126	2	AAW13534	Aaw13534 Anti-mela	957	59	66.3	17	6	ADA90826	Ada90826 MS-Roche
886	60	67.4	126	7	ADW41869	Adw41869 Human ant	958	59	66.3	17	6	ADA90913	Ada90913 MS-Roche
887	60	67.4	128	9	ADZ45413	Adz45413 Murine fa	959	59	66.3	17	6	ADA91188	Ada91188 MS-R Fab/
888	60	67.4	130	2	AAW71045	Aaw71045 Peptide s	960	59	66.3	17	6	ADA90827	Ada90827 MS-Roche
889	60	67.4	132	9	ADW04770	Adw04770 PAPP-A im	961	59	66.3	17	6	ADA90837	Ada90837 MS-Roche
890	60	67.4	132	9	ADW04882	Adw04882 PAPP-A im	962	59	66.3	17	6	ADA90418	Ada90418 MS-Roche
891	60	67.4	133	8	ADO25845	Ado25845 Camelidae	963	59	66.3	17	6	ADA90420	Ada90420 MS-Roche
892	60	67.4	136	9	ADZ57715	Adz57715 Germline	964	59	66.3	17	6	ADA91068	Ada91068 MS-R Fab/
893	60	67.4	138	7	ADC61100	Adc61100 Human ant	965	59	66.3	17	6	ADA91071	Ada91071 MS-R Fab/
894	60	67.4	142	3	AAR31532	Aar31532 IN2A8 MAb	966	59	66.3	17	6	ADA90577	Ada90577 MS-Roche
895	60	67.4	144	3	AAW43857	Aaw43857 Heavy cha	967	59	66.3	17	6	ADA90596	Ada90596 MS-Roche
896	60	67.4	149	8	ADO61377	Ado61377 Camelid b	968	59	66.3	17	6	ADA90598	Ada90598 MS-Roche
897	60	67.4	170	2	AAR77306	Aar77306 Mouse mon	969	59	66.3	17	6	ADA91194	Ada91194 MS-R Fab/
898	60	67.4	227	4	AAW75051	Aaw75051 TRO005 Hu	970	59	66.3	17	6	ADA90422	Ada90422 MS-Roche
899	60	67.4	241	9	ABE46931	Abe46931 Human CD1	971	59	66.3	17	6	ADA90585	Ada90585 MS-Roche
900	60	67.4	243	5	ABP46091	Abp46091 Human Bly	972	59	66.3	17	6	ADA90586	Ada90586 MS-Roche
							973	59	66.3	17	6	ADA90593	Ada90593 MS-Roche

974 59 66.3 17 6 ADA90595  
975 59 66.3 17 6 ADA91200  
976 59 66.3 17 6 ADA91312  
977 59 66.3 17 6 ADA91387  
978 59 66.3 17 7 ADC82812  
979 59 66.3 17 7 ADP93791  
980 59 66.3 17 7 ADJ32091  
981 59 66.3 17 7 ADM07759  
982 59 66.3 17 8 AD016873  
983 59 66.3 17 8 AD058072  
984 59 66.3 17 8 ADP47149  
985 59 66.3 17 8 ADP47170  
986 59 66.3 17 8 ADQ91433  
987 59 66.3 17 8 ADS92908  
988 59 66.3 17 8 ADS82665  
989 59 66.3 17 8 ADS52406  
990 59 66.3 17 8 ADS52412  
991 59 66.3 17 8 ADU86616  
992 59 66.3 17 9 ADW87167  
993 59 66.3 17 9 ADW87259  
994 59 66.3 17 9 ADW87265  
995 59 66.3 17 9 ADW87253  
996 59 66.3 17 9 ADW77425  
997 59 66.3 17 9 ADW77337  
998 59 66.3 17 9 AEA45672  
999 59 66.3 17 9 AEA46300  
1000 59 66.3 17 9 AEA46292

## ALIGNMENTS

RESULT 1  
ID AAB81980 standard; peptide; 17 AA.

XX  
AC AAB81980;

DT 03-JUL-2001 (first entry)

DE Ganglioside GD3 specific antibody related peptide SEQ ID NO: 4.

XX Ganglioside; GD3; complementarity determining region; CDR; antibody;  
KW cancer.

XX Mus musculus.

OS WO200123432-A1.

XX  
PD 05-APR-2001.

PF 29-SEP-2000; 2000WO-JP006774.

XX  
PR 30-SEP-1999; 99JP-00278291.

PR 06-APR-2000; 2000JP-00105088.

XX  
PA (KYOW ) KYOWA HAKKO KOGYO KK.

XX  
PI Hanai N, Shitara K, Nakamura K, Niwa R;

XX  
DR WPI; 2001-266143/27.

XX New human type complementation-determining region-transplanted antibody  
PT and derivatives against ganglioside GD3, useful in diagnosis and therapy  
PT of e.g. tumors, with low antigenicity, little side effects but potent  
PT activity in cancer.

XX  
PS Claim 5; Page 141; 183pp; Japanese.

XX The present invention describes a monoclonal antibody which can react  
CC specifically with ganglioside GD3. The antibody and its derivatives are  
CC useful in the diagnosis and therapy of tumors, particularly cancer  
CC diagnosis. The present sequence is a protein used in the exemplification

Ada90595 MS-Roche  
Ada91200 MS-R Fab/  
Ada91312 MS-R Fab/  
Ada91387 MS-R Fab/  
ADC82812 CDR regio  
ADP93791 Antibody  
ADJ32091 Human int  
ADM07759 Canine im  
AD016873 Murine an  
AD058072 S2 cell d  
ADP47149 Human pho  
ADP47170 Human pho  
ADQ91433 CDR2 of t  
ADS92908 Human Myo  
ADS82665 Anti-IL-2  
ADS52406 Fab targe  
ADU86616 Peptide d  
ADW87167 Anti-huma  
ADW87259 Anti-huma  
ADW87265 Anti-huma  
ADW87253 Anti-huma  
ADW77425 Human pia  
ADW77337 Human pia  
AEA45672 Apolipopr  
AEA46300 Apolipopr  
AEA46292 Apolipopr

CC of the invention  
XX  
SQ Sequence 17 AA;

Query Match 100.0%; Score 89; DB 4; Length 17;  
Best Local Similarity 100.0%; Pred. No. 5e-06;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YISGGSGTYSDSVKG 17  
|||||

Db 1 YISGGSGTYSDSVKG 17  
|||||

RESULT 2

ABU11005  
ID ABU11005 standard; peptide; 17 AA.

XX  
AC ABU11005;

DT 04-FEB-2003 (first entry)

DE Modified ganglioside GD3 antibody associated peptide #2.

XX Ganglioside GD3; anti-ganglioside GD3 antibody; tumour; melanoma.

XX Mus musculus.

XX WO200278739-A1.

XX  
PD 10-OCT-2002.

PF 29-MAR-2002; 2002WO-JP003170.

PR 29-MAR-2001; 2001JP-00097483.

XX  
PA (KYOW ) KYOWA HAKKO KOGYO KK.

XX  
PI Shitara K, Niwa R, Kanazawa J, Asada M;

XX  
DR WPI; 2003-067410/06.

XX Drugs containing genetically-modified antibody against ganglioside GD3,  
PT its fragment, immunocompetent cell activators or/and antitumor agents in  
PT combination, applicable in treating malignant tumor like melanoma.

XX  
PS Claim 6; Page 98; 121pp; Japanese.

XX The invention describes drugs contain a genetically-modified antibody  
CC against ganglioside GD3 or its fragment and at least 1 of a substance  
CC capable of activating immunocompetent cells and a substance having an  
CC antitumor activity in combination. The drugs can be used to treat tumour  
CC like melanoma and can provide a treatment with enhanced therapeutic  
CC effect and little side-reactions, particularly to relieve problems of  
CC side-effects during the conventional single administration. This sequence  
CC represents a peptide associated with the anti- ganglioside GD3 antibody

XX  
SQ Sequence 17 AA;

Query Match 100.0%; Score 89; DB 6; Length 17;  
Best Local Similarity 100.0%; Pred. No. 5e-06;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YISGGSGTYSDSVKG 17  
|||||

Db 1 YISGGSGTYSDSVKG 17  
|||||

RESULT 3

ADZ57811  
ID ADZ57811 standard; peptide; 17 AA.

XX  
AC ADZ57811;

DT 30-JUN-2005 (first entry)  
 XX Ganglioside GD3 binding antibody associated CDR2 SEQ ID NO 15.  
 DE cytostatic; antibody engineering; cancer; neoplasm; ganglioside; GD3;  
 XX pharmaceutical.  
 KW Mus musculus.  
 XX WO2005035577-A1.  
 XX 21-APR-2005.  
 XX 08-OCT-2004; 2004WO-JP015314.  
 XX 08-OCT-2003; 2003JP-00350161.  
 XX (KYOW ) KYOWA HAKKO KOGYO KK.  
 XX Iida S, Satoh M, Urakubo M, Wakitani M, Uchida K, Niwa R;  
 PI Shitara K;  
 XX WPI; 2005-346195/35.  
 XX Antibody composition for treating ganglioside GD3 associated disease e.g.  
 PT cancer, comprises genetically modified antibody molecule, which  
 PT specifically binds to ganglioside GD3 and has N-glycoside-binding sugar  
 PT chain in its Fc domain.  
 XX Claim 8; SEQ ID NO 15; 124pp; Japanese.  
 PS The invention describes an antibody composition (I), comprising a  
 CC genetically modified antibody molecule which specifically binds to  
 CC ganglioside GD3 and has an N-glycoside-binding complex sugar chain in its  
 CC Fc domain, where the N-glycoside-binding complex sugar chain is a sugar  
 CC chain having no fucose attached to N-acetylglucosamine at the reducing  
 CC end of the sugar chain. Also described are: a transformant (II) capable  
 CC of producing (I), obtained by introducing DNA that encodes the antibody  
 CC molecule which specifically binds with ganglioside GD3, to a host cell;  
 CC producing (I), involving cultivating (I) in a culture medium, such that  
 CC C1 (sic) is produced and accumulated in the culture, extracting and  
 CC purifying C1 from the culture medium; a pharmaceutical (III) containing  
 CC C1 as an active ingredient; and a therapeutic agent (A1) for ganglioside  
 CC GD3 associated disease, comprising C1 as an active ingredient. (I) is  
 CC useful for treating GD3 associated diseases, which involves administering  
 CC (I), where the GD3 associated diseases is cancer. (A1) is also useful for  
 CC treating GD3 associated disease. (II) is useful for producing (I). (I) is  
 CC useful for manufacturing a therapeutic agent for GD3 associated disease.  
 CC This sequence represents a ganglioside GD3 binding antibody associated  
 CC peptide.  
 XX Sequence 17 AA;  
 SQ Query Match 100.0%; Score 89; DB 9; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 5e-06;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YISGGSGTYYSDSVKG 17  
 Db |||||  
 1 YISGGSGTYYSDSVKG 17  
 RESULT 4  
 AAB81985  
 ID AAB81985 standard; protein; 119 AA.  
 XX AC AAB81985;  
 XX 03-JUL-2001 (first entry)  
 DT Ganglioside GD3 specific antibody related protein SEQ ID NO: 9.  
 DE Ganglioside; GD3; complementarity determining region; CDR; antibody;  
 KW Ganglioside; GD3; complementarity determining region; CDR; antibody;

KW cancer.  
 XX OS Synthetic.  
 XX WO200123432-A1.  
 XX 05-APR-2001.  
 XX 29-SEP-2000; 2000WO-JP006774.  
 XX 30-SEP-1999; 99JP-00278291.  
 PR 06-APR-2000; 2000JP-00105088.  
 XX (KYOW ) KYOWA HAKKO KOGYO KK.  
 XX Hanai N, Shitara K, Nakamura K, Niwa R;  
 PI WPI; 2001-266143/27.  
 XX New human type complementation-determining region-transplanted antibody  
 PT and derivatives against ganglioside GD3, useful in diagnosis and therapy  
 PT of e.g. tumors, with low antigenicity, little side effects but potent  
 PT activity in cancer.  
 XX Claim 20; Page 142-143; 183pp; Japanese.  
 PS The present invention describes a monoclonal antibody which can react  
 CC specifically with ganglioside GD3. The antibody and its derivatives are  
 CC useful in the diagnosis and therapy of tumors, particularly cancer  
 CC diagnosis. The present sequence is a protein used in the exemplification  
 CC of the invention  
 XX Sequence 119 AA;  
 SQ Query Match 100.0%; Score 89; DB 4; Length 119;  
 Best Local Similarity 100.0%; Pred. No. 4e-05;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YISGGSGTYYSDSVKG 17  
 Db |||||  
 50 YISGGSGTYYSDSVKG 66  
 RESULT 5  
 AAB81989  
 ID AAB81989 standard; protein; 119 AA.  
 XX AC AAB81989;  
 XX 03-JUL-2001 (first entry)  
 DT Ganglioside GD3 specific antibody related protein SEQ ID NO: 55.  
 DE Ganglioside; GD3; complementarity determining region; CDR; antibody;  
 KW Ganglioside; GD3; complementarity determining region; CDR; antibody;  
 XX Mus musculus.  
 XX WO200123432-A1.  
 XX 05-APR-2001.  
 XX 29-SEP-2000; 2000WO-JP006774.  
 XX 30-SEP-1999; 99JP-00278291.  
 PR 06-APR-2000; 2000JP-00105088.  
 XX (KYOW ) KYOWA HAKKO KOGYO KK.  
 XX Hanai N, Shitara K, Nakamura K, Niwa R;  
 PI WPI; 2001-266143/27.  
 XX



PT New human type complementation-determining region-transplanted antibody  
PT and derivatives against ganglioside GD3, useful in diagnosis and therapy  
PT of e.g. tumors, with low antigenicity, little side effects but potent  
PT activity in cancer.

XX Claim 10; Page 173-174; 183pp; Japanese.

XX The present invention describes a monoclonal antibody which can react  
CC specifically with ganglioside GD3. The antibody and its derivatives are  
CC useful in the diagnosis and therapy of tumors, particularly cancer  
CC diagnosis. The present sequence is a protein used in the exemplification  
CC of the invention

XX Sequence 119 AA;

Query Match 100.0%; Score 89; DB 4; Length 119;  
Best Local Similarity 100.0%; Pred. No. 4e-05;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YISSGGSGTYYSVSKG 17  
DB 50 YISSGGSGTYYSVSKG 66

RESULT 6

ABU11012  
ID ABU11012 standard; protein; 119 AA.

XX AC ABU11012;

XX DT 04-FEB-2003 (first entry)

XX DE Modified ganglioside GD3 antibody associated protein #5.

XX KW Ganglioside GD3; anti-ganglioside GD3 antibody; tumour; melanoma.

XX OS Mus musculus.

XX PN WO200278739-A1.

XX PD 10-OCT-2002.

XX PF 29-MAR-2002; 2002WO-JP003170.

XX PR 29-MAR-2001; 2001JP-00097483.

XX PA (KYOW ) KYOWA HAKKO KOGYO KK.

XX PI Shitara K, Niwa R, Kanazawa J, Asada M;

XX WPI; 2003-067410/06.

XX Drugs containing genetically-modified antibody against ganglioside GD3,  
PT its fragment, immunocompetent cell activators or/and antitumor agents in  
PT combination, applicable in treating malignant tumor like melanoma.

PS Claim 7; Page 112-113; 121pp; Japanese.

XX The invention describes drugs contain a genetically-modified antibody  
CC against ganglioside GD3 or its fragment and at least 1 of a substance  
CC capable of activating immunocompetent cells and a substance having an  
CC antitumor activity in combination. The drugs can be used to treat tumour  
CC like melanoma and can provide a treatment with enhanced therapeutic  
CC effect and little side-reactions, particularly to relieve problems of  
CC side-effects during the conventional single administration. This sequence  
CC represents a protein associated with the anti- ganglioside GD3 antibody

XX Sequence 119 AA;

Query Match 100.0%; Score 89; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 4e-05;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YISSGGSGTYYSVSKG 17  
DB 50 YISSGGSGTYYSVSKG 66

RESULT 7

ABU11010  
ID ABU11010 standard; protein; 119 AA.

XX AC ABU11010;

XX DT 04-FEB-2003 (first entry)

XX DE Modified ganglioside GD3 antibody associated protein #3.

XX KW Ganglioside GD3; anti-ganglioside GD3 antibody; tumour; melanoma.

XX OS Synthetic.

XX PN WO200278739-A1.

XX PD 10-OCT-2002.

XX PF 29-MAR-2002; 2002WO-JP003170.

XX PR 29-MAR-2001; 2001JP-00097483.

XX PA (KYOW ) KYOWA HAKKO KOGYO KK.

XX PI Shitara K, Niwa R, Kanazawa J, Asada M;

XX WPI; 2003-067410/06.

XX Drugs containing genetically-modified antibody against ganglioside GD3,  
PT its fragment, immunocompetent cell activators or/and antitumor agents in  
PT combination, applicable in treating malignant tumor like melanoma.

PS Claim 8; Page 99; 121pp; Japanese.

XX The invention describes drugs contain a genetically-modified antibody  
CC against ganglioside GD3 or its fragment and at least 1 of a substance  
CC capable of activating immunocompetent cells and a substance having an  
CC antitumor activity in combination. The drugs can be used to treat tumour  
CC like melanoma and can provide a treatment with enhanced therapeutic  
CC effect and little side-reactions, particularly to relieve problems of  
CC side-effects during the conventional single administration. This sequence  
CC represents a protein associated with the anti- ganglioside GD3 antibody

XX Sequence 119 AA;

Query Match 100.0%; Score 89; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 4e-05;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YISSGGSGTYYSVSKG 17  
DB 50 YISSGGSGTYYSVSKG 66

RESULT 8

ADZ57816  
ID ADZ57816 standard; protein; 119 AA.

XX AC ADZ57816;

XX DT 30-JUN-2005 (first entry)

XX DE Ganglioside GD3 binding antibody associated protein SEQ ID NO 20.

XX KW cytostatic; antibody engineering; cancer; neoplasm; ganglioside; GD3;  
XX pharmaceutical.

XX OS Mus musculus.



XX WO2005035577-A1.  
 PN  
 XX  
 XX  
 PD 21-APR-2005.  
 XX  
 XX  
 PF 08-OCT-2004; 2004WO-JP015314.  
 XX  
 PR 08-OCT-2003; 2003JP-00350161.  
 XX  
 XX (KYOW ) KYOWA HAKKO KOGYO KK.  
 PA  
 XX Iida S, Satoh M, Urakubo M, Wakitani M, Uchida K, Niwa R;  
 PI Shitara K;  
 XX  
 DR WPI; 2005-346195/35.  
 XX  
 PT Antibody composition for treating ganglioside GD3 associated disease e.g.  
 PT cancer, comprises genetically modified antibody molecule, which  
 PT specifically binds to ganglioside GD3 and has N-glycoside-binding sugar  
 PT chain in its Fc domain.  
 XX  
 PS Claim 13; SEQ ID NO 20; 124pp; Japanese.  
 XX  
 CC The invention describes an antibody composition (I), comprising a  
 CC genetically modified antibody molecule which specifically binds to  
 CC ganglioside GD3 and has an N-glycoside-binding complex sugar chain in its  
 CC Fc domain, where the N-glycoside-binding complex sugar chain is a sugar  
 CC chain having no fucose attached to N-acetylglucosamine at the reducing  
 CC end of the sugar chain. Also described are: a transformant (II) capable  
 CC of producing (I), obtained by introducing DNA that encodes the antibody  
 CC molecule which specifically binds with ganglioside GD3, to a host cell;  
 CC producing (I), involving cultivating (I) in a culture medium, such that  
 CC Cl (sic) is produced and accumulated in the culture, extracting and  
 CC purifying Cl from the culture medium; a pharmaceutical (III) containing  
 CC Cl as an active ingredient; and a therapeutic agent (A1) for ganglioside  
 CC GD3 associated disease, comprising Cl as an active ingredient. (I) is  
 CC useful for treating GD3 associated disease, which involves administering  
 CC (I), where the GD3 associated diseases is cancer. (A1) is also useful for  
 CC treating GD3 associated disease. (II) is useful for producing (I). (I) is  
 CC useful for manufacturing a therapeutic agent for GD3 associated disease.  
 CC This sequence represents a ganglioside GD3 binding antibody associated  
 CC protein.  
 XX  
 SQ Sequence 119 AA;  
 Query Match 100.0%; Score 89; DB 9; Length 119;  
 Best Local Similarity 100.0%; Pred. No. 4e-05;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YISGGSGTYSDSVKG 17  
 DB 50 YISGGSGTYSDSVKG 66  
 RESULT 9  
 ADZ57818  
 ID ADZ57818 standard; protein; 119 AA.  
 XX  
 XX ADZ57818;  
 AC  
 DT 30-JUN-2005 (first entry)  
 XX  
 DE Ganglioside GD3 binding antibody associated protein SEQ ID NO 22.  
 XX  
 KW cytostatic; antibody engineering; cancer; neoplasm; ganglioside; GD3;  
 KW pharmaceutical.  
 XX  
 OS Synthetic.  
 OS  
 PN WO2005035577-A1.  
 XX  
 PD 21-APR-2005.  
 XX

PF 08-OCT-2004; 2004WO-JP015314.  
 XX  
 PR 08-OCT-2003; 2003JP-00350161.  
 XX  
 PA (KYOW ) KYOWA HAKKO KOGYO KK.  
 XX  
 PI Iida S, Satoh M, Urakubo M, Wakitani M, Uchida K, Niwa R;  
 PI Shitara K;  
 XX  
 DR WPI; 2005-346195/35.  
 XX  
 XX Antibody composition for treating ganglioside GD3 associated disease e.g.  
 PT cancer, comprises genetically modified antibody molecule, which  
 PT specifically binds to ganglioside GD3 and has N-glycoside-binding sugar  
 PT chain in its Fc domain.  
 XX  
 PS Claim 19; SEQ ID NO 22; 124pp; Japanese.  
 XX  
 CC The invention describes an antibody composition (I), comprising a  
 CC genetically modified antibody molecule which specifically binds to  
 CC ganglioside GD3 and has an N-glycoside-binding complex sugar chain in its  
 CC Fc domain, where the N-glycoside-binding complex sugar chain is a sugar  
 CC chain having no fucose attached to N-acetylglucosamine at the reducing  
 CC end of the sugar chain. Also described are: a transformant (II) capable  
 CC of producing (I), obtained by introducing DNA that encodes the antibody  
 CC molecule which specifically binds with ganglioside GD3, to a host cell;  
 CC producing (I), involving cultivating (I) in a culture medium, such that  
 CC Cl (sic) is produced and accumulated in the culture, extracting and  
 CC purifying Cl from the culture medium; a pharmaceutical (III) containing  
 CC Cl as an active ingredient; and a therapeutic agent (A1) for ganglioside  
 CC GD3 associated disease, comprising Cl as an active ingredient. (I) is  
 CC useful for treating GD3 associated disease, which involves administering  
 CC (I), where the GD3 associated diseases is cancer. (A1) is also useful for  
 CC treating GD3 associated disease. (II) is useful for producing (I). (I) is  
 CC useful for manufacturing a therapeutic agent for GD3 associated disease.  
 CC This sequence represents a ganglioside GD3 binding antibody associated  
 CC protein.  
 XX  
 SQ Sequence 119 AA;  
 Query Match 100.0%; Score 89; DB 9; Length 119;  
 Best Local Similarity 100.0%; Pred. No. 4e-05;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YISGGSGTYSDSVKG 17  
 DB 50 YISGGSGTYSDSVKG 66  
 RESULT 10  
 ADZ57821  
 ID ADZ57821 standard; protein; 119 AA.  
 XX  
 XX ADZ57821;  
 AC  
 DT 30-JUN-2005 (first entry)  
 XX  
 DE Ganglioside GD3 binding antibody associated protein SEQ ID NO 25.  
 XX  
 KW cytostatic; antibody engineering; cancer; neoplasm; ganglioside; GD3;  
 KW pharmaceutical.  
 XX  
 OS Synthetic.  
 OS  
 PN WO2005035577-A1.  
 XX  
 PD 21-APR-2005.  
 XX  
 PF 08-OCT-2004; 2004WO-JP015314.  
 XX  
 PR 08-OCT-2003; 2003JP-00350161.  
 XX  
 XX (KYOW ) KYOWA HAKKO KOGYO KK.  
 PA

XX Iida S, Satoh M, Uzakubo M, Wakitani M, Uchida K, Niwa R;  
 PI Shitara K;  
 XX WPI; 2005-346195/35.  
 XX  
 XX Antibody composition for treating ganglioside GD3 associated disease e.g.  
 PT cancer, comprises genetically modified antibody molecule, which  
 PT specifically binds to ganglioside GD3 and has N-glycoside-binding sugar  
 PT chain in its Fc domain.  
 XX  
 XX Claim 24; SEQ ID NO 25; 124pp; Japanese.  
 PS  
 XX The invention describes an antibody composition (I), comprising a  
 CC genetically modified antibody molecule which specifically binds to  
 CC ganglioside GD3 and has an N-glycoside-binding complex sugar chain in its  
 CC Fc domain, where the N-glycoside-binding complex sugar chain is a sugar  
 CC chain having no fucose attached to N-acetylglucosamine at the reducing  
 CC end of the sugar chain. Also described are: a transformant (II) capable  
 CC of producing (I), obtained by introducing DNA that encodes the antibody  
 CC molecule which specifically binds with ganglioside GD3, to a host cell;  
 CC producing (I), involving cultivating (I) in a culture medium, such that  
 CC C1 (a) is produced and accumulated in the culture, extracting and  
 CC purifying C1 from the culture medium; a pharmaceutical (III) containing  
 CC C1 as an active ingredient; and a therapeutic agent (A1) for ganglioside  
 CC GD3 associated disease, comprising C1 as an active ingredient. (I) is  
 CC useful for treating GD3 associated disease, which involves administering  
 CC (I), where the GD3 associated disease is cancer. (A1) is also useful for  
 CC treating GD3 associated disease. (II) is useful for producing (I). (I) is  
 CC useful for manufacturing a therapeutic agent for GD3 associated disease.  
 CC This sequence represents a ganglioside GD3 binding antibody associated  
 CC protein.  
 XX  
 XX Sequence 119 AA;  
 SQ  
 Query Match 100.0%; Score 89; DB 9; Length 119;  
 Best Local Similarity 100.0%; Pred. No. 4e-05;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YISSGGSGTYSDSVKG 17  
 Db 50 YISSGGSGTYSDSVKG 66  
 RESULT 11  
 AAR33256  
 ID AAR33256 standard; protein; 130 AA.  
 AC  
 XX AAR33256;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 12-JUL-1993 (first entry)  
 XX  
 XX Rat immunoglobulin H chain variable region of pKM641HA3.  
 XX  
 XX Promoter; variable; region; rat; immunoglobulin; heavy; H; chain;  
 KW humanised; chimeric; antibody; expression vector.  
 XX  
 XX Rattus rattus.  
 OS  
 XX  
 XX Key Location/Qualifiers  
 FH Peptide 1..10  
 FT Protein /note= "signal peptide"  
 FT 11..130  
 FT /note= "Mature protein"  
 XX  
 XX EP533199-A2.  
 XX  
 XX 24-MAR-1993.  
 XX  
 XX 18-SEP-1992; 92EP-00116026.  
 XX  
 XX 18-SEP-1991; 91JP-00238375.

XX (KYOW ) KYOWA HAKKO KOGYO CO LTD.  
 PA Shitara K, Hanai N, Hasegawa M, Miyaji H, Kuwana Y;  
 PI  
 XX WPI; 1993-095510/12.  
 DR N-PSDB; AAQ33257.  
 XX  
 XX Humanised chimeric antibody prodn. against ganglioside GD3 - for treating  
 PT cancers, such as melanoma, neuroblastoma, etc.  
 PT  
 XX Claim 6; Page 29-30; 63pp; English.  
 PS  
 XX The sequences given in AAR33256-57 represent rat heavy and light chain  
 CC variable regions respectively. The DNA sequences encoding these proteins  
 CC were used in the construction of humanised chimeric antibody expression  
 CC vectors. In these humanised antibodies none of the amino acids of the non  
 CC -human animal Ab variable region have been changed. (Updated on 25-MAR-  
 CC 2003 to correct PN field.)  
 XX  
 XX Sequence 130 AA;  
 SQ  
 Query Match 100.0%; Score 89; DB 2; Length 130;  
 Best Local Similarity 100.0%; Pred. No. 4.4e-05;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YISSGGSGTYSDSVKG 17  
 Db 60 YISSGGSGTYSDSVKG 76  
 RESULT 12  
 AAR53341  
 ID AAR53341 standard; protein; 130 AA.  
 XX  
 AC AAR53341;  
 XX  
 DT 18-NOV-1994 (first entry)  
 XX  
 XX KM641 L chain variable region.  
 DE  
 XX Monoclonal antibody; Ab; ganglioside GM2; chimera; chimeric antibody;  
 KW expression vector; heavy; light; chain; hypervariable region; CDR;  
 KW constant region; hybridoma; Ig; immunoglobulin; promoter; enhancer.  
 XX  
 XX Mus musculus.  
 OS  
 XX  
 XX Key Location/Qualifiers  
 FH Peptide 1..10  
 FT /label= sig\_peptide  
 XX  
 XX AU9346181-A.  
 PN  
 XX 17-MAR-1994.  
 PD  
 XX 07-SEP-1993; 93AU-00046181.  
 PF  
 XX 07-SEP-1992; 92JP-00238452.  
 PR  
 XX (KYOW ) KYOWA HAKKO KOGYO KK.  
 PA  
 XX Nakamura K, Koike M, Shitara K, Hanai N, Kuwana Y, Hasegawa M;  
 PI  
 XX WPI; 1994-126857/16.  
 DR N-PSDB; AAQ45439.  
 XX  
 XX Humanised antibody specific for ganglioside GM2 - used for producing a  
 PT cytotoxic effect on cancers such as melanoma, neuroblastoma and glioma.  
 PT  
 XX Example 2; Page 116-117; 191pp; English.  
 PS  
 XX Example 2 describes the construction of the vector pCh1641HA1 for  
 CC chimeric human antibody H chain expression. mRNA from mouse anti-GD3

CC monoclonal Ab KM641-producing cells was isolated and KM641 H and L chain  
 CC cDNAs isolated. The base sequences of the Ig variable regions in KM641 H  
 CC chain cDNA (pKM641HA3) and KM641 L chain cDNA (pKM641LA2) are given in  
 CC AAQ5438-39. A KM641-derived chimeric human Ab H chain expression vector  
 CC was constructed by joining the H chain variable region gene from  
 CC pKM641HA3 to a vector for chimeric human Ab H chain expression using the  
 CC synthetic DNAs given in AAQ63439 and AAQ63440  
 XX  
 SQ Sequence 130 AA;

Query Match 100.0%; Score 89; DB 2; Length 130;  
 Best Local Similarity 100.0%; Pred. No. 4.4e-05;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YISGGSGTYYSDSVKG 17  
 |||||  
 Db 60 YISGGSGTYYSDSVKG 76

## RESULT 13

AAAY28369  
 ID AAY28369 standard; protein; 130 AA.

XX AC AAY28369;

XX DT 04-NOV-1999 (first entry)

XX DE pKM641 HA3 immunoglobulin heavy chain.

XX antibody; nucleotide; genomic; hypervariable region; chimeric;  
 KW light chain; amino acid.

XX OS Mus sp.

XX FN US939532-A.

XX PD 17-AUG-1999.

XX PF 07-JUN-1995; 95US-00483528.

XX PR 07-SEP-1993; 93US-00116778.

XX PA (KYOW ) KYOWA HAKKO KOGYO KK.

XX PI Nakamura K, Hanai N, Kuwana Y, Hasegawa M, Koike M, Shitara K;

XX WPI; 1999-468416/39.

XX DR N-PSDB; AAX99482.

XX PT Chimeric human antibody expression vectors.

XX PS Example 1; Col 99-101; 188pp; English.

XX This immunoglobulin region was isolated from pKM641HA3. This sequence has  
 CC no methionine initiation codon and the leader sequence was partly  
 CC lacking. The chimeric human antibodies are useful in the treatment of  
 CC cancer, especially that which is of neural ectodermal origin. In contrast  
 CC to prior art constructs based on mouse monoclonal antibodies, the  
 CC chimeric human antibodies do not cause anti-mouse immunoglobulin  
 CC production. The chimeric human antibodies have a prolonged half-life and  
 CC a reduced frequency of adverse effects when compared to mouse monoclonal  
 CC antibodies

XX SQ Sequence 130 AA;

Query Match 100.0%; Score 89; DB 2; Length 130;  
 Best Local Similarity 100.0%; Pred. No. 4.4e-05;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YISGGSGTYYSDSVKG 17  
 |||||  
 Db 60 YISGGSGTYYSDSVKG 76

## RESULT 14

AAAB01627  
 ID AAB01627 standard; protein; 130 AA.

XX AC AAB01627;

XX DT 07-DEC-2000 (first entry)

XX DE Murine immunoglobulin heavy chain variable region.

XX KW Mouse; immunoglobulin; H chain; heavy chain; variable region; cancer;  
 KW humanised antibody.

XX OS Mus sp.

XX FH Key Location/Qualifiers  
 FT Peptide 1..10  
 FT /label= signal\_peptide

FT Protein 11..130

FT /label= mature\_immunoglobulin\_heavy\_chain\_variable region

XX FN EP1013761-A2.

XX PD 28-JUN-2000.

XX PF 18-SEP-1992; 99EP-00124345.

XX PR 18-SEP-1991; 91JP-00238375.

XX PR 18-SEP-1992; 92EP-00116026.

XX PA (KYOW ) KYOWA HAKKO KOGYO KK.

XX PI Shitara K, Hanai N, Hasegawa M, Miyaji H, Kuwana Y;

XX WPI; 2000-402204/35.

XX DR N-PSDB; AAA51003.

XX PT New humanized chimera antibody KM-871 useful for treating cancer,  
 PT comprises variable region of mouse monoclonal antibody, reactive with  
 PT ganglioside and human antibody constant region.

XX PS Claim 14; Page 27-28; 65pp; English.

XX The present sequence is a murine immunoglobulin heavy chain variable  
 CC region from plasmid KM-641. The coding sequence was used in the creation  
 CC of an expression vector, along with the sequence for a human antibody, to  
 CC produce humanised chimaeric antibodies, which can be used to treat  
 CC cancer. Humanised chimaeric antibodies are more effective than mouse  
 CC antibodies as they do not provoke a reaction in the human and side  
 CC effects, such as the formation of anti-mouse immunoglobulin antibody and  
 CC the rapid half-life of the immunoglobulins, do not occur

XX SQ Sequence 130 AA;

Query Match 100.0%; Score 89; DB 3; Length 130;  
 Best Local Similarity 100.0%; Pred. No. 4.4e-05;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YISGGSGTYYSDSVKG 17  
 |||||  
 Db 60 YISGGSGTYYSDSVKG 76

## RESULT 15

AAAB81977  
 ID AAB81977 standard; protein; 138 AA.

XX AC AAB81977;

XX DT 03-JUL-2001 (first entry)

XX DE Ganglioside GD3 specific antibody related protein SEQ ID NO: 1.

XX Ganglioside; GD3; complementarity determining region; CDR; antibody;  
KW cancer.  
XX Mus musculus.  
OS WO200123432-A1.  
XX  
XX PD 05-APR-2001.  
XX PF 29-SEP-2000; 2000WO-JP006774.  
XX PR 30-SEP-1999; 99JP-00278291.  
XX PR 06-APR-2000; 2000JP-00105088.  
XX PA (KYOW ) KYOWA HAKKO KOGYO KK.  
XX PI Hanai N, Shitara K, Nakamura K, Niwa R;  
XX WPI; 2001-266143/27.  
XX PT New human type complementation-determining region-transplanted antibody  
PT and derivatives against ganglioside GD3; useful in diagnosis and therapy  
PT of e.g. tumors, with low antigenicity, little side effects but potent  
PT activity in cancer.  
XX Example 1; Page 138-139; 183pp; Japanese.  
XX CC The present invention describes a monoclonal antibody which can react  
CC specifically with ganglioside GD3. The antibody and its derivatives are  
CC useful in the diagnosis and therapy of tumors, particularly cancer  
CC diagnosis. The present sequence is a protein used in the exemplification  
CC of the invention  
XX SQ Sequence 138 AA;  
Query Match 100.0%; Score 89; DB 4; Length 138;  
Best Local Similarity 100.0%; Pred. No. 4.7e-05;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 YISGGSGTYYSVSKG 17  
Db 69 YISGGSGTYYSVSKG 85  
RESULT 16  
ABU11002  
ID ABU11002 standard; protein; 138 AA.  
XX AC ABU11002;  
XX DT 04-FEB-2003 (first entry)  
XX DE Modified ganglioside GD3 antibody associated protein #1.  
XX KW Ganglioside GD3; anti-ganglioside GD3 antibody; tumour; melanoma.  
XX OS Mus musculus.  
XX PN WO200278739-A1.  
XX PD 10-OCT-2002.  
XX PF 29-MAR-2002; 2002WO-JP003170.  
XX PR 29-MAR-2001; 2001JP-00097483.  
XX PA (KYOW ) KYOWA HAKKO KOGYO KK.  
XX PI Shitara K, Niwa R, Kanazawa J, Asada M;  
XX WPI; 2003-067410/06.  
XX

PT Drugs containing genetically-modified antibody against ganglioside GD3,  
PT its fragment, immunocompetent cell activators or/and antitumor agents in  
PT combination, applicable in treating malignant tumor like melanoma.  
XX Example 3; Page 97; 121pp; Japanese.  
XX CC The invention describes drugs contain a genetically-modified antibody  
CC against ganglioside GD3 or its fragment and at least 1 of a substance  
CC capable of activating immunocompetent cells and a substance having an  
CC antitumor activity in combination. The drugs can be used to treat tumour  
CC like melanoma and can provide a treatment with enhanced therapeutic  
CC effect and little side-reactions, particularly to relieve problems of  
CC side-effects during the conventional single administration. This sequence  
CC represents a protein associated with the anti- ganglioside GD3 antibody  
XX SQ Sequence 138 AA;  
Query Match 100.0%; Score 89; DB 6; Length 138;  
Best Local Similarity 100.0%; Pred. No. 4.7e-05;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 YISGGSGTYYSVSKG 17  
Db 69 YISGGSGTYYSVSKG 85  
RESULT 17  
AAB81987  
ID AAB81987 standard; protein; 582 AA.  
XX AC AAB81987;  
XX DT 03-JUL-2001 (first entry)  
XX DE Ganglioside GD3 specific antibody related protein SEQ ID NO: 53.  
XX KW Ganglioside; GD3; complementarity determining region; CDR; antibody;  
XX cancer.  
XX OS Synthetic.  
XX PN WO200123432-A1.  
XX PD 05-APR-2001.  
XX PF 29-SEP-2000; 2000WO-JP006774.  
XX PR 30-SEP-1999; 99JP-00278291.  
XX PR 06-APR-2000; 2000JP-00105088.  
XX PA (KYOW ) KYOWA HAKKO KOGYO KK.  
XX PI Hanai N, Shitara K, Nakamura K, Niwa R;  
XX WPI; 2001-266143/27.  
XX PT New human type complementation-determining region-transplanted antibody  
PT and derivatives against ganglioside GD3; useful in diagnosis and therapy  
PT of e.g. tumors, with low antigenicity, little side effects but potent  
PT activity in cancer.  
XX PS Claim 41; Page 168-172; 183pp; Japanese.  
XX CC The present invention describes a monoclonal antibody which can react  
CC specifically with ganglioside GD3. The antibody and its derivatives are  
CC useful in the diagnosis and therapy of tumors, particularly cancer  
CC diagnosis. The present sequence is a protein used in the exemplification  
CC of the invention  
XX SQ Sequence 582 AA;  
Query Match 100.0%; Score 89; DB 4; Length 582;  
Best Local Similarity 100.0%; Pred. No. 0.00022;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		KW chimeric antibody; antibody engineering; monoclonal antibody; Mab;	
QY	1 YISSGGSGTYSDSVKG 17	XX SK48-E26; inflammation; therapy.	
Db	50 YISSGGSGTYSDSVKG 66	OS Homo, sapiens.	
		OS Mus sp.	
		OS Chimeric.	
RESULT 18		XX Key	Location/Qualifiers
AAB81991		FT Region	1..30
ID AAB81991 standard; protein; 582 AA.		FT	/label= FR1
XX		FT	/note= "framework region 1"
AC AAB81991;		FT	31..35
XX		FT	/label= CDR1
DT 03-JUL-2001 (first entry)		FT	/note= "complementarity determining region 1 (Claim 10,
XX		FT	page 48)"
DE Ganglioside GD3 specific antibody related protein SEQ ID NO: 57.		FT	36..49
XX		FT	/label= FR2
KW Ganglioside; GD3; complementarity determining region; CDR; antibody;		FT	/note= "framework region 2"
KW cancer.		FT	50..66
XX Synthetic.		FT	/label= CDR2
OS		FT	/note= "complementarity determining region 2 (Claim 10,
XX		FT	page 48)"
PN WO200123432-A1.		FT	67..98
XX		FT	/label= FR3
PD 05-APR-2001.		FT	/note= "framework region 3"
XX		FT	99..108
PF 29-SEP-2000; 2000WO-JP006774.		FT	/label= CDR3
XX		FT	/note= "complementarity determining region 3 (Claim 10,
PR 30-SEP-1999; 99JP-00278291.		FT	page 48)"
PR 06-APR-2000; 2000JP-00105088.		FT	109..119
XX		FT	/label= FR4
PA (KYOW ) KYOWA HAKKO KOGYO KK.		FT	/note= "framework region 4"
XX		XX	WO9501997-A1.
PI Hanai N, Shitara K, Nakamura K, Niwa R;		PN	
XX		XX	19-JAN-1995.
DR WPI; 2001-266143/27.		PD	
XX		XX	07-JUL-1994; 94WO-US007659.
PT New human type complementation-determining region-transplanted antibody		PF	
PT and derivatives against ganglioside GD3, useful in diagnosis and therapy		XX	
PT of e.g. tumors, with low antigenicity, little side effects but potent		PR	09-JUL-1993; 93US-00090534.
PT activity in cancer.		PR	04-MAR-1994; 94US-00206130.
XX		XX	(SMIK ) SMITHKLINE BEECHAM CORP.
PS Claim 39; Page 175-179; 183pp; Japanese.		PA	
XX		XX	Young PR, Gross MS, Jonak ZL, Theisen TW, Hurle MR, Jackson JR;
CC The present invention describes a monoclonal antibody which can react		PI	
CC specifically with ganglioside GD3. The antibody and its derivatives are		XX	
CC useful in the diagnosis and therapy of tumors, particularly cancer		DR	WPI; 1995-066868/09.
CC diagnosis. The present sequence is a protein used in the exemplification		DR	N-PSDB; AAT51438.
CC of the invention		XX	
XX		PT	Recombinant and humanised chimeric antibodies against human interleukin-1
SQ Sequence 582 AA;		PT	-beta - for preventing and treating interleukin-mediated inflammatory
		PT	disorders.
Query Match	100.0%; Score 89; DB 4; Length 582;	PS	Claim 39; Page 40-41; 62pp; English.
Best Local Similarity	100.0%; Pred. No. 0.00022;	XX	
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		XX	
QY	1 YISSGGSGTYSDSVKG 17	CC	The heavy chain variable region (AAW11919) and light chain variable
Db	50 YISSGGSGTYSDSVKG 66	CC	region (AAW11920) of humanised anti-human interleukin-1 beta (IL-1 beta)
		CC	murine monoclonal antibody (Mab) SK48-E26 comprise the complementarity
		CC	determining regions from Mab SK48-E26 (see also AAW11917-18) grafted into
		CC	human frameworks. The humanised antibody can be produced in e.g. COS
		CC	cells transfected with vectors carrying humanised heavy and light chain
		CC	nucleic acids (AARS1437-39) for use in the treatment and prevention of IL
		CC	-1 mediated inflammatory disorders. (Updated on 16-OCT-2003 to
		CC	standardise OS field)
		XX	
		SQ	Sequence 119 AA;
RESULT 19		Query Match	
AAW11919		Best Local Similarity	
ID AAW11919 standard; protein; 119 AA.		86.5%; Score 77; DB 2; Length 119;	
XX		Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;	
AC AAW11919;			
XX			
DT 16-OCT-2003 (revised)			
DT 24-JUN-1997 (first entry)			
XX			
DE Humanised Mab SK48-E26 heavy chain.			
XX			
KW Interleukin-1 beta; IL-1 beta; recombinant antibody; humanised antibody;			
QY	1 YISSGGSGTYSDSVKG 17		
	:		



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XX AC ADJ95630;
XX ADZ08153
XX DT 06-MAY-2004 (first entry)
XX DE Rat insulin-like growth factor (IGF)-related peptide #2.
XX KW insulin-like growth factor; IGF-I; IGF-II; diabetes;
XX KW rheumatoid arthritis; cancer; rat.
XX OS Rattus norvegicus.
XX PN WO2003093317-A1.
XX PD 13-NOV-2003.
XX PF 30-APR-2003; 2003WO-JP005505.
XX PR 30-APR-2002; 2002JP-00129046.
XX PA (KYOW ) KYOWA HAKKO KOGYO KK.
XX PI Shitara K, Nakamura K, Furuya A, Niwa R, Ohki Y, Hanai N;
XX WIPI; 2003-854482/79.
XX DR Antibodies and antibody fragments recognising human insulin-like growth
XX PT factor for treatment and diagnosis of cancer, diabetes and rheumatoid
XX PT arthritis.
XX PS Claim 3; SEQ ID NO 6; 115pp; Japanese.
XX CC The invention comprises antibodies and antibody fragments which bind to
XX CC and inhibit the function of human insulin-like growth factor (IGF-I
XX CC and/or IGF-II). The antibodies and antibody fragments of the invention
XX CC are useful for the treatment, prevention, and diagnosis of diabetes,
XX CC rheumatoid arthritis and cancer. The present amino acid sequence
XX CC represents a rat insulin-like growth factor-related peptide of the
XX CC invention.
XX SQ Sequence 17 AA;

Query Match 83.1%; Score 74; DB 7; Length 17;
Best Local Similarity 82.4%; Pred. No. 0.00076;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 YISGGSGTYSDSVKG 17
DB 1 YISGGSGTYRDSVKG 17

RESULT 23
ADZ08153
ID ADZ08153 standard; peptide; 17 AA.
XX AC ADZ08153;
XX DT 16-JUN-2005 (first entry)
XX DE Rat IGF-specific antibody heavy chain variable region CDR - SEQ ID 6.
XX KW Insulin-like growth factor 1 antagonist;
XX KW Insulin-like growth factor 2 antagonist; antibody; cancer; cytostatic;
XX KW acromegaly; osteopathic; diabetic complication;
XX KW heavy chain variable region.
XX OS Rattus norvegicus.
XX PN WO2005028515-A1.
XX PD 31-MAR-2005.
XX PF -24-SEP-2004; 2004WO-JP014453.

XX PR 24-SEP-2003; 2003JP-00331509.
XX PA (KYOW ) KYOWA HAKKO KOGYO KK.
XX PI Shitara K, Nakamura K, Ohki Y;
XX WIPI; 2005-305821/31.
XX DR Recombinant antibody (fragment) binding to and inhibiting human insulin-
XX PT like growth factors IGF-1 and IGF-2, useful for treating diseases such as
XX PT cancer, acromegaly, and diabetic complications.
XX PS Claim 6; SEQ ID NO 6; 154pp; Japanese.
XX CC The invention comprises a recombinant antibody which targets human
XX CC insulin-like growth factor (IGF-1 and IGF-2), and is capable of
XX CC inhibiting the biological function of human IGF-1 and IGF-2. The antibody
XX CC of the invention is useful in the treatment of IGF-associated disease,
XX CC such as cancer, acromegaly and diabetic complications. The present amino
XX CC acid sequence represents a rat IGF-specific antibody heavy chain variable
XX CC region CDR.
XX SQ Sequence 17 AA;

Query Match 83.1%; Score 74; DB 9; Length 17;
Best Local Similarity 82.4%; Pred. No. 0.00076;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 YISGGSGTYSDSVKG 17
DB 1 YISGGSGTYRDSVKG 17

RESULT 24
ADJ95639
ID ADJ95639 standard; protein; 118 AA.
XX AC ADJ95639;
XX DT 06-MAY-2004 (first entry)
XX DE Insulin-like growth factor (IGF)-related protein #1.
XX KW insulin-like growth factor; IGF-I; IGF-II; diabetes;
XX KW rheumatoid arthritis; cancer.
XX OS Unidentified.
XX PN WO2003093317-A1.
XX PD 13-NOV-2003.
XX PF 30-APR-2003; 2003WO-JP005505.
XX PR 30-APR-2002; 2002JP-00129046.
XX PA (KYOW ) KYOWA HAKKO KOGYO KK.
XX PI Shitara K, Nakamura K, Furuya A, Niwa R, Ohki Y, Hanai N;
XX WIPI; 2003-854482/79.
XX DR Antibodies and antibody fragments recognising human insulin-like growth
XX PT factor for treatment and diagnosis of cancer, diabetes and rheumatoid
XX PT arthritis.
XX PS Example 7; SEQ ID NO 15; 115pp; Japanese.
XX CC The invention comprises antibodies and antibody fragments which bind to
XX CC and inhibit the function of human insulin-like growth factor (IGF-I
XX CC and/or IGF-II). The antibodies and antibody fragments of the invention
XX CC are useful for the treatment, prevention, and diagnosis of diabetes,

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CC rheumatoid arthritis and cancer. The present amino acid sequence  
CC represents an insulin-like growth factor-related protein of the  
CC invention.

XX SQ Sequence 118 AA;

Query Match 83.1%; Score 74; DB 7; Length 118;  
Best Local Similarity 82.4%; Pred. No. 0.0061;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 YISSGGSGTYRDSVKG 17  
||||| ||| |||||  
Db 50 YISSGGSGTYRDSVKG 66

## RESULT 25

ADZ08201  
ID ADZ08201 standard; protein; 118 AA.

XX AC ADZ08201;

XX DT 16-JUN-2005 (first entry)

XX DE IGF-specific antibody-related protein - SEQ ID 54.

XX KW Insulin-like growth factor 1 antagonist;  
XX KW Insulin-like growth factor 2 antagonist; antibody; cancer; cytostatic;  
XX KW acromegaly; osteopathic; diabetic complication.

XX OS Unidentified.

XX PN WO2005028515-A1.

XX PD 31-MAR-2005.

XX PF 24-SEP-2004; 2004WO-JP014453.

XX PR 24-SEP-2003; 2003JP-00331509.

XX PA (KYOW ) KYOWA HAKKO KOGYO KK.

XX PI Shitara K, Nakamura K, Ohki Y;

XX WPI; 2005-305821/31.

XX PT Recombinant antibody (fragment) binding to and inhibiting human insulin-  
PT like growth factors IGF-1 and IGF-2, useful for treating diseases such as  
PT cancer, acromegaly, and diabetic complications.

XX PS Claim 11; SEQ ID NO 54; 154pp; Japanese.

XX CC The invention comprises a recombinant antibody which targets human  
CC insulin-like growth factor (IGF-1 and IGF-2), and is capable of  
CC inhibiting the biological function of human IGF-1 and IGF-2. The antibody  
CC of the invention is useful in the treatment of IGF-associated disease,  
CC such as cancer, acromegaly and diabetic complications. The present amino  
CC acid sequence represents an IGF-specific antibody-related protein of the  
CC invention.

XX SQ Sequence 118 AA;

Query Match 83.1%; Score 74; DB 9; Length 118;  
Best Local Similarity 82.4%; Pred. No. 0.0061;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 YISSGGSGTYRDSVKG 17  
||||| ||| |||||  
Db 50 YISSGGSGTYRDSVKG 66

## RESULT 26

ADZ08173  
ID ADZ08173 standard; protein; 118 AA.

XX AC ADZ08173;  
XX DT 16-JUN-2005 (first entry)  
XX DE IGF-specific antibody-related protein - SEQ ID 26.

XX KW Insulin-like growth factor 1 antagonist;  
XX KW Insulin-like growth factor 2 antagonist; antibody; cancer; cytostatic;  
XX KW acromegaly; osteopathic; diabetic complication.

XX OS Unidentified.

XX PN WO2005028515-A1.

XX PD 31-MAR-2005.

XX PF 24-SEP-2004; 2004WO-JP014453.

XX PR 24-SEP-2003; 2003JP-00331509.

XX PA (KYOW ) KYOWA HAKKO KOGYO KK.

XX PI Shitara K, Nakamura K, Ohki Y;

XX WPI; 2005-305821/31.

XX PT Recombinant antibody (fragment) binding to and inhibiting human insulin-  
PT like growth factors IGF-1 and IGF-2, useful for treating diseases such as  
PT cancer, acromegaly, and diabetic complications.

XX PS Claim 14; SEQ ID NO 26; 154pp; Japanese.

XX CC The invention comprises a recombinant antibody which targets human  
CC insulin-like growth factor (IGF-1 and IGF-2), and is capable of  
CC inhibiting the biological function of human IGF-1 and IGF-2. The antibody  
CC of the invention is useful in the treatment of IGF-associated disease,  
CC such as cancer, acromegaly and diabetic complications. The present amino  
CC acid sequence represents an IGF-specific antibody-related protein that  
CC was used in an example of the invention.

XX SQ Sequence 118 AA;

Query Match 83.1%; Score 74; DB 9; Length 118;  
Best Local Similarity 82.4%; Pred. No. 0.0061;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 YISSGGSGTYRDSVKG 17  
||||| ||| |||||  
Db 50 YISSGGSGTYRDSVKG 66

## RESULT 27

ADZ08158  
ID ADZ08158 standard; protein; 118 AA.

XX AC ADZ08158;

XX DT 16-JUN-2005 (first entry)

XX DE IGF-specific antibody-related protein - SEQ ID 11.

XX KW Insulin-like growth factor 1 antagonist;  
XX KW Insulin-like growth factor 2 antagonist; antibody; cancer; cytostatic;  
XX KW acromegaly; osteopathic; diabetic complication.

XX OS Unidentified.

XX PN WO2005028515-A1.

XX PD 31-MAR-2005.

XX PF 24-SEP-2004; 2004WO-JP014453.



XX 24-SEP-2003; 2003JP-00331509.  
 XX (KYOW ) KYOWA HAKKO KOGYO KK.  
 XX Shitara K, Nakamura K, Ohki Y;  
 XX WPI; 2005-305821/31.  
 XX Recombinant antibody (fragment) binding to and inhibiting human insulin-  
 PT like growth factors IGF-1 and IGF-2, useful for treating diseases such as  
 PT cancer, acromegaly, and diabetic complications.  
 XX Claim 9; SEQ ID NO 11; 154pp; Japanese.  
 XX The invention comprises a recombinant antibody which targets human  
 CC insulin-like growth factor (IGF-1 and IGF-2), and is capable of  
 CC inhibiting the biological function of human IGF-1 and IGF-2. The antibody  
 CC of the invention is useful in the treatment of IGF-associated disease,  
 CC such as cancer, acromegaly and diabetic complications. The present amino  
 CC acid sequence represents a protein that was used in the exemplification  
 CC of the invention.  
 XX Sequence 118 AA;  
 SQ  
 Query Match 83.1%; Score 74; DB 9; Length 118;  
 Best Local Similarity 82.4%; Pred. No. 0.0061;  
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 YISSGGSGTYYSDSVKG 17  
 ||||| |||||  
 DB 50 YISSGGSGTYRDSVKG 66  
 RESULT 28  
 ADJ95626  
 ID ADJ95626 standard; protein; 137 AA.  
 XX AC ADJ95626;  
 XX 06-MAY-2004 (first entry)  
 XX Rat insulin-like growth factor (IGF)-related protein #1.  
 XX insulin-like growth factor; IGF-I; IGF-II; diabetes;  
 KW rheumatoid arthritis; cancer; rat.  
 XX Rattus norvegicus.  
 XX WO2003093317-A1.  
 XX 13-NOV-2003.  
 XX 30-APR-2003; 2003WO-JP005505.  
 XX 30-APR-2002; 2002JP-00129046.  
 XX (KYOW ) KYOWA HAKKO KOGYO KK.  
 XX Shitara K, Nakamura K, Furuya A, Niwa R, Ohki Y, Hanai N;  
 XX WPI; 2003-854482/79.  
 DR N-PSDB; ADJ95625.  
 XX Antibodies and antibody fragments recognising human insulin-like growth  
 PT factor for treatment and diagnosis of cancer, diabetes and rheumatoid  
 PT arthritis.  
 XX Claim 6; SEQ ID NO 2; 115pp; Japanese.  
 XX The invention comprises antibodies and antibody fragments which bind to  
 CC and inhibit the function of human insulin-like growth factor (IGF-I  
 CC and/or IGF-II). The antibodies and antibody fragments of the invention

CC are useful for the treatment, prevention, and diagnosis of diabetes,  
 CC rheumatoid arthritis and cancer. The present amino acid sequence  
 CC represents a rat insulin-like growth factor-related protein of the  
 CC invention.  
 XX Sequence 137 AA;  
 SQ  
 Query Match 83.1%; Score 74; DB 7; Length 137;  
 Best Local Similarity 82.4%; Pred. No. 0.0071;  
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 YISSGGSGTYYSDSVKG 17  
 ||||| |||||  
 DB 69 YISSGGSGTYRDSVKG 85  
 RESULT 29  
 ADZ08159  
 ID ADZ08159 standard; protein; 137 AA.  
 XX AC ADZ08159;  
 XX 16-JUN-2005 (first entry)  
 XX IGF-specific antibody-related protein - SEQ ID 12.  
 XX Insulin-like growth factor 1 antagonist;  
 KW Insulin-like growth factor 2 antagonist; antibody; cancer; cytostatic;  
 KW acromegaly; osteopathic; diabetic complication.  
 XX Unidentified.  
 XX WO2005028515-A1.  
 XX 31-MAR-2005.  
 XX 24-SEP-2004; 2004WO-JP014453.  
 XX 24-SEP-2003; 2003JP-00331509.  
 XX (KYOW ) KYOWA HAKKO KOGYO KK.  
 XX Shitara K, Nakamura K, Ohki Y;  
 XX WPI; 2005-305821/31.  
 DR N-PSDB; ADZ08160.  
 XX Recombinant antibody (fragment) binding to and inhibiting human insulin-  
 PT like growth factors IGF-1 and IGF-2, useful for treating diseases such as  
 PT cancer, acromegaly, and diabetic complications.  
 XX Example 1; SEQ ID NO 12; 154pp; Japanese.  
 XX The invention comprises a recombinant antibody which targets human  
 CC insulin-like growth factor (IGF-1 and IGF-2), and is capable of  
 CC inhibiting the biological function of human IGF-1 and IGF-2. The antibody  
 CC of the invention is useful in the treatment of IGF-associated disease,  
 CC such as cancer, acromegaly and diabetic complications. The present amino  
 CC acid sequence represents a protein that was used in the exemplification  
 CC of the invention.  
 XX Sequence 137 AA;  
 SQ  
 Query Match 83.1%; Score 74; DB 9; Length 137;  
 Best Local Similarity 82.4%; Pred. No. 0.0071;  
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 YISSGGSGTYYSDSVKG 17  
 ||||| |||||  
 DB 69 YISSGGSGTYRDSVKG 85  
 RESULT 30

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ADZ08220
ID ADZ08220 standard; protein; 137 AA.
XX
AC ADZ08220;
XX
DT 16-JUN-2005 (first entry)
DE
DE IGF-specific antibody-related protein - SEQ ID 17.
XX
KW Insulin-like growth factor 1 antagonist;
KW Insulin-like growth factor 2 antagonist; antibody; cancer; cytostatic;
KW acromegaly; osteopathic; diabetic complication.
XX
OS Unidentified.
XX
XX WO2005028515-A1.
PN
XX
XX 31-MAR-2005.
XX
XX 24-SEP-2004; 2004WO-JP014453.
XX
XX 24-SEP-2003; 2003JP-00331509.
XX
XX (KYOW ) KYOWA HAKKO KOGYO KK.
XX
XX Shitara K, Nakamura K, Ohki Y;
XX
XX WPI; 2005-305821/31.
DR N-PSDB; ADZ08164.
XX
XX Recombinant antibody (fragment) binding to and inhibiting human insulin-
XX like growth factors IGF-1 and IGF-2, useful for treating diseases such as
XX cancer, acromegaly, and diabetic complications.
XX
XX Example 1; SEQ ID NO 17; 154pp; Japanese.
XX
XX The invention comprises a recombinant antibody which targets human
XX insulin-like growth factor (IGF-1 and IGF-2), and is capable of
XX inhibiting the biological function of human IGF-1 and IGF-2. The antibody
XX of the invention is useful in the treatment of IGF-associated disease,
XX such as cancer, acromegaly and diabetic complications. The present amino
XX acid sequence represents a protein that was used in the exemplification
XX of the invention.
XX
XX Sequence 137 AA;
SQ
Query Match 83.1%; Score 74; DB 9; Length 137;
Best Local Similarity 82.4%; Pred. No. 0.0071;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 YISSGGSGTYSDSVKG 17
DB 69 YISSGGSGTYRDSVKG 85
RESULT 31
ADZ08149
ID ADZ08149 standard; protein; 137 AA.
XX
AC ADZ08149;
XX
DT 16-JUN-2005 (first entry)
DE
DE Rat IGF-specific antibody-related protein - SEQ ID 2.
XX
XX Insulin-like growth factor 1 antagonist;
XX Insulin-like growth factor 2 antagonist; antibody; cancer; cytostatic;
XX acromegaly; osteopathic; diabetic complication.
XX
XX Rattus norvegicus.
XX
XX WO2005028515-A1.
PN
XX
ADZ08220
ID ADZ08220 standard; protein; 137 AA.
XX
AC ADZ08220;
XX
DT 16-JUN-2005 (first entry)
DE
DE IGF-specific antibody-related protein - SEQ ID 17.
XX
KW Insulin-like growth factor 1 antagonist;
KW Insulin-like growth factor 2 antagonist; antibody; cancer; cytostatic;
KW acromegaly; osteopathic; diabetic complication.
XX
OS Unidentified.
XX
XX WO2005028515-A1.
PN
XX
XX 31-MAR-2005.
XX
XX 24-SEP-2004; 2004WO-JP014453.
XX
XX 24-SEP-2003; 2003JP-00331509.
XX
XX (KYOW ) KYOWA HAKKO KOGYO KK.
XX
XX Shitara K, Nakamura K, Ohki Y;
XX
XX WPI; 2005-305821/31.
DR N-PSDB; ADZ08164.
XX
XX Recombinant antibody (fragment) binding to and inhibiting human insulin-
XX like growth factors IGF-1 and IGF-2, useful for treating diseases such as
XX cancer, acromegaly, and diabetic complications.
XX
XX Example 1; SEQ ID NO 17; 154pp; Japanese.
XX
XX The invention comprises a recombinant antibody which targets human
XX insulin-like growth factor (IGF-1 and IGF-2), and is capable of
XX inhibiting the biological function of human IGF-1 and IGF-2. The antibody
XX of the invention is useful in the treatment of IGF-associated disease,
XX such as cancer, acromegaly and diabetic complications. The present amino
XX acid sequence represents a protein that was used in the exemplification
XX of the invention.
XX
XX Sequence 137 AA;
SQ
Query Match 83.1%; Score 74; DB 9; Length 137;
Best Local Similarity 82.4%; Pred. No. 0.0071;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 YISSGGSGTYSDSVKG 17
DB 69 YISSGGSGTYRDSVKG 85
RESULT 32
ADZ08221
ID ADZ08221 standard; protein; 137 AA.
XX
AC ADZ08221;
XX
DT 16-JUN-2005 (first entry)
DE
DE IGF-specific antibody-related protein - SEQ ID 18.
XX
XX Insulin-like growth factor 1 antagonist;
XX Insulin-like growth factor 2 antagonist; antibody; cancer; cytostatic;
XX acromegaly; osteopathic; diabetic complication.
XX
XX Unidentified.
XX
XX WO2005028515-A1.
PN
XX
XX 31-MAR-2005.
XX
XX 24-SEP-2004; 2004WO-JP014453.
XX
XX 24-SEP-2003; 2003JP-00331509.
XX
XX (KYOW ) KYOWA HAKKO KOGYO KK.
XX
XX Shitara K, Nakamura K, Ohki Y;
XX
XX WPI; 2005-305821/31.
DR N-PSDB; ADZ08165.
XX
XX Recombinant antibody (fragment) binding to and inhibiting human insulin-
XX like growth factors IGF-1 and IGF-2, useful for treating diseases such as
XX cancer, acromegaly, and diabetic complications.
XX
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PS Disclosure; SEQ ID NO 18; 15app; Japanese.

XX The invention comprises a recombinant antibody which targets human

CC insulin-like growth factor (IGF-1 and IGF-2), and is capable of

CC inhibiting the biological function of human IGF-1 and IGF-2. The antibody

CC of the invention is useful in the treatment of IGF-associated disease,

CC such as cancer, acromegaly and diabetic complications. The present amino

CC acid sequence represents a protein that was used in the exemplification

CC of the invention.

XX SQ Sequence 137 AA;

Query Match 83.1%; Score 74; DB 9; Length 137;

Best Local Similarity 82.4%; Pred. No. 0.0071; 3; Indels 0; Gaps 0;

Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 YISSGGSGTYRDSVKG 17

DB 69 YISSGGSGTYRDSVKG 85

RESULT 33

ID ADS09261

ADSD09261 standard; protein; 240 AA.

XX ADS09261;

XX 18-NOV-2004 (first entry)

XX Human c-Met protein tyrosine kinase antibody, PGIA-2-A9.

XX c-Met; tyrosine kinase antibody; antigen binding; cytostatic;

XX ophthalmological; antiinflammatory; analgesic; vasotropic; antipsoriatic;

XX osteopathic; cancer; tumour; ophthalmic disease; glaucoma; retinitis;

XX retinopathy; uveitis; ocular photophobia; macular degeneration; pain;

XX acute injury; eye; hyperproliferative disorder; restenosis; angioplasty;

XX psoriasis; HGF; osteoporosis; cancer.

XX Homo sapiens.

OS WO2004072117-A2.

XX 26-AUG-2004.

XX 11-FEB-2004; 2004WO-IB000503.

XX 13-FEB-2003; 2003US-0447073P.

XX (PHAA ) PHARMACIA CORP.

XX Morton PA, Arbuckle JA, Evans ML, Joy WD, Kahn LE, Shieh JJ;

PI WPI; 2004-616044/59.

XX N-PSDB; ADS09321.

XX Novel c-Met protein tyrosine kinase antibody or its antigen-binding

PT portion specifically binding to c-Met, useful for manufacture of

PT medicament for treating cancer or tumor and for treatment of ophthalmic

PT diseases such as glaucoma.

XX Claim 1; SEQ ID NO 23; 303pp; English.

XX The invention relates to a novel c-Met protein tyrosine kinase antibody

CC or its antigen binding portion that specifically binds to c-Met. The c-

CC Met antibody comprises any one of 1-60 fully defined sequence of 238,

CC 244, 240, 250, 251, 242, 245, 247, 246, 253, 249, 243, 241, etc., amino

CC acids as given in the specification, or its fragment. The invention

CC further comprises: a pharmaceutical composition comprising the c-Met

CC protein tyrosine kinase antibody and a carrier; an isolated cell that

CC produces the c-Met protein tyrosine kinase antibody; and an isolated

CC nucleic acid molecule that comprises a nucleic acid sequence that encodes

CC a heavy chain or its antigen-binding portion or light chain or its

CC antigen-binding portion of the c-Met protein tyrosine kinase antibody.

CC The c-Met protein tyrosine kinase antibody has cytostatic,

CC ophthalmological, antiinflammatory, analgesic, vasotropic, antipsoriatic,

CC and osteopathic activities. The c-Met protein tyrosine kinase antibody is

CC useful for the manufacture of medicament for the treatment of cancer or

CC tumour. The c-Met protein tyrosine kinase antibody is useful for

CC diagnosing the presence or ligation of c-Met expressing tissue. The c-Met

CC protein tyrosine kinase antibody is useful for detecting c-Met in a

CC biological sample in vitro or in vivo. The c-Met protein tyrosine kinase

CC antibody is also useful in the treatment or prevention of ophthalmic

CC diseases such as glaucoma, retinitis, retnopathies (e.g., diabetic

CC retinopathy), uveitis, ocular photophobia, macular degeneration and pain

CC associated with acute injury to the eye. The pharmaceutical composition

CC is useful for the treatment of hyperproliferative disorders such as

CC restenosis after angioplasty, and psoriasis, and for the treatment of

CC animals that lack sufficient HGF, e.g. osteoporosis and cancer. This

CC sequence represents the protein of a phage display generated human c-Met

CC antibody of the invention.

XX SQ Sequence 240 AA;

Query Match 83.1%; Score 74; DB 8; Length 240;

Best Local Similarity 82.4%; Pred. No. 0.013;

Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YISSGGSGTYRDSVKG 17

DB 50 YISSGGSGTYRDSVKG 66

RESULT 34

ID ADW44417

ADW44417 standard; protein; 468 AA.

XX ADW44417;

XX 07-APR-2005 (first entry)

XX Dog immunoglobulin gamma chain amino acid sequence - SEQ ID 10.

XX antibody; parvovirus infection.

XX Canis familiaris.

XX JP2005006593-A.

XX 13-JAN-2005.

XX 20-JUN-2003; 2003JP-00175932.

XX 20-JUN-2003; 2003JP-00175932.

XX (NISK ) NIPPON SEIBUTSU KAGAKU KENKYUSHO ZH.

XX WPI; 2005-104478/12.

XX N-PSDB; ADW44416.

XX Novel canine-sized antibody protein having variable region, preferably

PT transplanted complementary determining region of neutralized monoclonal

PT antibody of canine parvovirus, useful for treating canine parvovirus

PT infectious disease.

XX Claim 8; SEQ ID NO 10; 107pp; Japanese.

XX The invention relates to the production and use of a canine-sized antibody

CC that recognizes canine parvovirus. The antibody of the invention is

CC useful for treating canine parvovirus infectious disease. The present

CC amino acid sequence represents a dog immunoglobulin gamma chain of the

CC invention.

XX SQ Sequence 468 AA;

Query Match 83.1%; Score 74; DB 9; Length 468;

Best Local Similarity 76.5%; Pred. No. 0.027;

Matches 13; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 YISGGSGTYYSVSKG 17  
 DB 69 YISGGSGTYYSVSKG 85

RESULT 35  
 ADG25805  
 ID ADG25805 standard; protein; 117 AA.  
 AC ADG25805;  
 KW 11-MAR-2004 (first entry)  
 DT  
 DE Anti-CD30 monoclonal antibody VH variable region T14 SEQ ID NO:5.  
 XX antibody; CD30; anti-CD30 antibody; cytostatic; gene therapy; cancer.  
 KW Synthetic.  
 OS  
 XX WO200310432-A2.  
 PN 18-DEC-2003.  
 XX 09-JUN-2003; 2003WO-US018373.  
 PF 07-JUN-2002; 2002US-0387293P.  
 PR 16-SEP-2002; 2002US-0411032P.  
 XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 PA Pastan IH, Nagata S, Onda M, Numata Y, Santora K, Beers R;  
 PI Kreitman R, Sinha A;  
 XX WPI; 2004-062352/06.  
 DR New antibody that binds specifically to a stalk of CD30 of a cell, or to  
 PT an epitope destroyed upon cleavage of soluble CD30 (sCD30) from intact  
 PT CD30, useful for inhibiting the growth of a CD30+ cancer cell.  
 XX Example 1; SEQ ID NO 5; 102pp; English.

CC The present invention describes an isolated antibody that binds  
 CC specifically to a stalk of CD30 of a cell, or to an epitope destroyed  
 CC upon cleavage of soluble CD30 (sCD30) from intact CD30. Also described:  
 CC (1) a composition comprising the antibody conjugated or fused to a  
 CC therapeutic part; (2) a nucleic acid encoding an antibody that binds  
 CC specifically to a stalk of CD30 of a cell, or to an epitope destroyed  
 CC upon cleavage of sCD30 from intact CD30; (3) an expression vector  
 CC comprising the nucleic acid operably linked to a promoter; (4) inhibiting  
 CC growth of a CD30+ cancer cell; (5) detecting the presence of a CD30+ cell  
 CC in a biological sample; (6) a host cell expressing the isolated nucleic  
 CC acid encoding the antibody having variable heavy and variable light  
 CC chains; and (7) a kit for detecting the presence of a CD30+ cancer cell  
 CC in a biological sample comprising a container and an anti-CD30 antibody.  
 CC An anti-CD30 antibody has cytostatic activity, and can be used in gene  
 CC therapy. The anti-CD30 antibody that binds specifically to a stalk of  
 CC CD30 of a cell, or to an epitope destroyed upon cleavage of sCD30 from  
 CC intact CD30 is useful for the manufacture of a medicament for inhibiting  
 CC the growth of a CD30+ cancer cell. The present sequence is used in the  
 CC exemplification of the present invention.

QY 2 ISSGGSGTYYSVSKG 17  
 DB 51 ISSGGSGTYYSVSKG 66

Query Match 82.0%; Score 73; DB 8; Length 117;  
 Best Local Similarity 93.8%; Pred. No. 0.0084;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 36  
 ADC27437  
 ID ADC27437 standard; protein; 120 AA.  
 XX ADC27437;  
 AC  
 XX 18-DEC-2003 (first entry)  
 DT  
 DE TMEFF2#10 heavy chain variable region SEQ ID NO:6.  
 XX antibody; TMEFF2#19; TMEFF2; binding inhibitor; prostate cancer;  
 KW cytostatic; vaccine; primary prostate cancer; metastatic prostate cancer;  
 KW locally advanced prostate cancer; androgen independent prostate cancer.  
 XX Synthetic.  
 OS  
 XX WO2003075855-A2.  
 PN 18-SEP-2003.  
 XX 07-MAR-2003; 2003WO-US007209.  
 PF 08-MAR-2002; 2002US-0362837P.  
 PR 27-DEC-2002; 2002US-0436812P.  
 XX (EOSB-) EOS BIOTECHNOLOGY INC.  
 PA Bhaskar V, De La Calle A, Law D, Caras I, Ramakrishnan V;  
 PI Murray R, Afar D, Powers D;  
 XX WPI; 2003-756783/71.  
 DR N-PSDB; ADC27436.

CC New antibody that competitively inhibits binding of TMEFF219 to TMEFF2,  
 CC useful for treating prostate cancer, e.g. primary, metastatic, locally  
 CC advanced, or androgen independent prostate cancer.  
 XX Example 1; SEQ ID NO 6; 51pp; English.  
 PS The present invention describes an antibody (I) that competitively  
 CC inhibits binding of TMEFF2#19 to TMEFF2. Also described: (1) a  
 CC pharmaceutical composition comprising the antibody and a carrier; (2)  
 CC detecting a prostate cancer cell in a biological sample from a patient by  
 CC contacting the biological sample with the antibody; (3) inhibiting the cell  
 CC proliferation of a prostate cancer-associated cell by contacting the cell  
 CC with the antibody; and (4) treating prostate cancer with an antibody to  
 CC TMEFF2. (I) has cytostatic activity and can be used in vaccines. The  
 CC antibody, composition and method are useful for treating prostate cancer,  
 CC e.g. primary prostate cancer, metastatic prostate cancer, locally  
 CC advanced prostate cancer, androgen independent prostate cancer, prostate  
 CC cancer that has been treated with neoadjuvant therapy, or prostate cancer  
 CC that is refractory to treatment with neoadjuvant therapy. The present  
 CC sequence is used in the exemplification of the present invention.

QY 1 YISGGSGTYYSVSKG 17  
 DB 50 YISGGSGTYYSVSKG 66

Query Match 82.0%; Score 73; DB 7; Length 120;  
 Best Local Similarity 76.5%; Pred. No. 0.0087;  
 Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

RESULT 37  
 ADZ45351  
 ID ADZ45351 standard; peptide; 17 AA.  
 XX ADZ45351;  
 AC  
 XX 30-JUN-2005 (first entry)

XX DE Murine factor IX directed antibody CDR2 SEQ ID NO 55.  
 XX DE bispecific antibody; blood coagulation factor VIII; bleeding;  
 KW fibrinolysis; blood coagulation factor X; blood-coagulation factor IX;  
 KW factor VIII deficiency; von Willebrand disease; hemostatic;  
 KW immunostimulator; antibody engineering.  
 XX OS Mus musculus.  
 XX PN WO2005035756-A1.  
 XX PD 21-APR-2005.  
 XX PF 08-OCT-2004; 2004WO-JP014911.  
 XX PR 10-OCT-2003; 2003WO-JP013062.  
 XX PR 14-OCT-2003; 2003WO-JP013123.  
 XX PA (CHUS ) CHUGAI SEIYAKU KK.  
 XX PI Hattori K, Kojima T, Miyazaki T, Soeda T;  
 XX PI WPI; 2005-315563/32.  
 XX PT Novel bispecific antibody substituting for function of cofactor that  
 PT enhances enzyme reaction, and recognizing both enzyme and substrates of  
 PT enzyme, useful for treating hemophilia A.  
 XX PS Claim 5; SEQ ID NO 55; 69pp; Japanese.  
 XX CC This invention describes a novel bispecific antibody which can act as a  
 CC cofactor to enhance an enzyme reaction and can recognize the enzyme and  
 CC the enzyme substrate. The antibody specifically binds to blood  
 CC coagulation factor VIII. The invention also describes a composition  
 CC comprising the antibody and a carrier, a kit useful in preventing and/or  
 CC treating bleeding associated with a disorder or from a disease caused by  
 CC bleeding. The composition includes blood coagulation factor VIII. The  
 CC antibody of the invention can be a blood-coagulation fibrinolysis related  
 CC factor including blood-coagulation factor VIII, blood coagulation factor  
 CC X, or blood-coagulation factor IX. The antibody comprises a complementary  
 CC determining region (CDR) of anti-blood-coagulation factor IX/IXa factor  
 CC antibody. The novel antibody or composition is useful for preventing  
 CC and/or treating a disease accompanying bleeding, or the disease resulting  
 CC from bleeding, where the disease accompanying bleeding or the disease  
 CC resulting from bleeding develops and/or progresses by an active reduction  
 CC or deletion of the blood coagulation factor VIII. The disease the  
 CC develops and/or progresses by an active reduction or deletion of the  
 CC blood coagulation factor VIII and/or activation blood coagulation factor  
 CC VIII, is hemophilia A or von Willebrand disease, where the hemophilia is  
 CC an acquired hemophilia A. This sequence represents a fragment of the  
 CC antibody described in the method of the invention. Note: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pt\_sequences.  
 XX SQ Sequence 17 AA;  
 Query Match 80.9%; Score 72; DB 9; Length 17;  
 Best Local Similarity 76.5%; Pred. No. 0.0015;  
 Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 YISGGSGTYTSDSVKG 17  
 |||:|:| ||| |||  
 Db 1 YISNGGANTYTPDSVKG 17  
 RESULT 38  
 ADZ51264  
 ID ADZ51264 standard; peptide; 17 AA.  
 XX AC ADZ51264;  
 XX PN

DT 30-JUN-2005 (first entry)  
 XX Amino acid sequence of a variable heavy chain region CDR.  
 DE bispecific antibody; AR1 chain; AR2 chain; hemostatic; bleeding;  
 XX antibody therapy; blood coagulation factor VIII; factor VIII deficiency;  
 KW von Willebrand disease; heavy chain; complementarity determining region;  
 KW CDR.  
 XX OS Mus musculus.  
 XX PN WO2005035753-A1.  
 XX PD 21-APR-2005.  
 XX PF 10-OCT-2003; 2003WO-JP013062.  
 XX PR 10-OCT-2003; 2003WO-JP013062.  
 XX PA (CHUS ) CHUGAI SEIYAKU KK.  
 XX PI Hattori K, Kojima T, Miyazaki T, Soeda T, Senoo C, Natori O;  
 XX PI Kasutani K, Ishii S;  
 XX PI WPI; 2005-315560/32.  
 XX PT Novel bispecific antibody substituting for functional protein or  
 PT substituting for ligand for receptor comprising two types of molecules,  
 PT useful as pharmaceutical for treating or preventing diseases e.g.  
 PT bleeding.  
 XX PS Claim 18; SEQ ID NO 81; 143pp; Japanese.  
 XX CC The specification describes a bispecific antibody substituting for  
 CC functional protein or substituting for a ligand for a receptor comprising  
 CC two types of molecules. The antibody comprises AR1 and AR2 chains.  
 CC Bispecific antibodies of the invention are useful for preventing and  
 CC treating bleeding, diseases accompanying bleeding or diseases resulting  
 CC from bleeding. These diseases develop or progress by active reduction of  
 CC blood coagulation factor VII/activated blood coagulation factor VIII,  
 CC e.g. hemophilia A, acquired hemophilia or von Willebrand disease. The  
 CC present sequence represents a complementarity determining region (CDR)  
 CC from a variable heavy chain region, which was used to construct  
 CC bispecific antibodies of the invention.  
 XX SQ Sequence 17 AA;  
 Query Match 80.9%; Score 72; DB 9; Length 17;  
 Best Local Similarity 76.5%; Pred. No. 0.0015;  
 Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 YISGGSGTYTSDSVKG 17  
 |||:|:| ||| |||  
 Db 1 YISNGGANTYTPDSVKG 17  
 RESULT 39  
 ADZ42138  
 ID ADZ42138 standard; peptide; 17 AA.  
 XX AC ADZ42138;  
 XX DT 30-JUN-2005 (first entry)  
 XX DE Mouse anti-s AR antibody heavy chain CDR 2 SEQ ID NO 81.  
 KW viral infection; neoplasm; immune disorder; bleeding; infection;  
 KW cardiovascular disease; Virucide; Hepatotropic; Antiinflammatory;  
 KW Neuroprotective; Hemostatic; Cytostatic; Immunotherapy; antibody.  
 XX OS Mus musculus.  
 XX PN WO2005035754-A1.

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XX 21-APR-2005.
PD 14-OCT-2003; 2003WO-JP013123.
XX PF
XX 14-OCT-2003; 2003WO-JP013123.
XX PF
XX 14-OCT-2003; 2003WO-JP013123.
XX PR
XX (CHUS ) CHUGAI SEIYAKU KK.
XX PA
XX Hattori K, Kojima T, Miyazaki T, Soeda T, Senoo C, Natori O;
PI Kasutani K, Ishii S;
XX WPI; 2005-315561/32.
XX DR
XX Novel bispecific antibody substituting for functional protein and having
PT ligand functional alternative activity to receptor containing
PT heteromolecule, useful for preventing/treating viral disease,
PT immunological disease or bleeding.
XX
XX Claim 28; SEQ ID NO 81; 151pp; Japanese.
XX
XX The invention relates to a bispecific antibody (I) substituting for: a
CC functional protein and having ligand functional alternative activity with
CC respect to receptor containing heteromolecule; or a functional cofactor
CC which enhances an enzyme reaction and recognizes both substrates of
CC enzyme. Also claimed are a composition (II) containing (I). (I) and (II)
CC are useful for preventing and/or treating viral disease, neoplasm, or
CC immunological disease, or bleeding or disease resulting from bleeding.
CC The viral disease is a hepatitis C virus or hepatitis B virus infection
CC such as an acute or chronic liver cirrhosis or hepatic carcinoma. The
CC neoplasms are chronic myeloid leukemia, malignant melanoma, multiple
CC myeloma, renal carcinoma, glioblastoma, medulloblastoma, astrocytoma,
CC hairy cell leukemia, AIDS-related Kaposi's sarcoma, skin T cell lymphoma
CC or non-Hodgkin's lymphoma. The immunological disease is multiple
CC sclerosis. The bleeding disease is the disease resulting from the active
CC reduction or a defect of blood coagulation factor VIII such as hemophilia
CC or von Willebrand disease. (II) is useful for manufacturing (I). (I) has
CC high stability and low antigenicity in blood. The present sequence
CC represents a mouse anti-s AR antibody CDR.
XX
XX Sequence 17 AA;
SQ
Query Match 80.9%; Score 72; DB 9; Length 17;
Best Local Similarity 76.5%; Pred. No. 0.0015;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 YISGGSGTYSDSVK 17
DB 1 YISNGGANTYPDSVK 17
|||:|:|:|:|:|:|
1 YISNGGANTYPDSVK 17
RESULT 40
ADZ45349
ID ADZ45349 standard; protein; 121 AA.
XX AC
XX ADZ45349;
XX
XX 30-JUN-2005 (first entry)
XX
XX Murine factor IX directed antibody fragment SEQ ID NO 53.
XX
XX bispecific antibody; blood coagulation factor VIII; bleeding;
KW fibrinolysis; blood coagulation factor X; blood-coagulation factor IX;
KW factor VIII deficiency; von Willebrand disease; hemostatic;
KW immunostimulator; antibody engineering.
XX
XX Mus musculus.
XX
XX WO2005035756-A1.
XX PN
XX 21-APR-2005.
XX PD
XX 08-OCT-2004; 2004WO-JP014911.
XX PF
10-OCT-2003; 2003WO-JP013062.
14-OCT-2003; 2003WO-JP013123.
(CHUS ) CHUGAI SEIYAKU KK.
Hattori K, Kojima T, Miyazaki T, Soeda T;
WPI; 2005-315563/32.
Novel bispecific antibody substituting for function of cofactor that
enhances enzyme reaction, and recognizing both enzyme and substrates of
enzyme, useful for treating hemophilia A.
Discloure; SEQ ID NO 53; 69pp; Japanese.
This invention describes a novel bispecific antibody which can act as a
cofactor to enhance an enzyme reaction and can recognize the enzyme and
the enzyme substrate. The antibody specifically binds to blood
coagulation factor VIII. The invention also describes a composition
comprising the antibody and a carrier, a kit useful in preventing and/or
treating bleeding associated with a disorder or from a disease caused by
bleeding. The composition includes blood coagulation factor VIII. The
antibody of the invention can be a blood-coagulation fibrinolysis related
factor including blood-coagulation factor VIII, blood coagulation factor
X, or blood-coagulation factor IX. The antibody comprises a complementary
determining region (CDR) of anti-blood-coagulation factor IX/IXa factor
antibody. The novel antibody or composition is useful for preventing
and/or treating a disease accompanying bleeding, or the disease resulting
from bleeding, where the disease accompanying bleeding or the disease
resulting from bleeding develops and/or progresses by an active reduction
or deletion of the blood coagulation factor VIII. The disease the
develops and/or progresses by an active reduction or deletion of the
blood coagulation factor VIII and/or activation blood coagulation factor
VIII, is hemophilia A or von Willebrand disease, where the hemophilia is
an acquired hemophilia A. This sequence represents a fragment of the
antibody described in the method of the invention. Note: The sequence
data for this patent did not form part of the printed specification, but
was obtained in electronic format directly from WIPO at
ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 121 AA;
SQ
Query Match 80.9%; Score 72; DB 9; Length 121;
Best Local Similarity 76.5%; Pred. No. 0.012;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 YISGGSGTYSDSVK 17
DB 51 YISNGGANTYPDSVK 67
|||:|:|:|:|:|:|
51 YISNGGANTYPDSVK 67
RESULT 41
ADZ51262
ID ADZ51262 standard; protein; 121 AA.
XX AC
XX ADZ51262;
XX
XX 30-JUN-2005 (first entry)
XX
XX Amino acid sequence of polypeptide #13.
XX
XX bispecific antibody; ARI chain; AR2 chain; hemostatic; bleeding;
KW antibody therapy; blood coagulation factor VIII; factor VIII deficiency;
KW von Willebrand disease.
XX
XX Mus musculus.
XX
XX WO2005035753-A1.
XX PN
XX 21-APR-2005.
XX PD
XX 10-OCT-2003; 2003WO-JP013062.
XX PF
```

XX 10-OCT-2003; 2003WO-JP013062.  
 XX (CHUS ) CHUGAI SEIYAKU KK.  
 XX Hattori K, Kojima T, Miyazaki T, Soeda T, Senoo C, Natori O;  
 PI Kasutani K, Ishii S;  
 XX WPI; 2005-315560/32.  
 XX Novel bispecific antibody substituting for functional protein or  
 PT substituting for ligand for receptor comprising two types of molecules,  
 PT useful as pharmaceutical for treating or preventing diseases e.g.  
 PT bleeding.  
 XX Disclosure; SEQ ID NO 79; 143pp; Japanese.  
 XX The specification describes a bispecific antibody substituting for  
 CC functional protein or substituting for a ligand for a receptor comprising  
 CC two types of molecules. The antibody comprises AR1 and AR2 chains.  
 CC Bispecific antibodies of the invention are useful for preventing and  
 CC treating bleeding, diseases accompanying bleeding or diseases resulting  
 CC from bleeding. These diseases develop or progress by active reduction of  
 CC blood coagulation factor VIII/activated blood coagulation factor VIII,  
 CC e.g. hemophilia A, acquired hemophilia or Von Willebrand disease. The  
 CC present primer represents a polypeptide used in the course of the  
 CC invention.  
 XX Sequence 121 AA;  
 SQ Query Match 80.9%; Score 72; DB 9; Length 121;  
 Best Local Similarity 76.5%; Pred. No. 0.012;  
 Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 YISGSGGTYSDSVKG 17  
 DB 51 YISNGGANTYYPDSVKG 67  
 RESULT 42  
 ADZ42136  
 ID ADZ42136 standard; protein; 121 AA.  
 AC ADZ42136;  
 XX 30-JUN-2005 (first entry)  
 XX Mouse anti-s AR antibody associated protein SEQ ID NO 79.  
 XX viral infection; neoplasm; immune disorder; bleeding; infection;  
 KW cardiovascular disease; Viricide; Hepatotropic; Antiinflammatory;  
 KW Neuroprotective; Hemostatic; Cytostatic; Immunotherapy.  
 XX Mus musculus.  
 XX WO2005035754-A1.  
 PN 21-APR-2005.  
 XX 14-OCT-2003; 2003WO-JP013123.  
 XX 14-OCT-2003; 2003WO-JP013123.  
 XX (CHUS ) CHUGAI SEIYAKU KK.  
 XX Hattori K, Kojima T, Miyazaki T, Soeda T, Senoo C, Natori O;  
 PI Kasutani K, Ishii S;  
 XX WPI; 2005-315561/32.  
 XX Novel bispecific antibody substituting for functional protein and having  
 PT ligand functional alternative activity to receptor containing  
 PT heteromolecule, useful for preventing/treating viral disease,

PT immunological disease or bleeding.  
 XX Disclosure; SEQ ID NO 79; 151pp; Japanese.  
 XX The invention relates to a bispecific antibody (I) substituting for: a  
 CC functional protein and having ligand functional alternative activity with  
 CC respect to receptor containing heteromolecule; or a functional cofactor  
 CC which enhances an enzyme reaction and recognizes both substrates of  
 CC enzyme. Also claimed are a composition (II) containing (I), (I) and (II)  
 CC are useful for preventing and/or treating viral disease, neoplasm, or  
 CC immunological disease, or bleeding or disease resulting from bleeding.  
 CC The viral disease is a hepatitis C virus or hepatitis B virus infection.  
 CC such as an acute or chronic liver cirrhosis or hepatic carcinoma. The  
 CC neoplasms are chronic myeloid leukemia, malignant melanoma, multiple  
 CC myeloma, renal carcinoma, glioblastoma, medulloblastoma, astrocytoma,  
 CC hairy cell leukemia, AIDS-related Kaposi's sarcoma, skin T cell lymphoma  
 CC or non-Hodgkin's lymphoma. The immunological disease is multiple  
 CC sclerosis. The bleeding disease is the disease resulting from the active  
 CC reduction or a defect of blood coagulation factor VIII such as hemophilia  
 CC or von Willebrand disease. (II) is useful for manufacturing (I). (I) has  
 CC high stability and low antigenicity in blood. The present sequence  
 CC represents a mouse anti-s AR antibody associated protein.  
 XX Sequence 121 AA;  
 SQ Query Match 80.9%; Score 72; DB 9; Length 121;  
 Best Local Similarity 76.5%; Pred. No. 0.012;  
 Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 YISGSGGTYSDSVKG 17  
 DB 51 YISNGGANTYYPDSVKG 67  
 RESULT 43  
 ABP46028  
 ID ABP46028 standard; protein; 237 AA.  
 XX AC ABP46028;  
 XX 19-AUG-2002 (first entry)  
 XX Human BlyS binding scFv SEQ ID 2039.  
 XX BlyS, B lymphocyte stimulator; TNF superfamily; human; cytostatic;  
 KW tumour necrosis factor; B cell proliferation; B cell differentiation;  
 KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;  
 KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;  
 KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;  
 KW common variable immunodeficiency; acquired immunodeficiency syndrome.  
 XX Homo sapiens.  
 OS WO200202641-A1.  
 PN 10-JAN-2002.  
 PD 15-JUN-2001; 2001WO-US019110.  
 PF 16-JUN-2000; 2000US-0212210P.  
 PR 17-OCT-2000; 2000US-0240816P.  
 PR 16-MAR-2001; 2001US-0276248P.  
 PR 21-MAR-2001; 2001US-0277379P.  
 PR 25-MAY-2001; 2001US-0293499P.  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 PA (CAME-) CAMBRIDGE ANTIBODY TECHNOLOGY.  
 XX Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;  
 PI WPI; 2002-114799/15.  
 XX Antibodies against B Lymphocyte Stimulating polypeptides, useful for the

PT diagnosis and treatment of cancers and immune disorders.

XX Claim 1; Page 2831-2832; 3148pp; English.

XX This invention describes novel antibodies that immunospecifically bind to  
 CC B Lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the  
 CC tumour necrosis factor (TNF) super family and induces B cell  
 CC proliferation and differentiation. The antibodies of the invention have  
 CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,  
 CC antirheumatic and antiAIDS activity and can be used in vaccines to  
 CC inhibit the expression and activity of Blys. The antibodies bind to Blys  
 CC and so may be used to detect and quantitate the presence of Blys in  
 CC biological samples and may be used in this way to diagnose disease  
 CC associated with aberrant expression of Blys. They may also be  
 CC administered to treat diseases associated with aberrant Blys expression  
 CC and activity such as cancer, immune, and autoimmune disorders and  
 CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,  
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and  
 CC acquired immunodeficiency syndrome (AIDS)). ABP4390-ABP4728 represent  
 CC the antibodies and fragments of the antibodies described in the method of  
 CC the invention

XX SQ Sequence 237 AA;

Query Match 80.9%; Score 72; DB 5; Length 237;  
 Best Local Similarity 82.4%; Pred. No. 0.025;  
 Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YISSGGSGTYSDSVKG 17  
 ||||| ||||| |||||  
 Db 50 YISSGGSTTYADSVKG 66

RESULT 44

ABP45895  
 ID ABP45895 standard; protein; 237 AA.

XX AC ABP45895;

XX DT 19-AUG-2002 (first entry)

XX DE Human Blys binding scFv SEQ ID 1906.

XX Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;  
 KW tumour necrosis factor; B cell proliferation; B cell differentiation;  
 KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;  
 KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;  
 KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;  
 KW common variable immunodeficiency; acquired immunodeficiency syndrome.

XX OS Homo sapiens.

XX PN WO200202641-A1.

XX PD 10-JAN-2002.

XX PF 15-JUN-2001; 2001WO-US019110.

XX PR 16-JUN-2000; 2000US-0212210P.

XX PR 17-OCT-2000; 2000US-0240816P.

XX PR 16-MAR-2001; 2001US-0276248P.

XX PR 21-MAR-2001; 2001US-0277379P.

XX PR 25-MAY-2001; 2001US-0293499P.

XX (HUMA-) HUMAN GENOME SCI INC.

PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.

XX Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;

XX WPI; 2002-114799/15.

XX Antibodies against B Lymphocyte Stimulating polypeptides, useful for the  
 PT diagnosis and treatment of cancers and immune disorders.

XX Claim 1; Page 2675-2676; 3148pp; English.

XX This invention describes novel antibodies that immunospecifically bind to  
 CC B Lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the  
 CC tumour necrosis factor (TNF) super family and induces B cell  
 CC proliferation and differentiation. The antibodies of the invention have  
 CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,  
 CC antirheumatic and antiAIDS activity and can be used in vaccines to  
 CC inhibit the expression and activity of Blys. The antibodies bind to Blys  
 CC and so may be used to detect and quantitate the presence of Blys in  
 CC biological samples and may be used in this way to diagnose disease  
 CC associated with aberrant expression of Blys. They may also be  
 CC administered to treat diseases associated with aberrant Blys expression  
 CC and activity such as cancer, immune, and autoimmune disorders and  
 CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,  
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and  
 CC acquired immunodeficiency syndrome (AIDS)). ABP4390-ABP4728 represent  
 CC the antibodies and fragments of the antibodies described in the method of  
 CC the invention

XX SQ Sequence 237 AA;

Query Match 80.9%; Score 72; DB 5; Length 237;  
 Best Local Similarity 82.4%; Pred. No. 0.025;  
 Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YISSGGSGTYSDSVKG 17  
 ||||| ||||| |||||  
 Db 50 YISSGGSTTYADSVKG 66

RESULT 45

ADG96722

ID ADG96722 standard; protein; 237 AA.

XX AC ADG96722;

XX DT 11-MAR-2004 (first entry)

XX DE Single chain antibody that immunospecifically binds Blys SeqID 1906.

XX antibody; B lymphocyte stimulator; Blys; tumour necrosis factor;

KW B cell proliferation; differentiation; scFv; myasthenia gravis;

KW multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia;

KW carcinoma; lymphoma; antirheumatic; antiallergic; neuroprotective;

KW antinflammatory; antiasthmatic; antiallergic; cytostatic.

XX Unidentified.

XX WO2003055979-A2.

XX PD 10-JUL-2003.

XX PF 14-NOV-2002; 2002WO-US036496.

XX PR 16-NOV-2001; 2001US-0331469P.

XX PR 19-DEC-2001; 2001US-0340817P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Ruben SM, Barash SC, Choi GH, Vaughan TJ, Hilbert D;

XX WPI; 2003-505530/47.

XX Novel antibody that immunospecifically binds to a B lymphocyte stimulator

PT (Blys), useful for detecting and treating diseases or disorders e.g.

PT rheumatoid arthritis, asthma and leukemia.

XX Example 1; SEQ ID NO 1906; 394pp; English.

XX This invention relates to novel antibodies that immunospecifically bind

CC to B lymphocyte stimulator (Blys). The Blys gene has been mapped to



CC chromosome 13q34 and encodes a protein that is a member of the tumour  
 CC necrosis factor superfamily and induces both in vivo and in vitro B cell  
 CC proliferation and differentiation. Specifically, it refers to single  
 CC chain antibody molecules (scfvs) derived, preferably, from the variable  
 CC heavy CDR3 region that immunospecifically bind to a polypeptide, or  
 CC fragment thereof, of either human, murine, rat or monkey BlyS. The  
 CC present invention refers to the use of such antibodies in various methods  
 CC for the detection, diagnosis and prognosis of diseases related to the  
 CC aberrant expression or inappropriate function of BlyS or its receptor. As  
 CC such, these compositions are useful for identifying immune disorders  
 CC including myasthenia gravis and multiple sclerosis, inflammatory  
 CC disorders e.g. asthma and rheumatoid arthritis, infectious diseases such  
 CC as AIDS and proliferative disorders including leukaemia, carcinoma and  
 CC lymphoma. Accordingly, they can be described as exhibiting various  
 CC activities such as antirheumatic, antiarthritic, neuroprotective,  
 CC antiinflammatory, antiasthmatic, antiallergic and cytostatic. This  
 CC polypeptide sequence is a single chain antibody that binds BlyS of the  
 CC invention. NOTE: The sequence data for this patent did not form part of  
 CC the printed specification, but was obtained in electronic format  
 CC directly from WIPO at ftp.wipo.int/pub/published pct\_sequences.

XX  
 SQ Sequence 237 AA;

Query Match 80.9%; Score 72; DB 7; Length 237;  
 Best Local Similarity 82.4%; Pred. No. 0.025;  
 Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 YISGGSGTYSDSVK 17  
 ||||| |||||  
 Db 50 YISGGSGTYSDSVK 66

RESULT 46  
 ADG96855  
 ID ADG96855 standard; protein; 237 AA.  
 AC ADG96855;

DT 11-MAR-2004 (first entry)

DE Single chain antibody that immunospecifically binds BlyS SeqID 2039.

KW antibody; B lymphocyte stimulator; BlyS; tumour necrosis factor;  
 KW B cell proliferation; differentiation; scFv; myasthenia gravis;  
 KW multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia;  
 KW carcinoma; lymphoma; antirheumatic; antiallergic; neuroprotective;  
 KW antiinflammatory; antiasthmatic; antiallergic; cytostatic.

XX Unidentified.

OS WO2003055979-A2.

PN 10-JUL-2003.

PD 14-NOV-2002; 2002WO-US036496.

PF 16-NOV-2001; 2001US-0331469P.

PR 19-DEC-2001; 2001US-0340817P.

XX (HUMA-) HUMAN GENOME SCI INC.

PI Ruben SM, Barash SC, Choi GH, Vaughan TJ, Hilbert D;

DR WPI; 2003-505530/47.

XX Novel antibody that immunospecifically binds to a B lymphocyte stimulator  
 PT (BlyS), useful for detecting and treating diseases or disorders e.g.  
 PT rheumatoid arthritis, asthma and leukaemia.

PS Example 1; SEQ ID NO 2039; 394pp; English.

XX This invention relates to novel antibodies that immunospecifically bind  
 CC to B lymphocyte stimulator (BlyS). The BlyS gene has been mapped to

CC chromosome 13q34 and encodes a protein that is a member of the tumour  
 CC necrosis factor superfamily and induces both in vivo and in vitro B cell  
 CC proliferation and differentiation. Specifically, it refers to single  
 CC chain antibody molecules (scfvs) derived, preferably, from the variable  
 CC heavy CDR3 region that immunospecifically bind to a polypeptide, or  
 CC fragment thereof, of either human, murine, rat or monkey BlyS. The  
 CC present invention refers to the use of such antibodies in various methods  
 CC for the detection, diagnosis and prognosis of diseases related to the  
 CC aberrant expression or inappropriate function of BlyS or its receptor. As  
 CC such, these compositions are useful for identifying immune disorders  
 CC including myasthenia gravis and multiple sclerosis, inflammatory  
 CC disorders e.g. asthma and rheumatoid arthritis, infectious diseases such  
 CC as AIDS and proliferative disorders including leukaemia, carcinoma and  
 CC lymphoma. Accordingly, they can be described as exhibiting various  
 CC activities such as antirheumatic, antiarthritic, neuroprotective,  
 CC antiinflammatory, antiasthmatic, antiallergic and cytostatic. This  
 CC polypeptide sequence is a single chain antibody that binds BlyS of the  
 CC invention. NOTE: The sequence data for this patent did not form part of  
 CC the printed specification, but was obtained in electronic format  
 CC directly from WIPO at ftp.wipo.int/pub/published pct\_sequences.

XX  
 SQ Sequence 237 AA;

Query Match 80.9%; Score 72; DB 7; Length 237;  
 Best Local Similarity 82.4%; Pred. No. 0.025;  
 Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 YISGGSGTYSDSVK 17  
 ||||| |||||  
 Db 50 YISGGSGTYSDSVK 66

RESULT 47  
 ABP45894  
 ID ABP45894 standard; protein; 240 AA.  
 AC ABP45894;

DT 19-AUG-2002 (first entry)

DE Human BlyS binding scFv SEQ ID 1905.

KW BlyS; B lymphocyte stimulator; TNF superfamily; human; cytostatic;  
 KW tumour necrosis factor; B cell proliferation; B cell differentiation;  
 KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;  
 KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;  
 KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;  
 KW common variable immunodeficiency; acquired immunodeficiency syndrome.

XX Homo sapiens.

OS WO200202641-A1.

PN 10-JAN-2002.

PD 15-JUN-2001; 2001WO-US019110.

PF 16-JUN-2000; 2000US-0212210P.

PR 17-OCT-2000; 2000US-0240816P.

PR 16-MAR-2001; 2001US-0276248P.

PR 21-MAR-2001; 2001US-0277379P.

PR 25-MAY-2001; 2001US-0293499P.

XX (HUMA-) HUMAN GENOME SCI INC.

PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.

XX Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;

DR WPI; 2002-114799/15.

PT Antibodies against B lymphocyte stimulating polypeptides, useful for the  
 PT diagnosis and treatment of cancers and immune disorders.



CC treating, preventing or ameliorating type II diabetes. The current  
 CC sequence is that of the human scFv protein of the invention.

XX  
 SQ Sequence 246 AA;  
 Query Match 80.9%; Score 72; DB 7; Length 246;  
 Best Local Similarity 82.4%; Pred. No. 0.026;  
 Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YISSGGSGTYSDSVKG 17  
 ||||| |||||  
 Db 50 YISSGSGTYYTDSVKG 66

RESULT 50

AAR06251  
 ID AAR06251 standard; protein; 136 AA.

XX AC AAR06251,  
 XX DT 10-DEC-1990 (first entry)  
 XX DE Variable region of murine AHT 54 heavy chain.  
 XX KW Interleukin-2 receptor; IL-2; tumour necrosis factor; TNF; ss.  
 XX OS Mus sp.

XX PN EP380068-A.  
 XX PD 01-AUG-1990.  
 XX PF 24-JAN-1990; 90BP-00101351.  
 XX PR 24-JAN-1989; 89US-00301216.  
 XX PR 04-DEC-1989; 89US-00441702.  
 XX PA (MOLE-) MOLECULAR THERAPEU.

XX PI Zerler B;  
 XX DR WPI; 1990-232892/31.  
 XX DR N-PSDB; AAQ05555.  
 XX PT Expression vectors for producing chimeric monoclonal antibodies - which  
 XX express human constant region and non-human variable region.

XX PS Disclosure; Page ?; -pp; English.  
 XX CC Mabs comprising mouse CH and CL constant regions with human variable  
 XX CC regions may be used to create mouse/human hybrid Mabs, which have a  
 XX CC longer serum half-life. Method can be used to produce Abs against  
 XX CC interleukin-2 receptor and tumour necrosis factor

XX SQ Sequence 136 AA;  
 Query Match 79.8%; Score 71; DB 2; Length 136;  
 Best Local Similarity 76.5%; Pred. No. 0.019;  
 Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 YISSGGSGTYSDSVKG 17  
 ||||| |||||  
 Db 69 YISSGGDNTYYPTVKG 85

Search completed: April 6, 2006, 09:04:37  
 Job time : 141.203 secs

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OM protein - protein search, using sw model

Run on: April 6, 2006, 08:56:41 ; Search time 17 Seconds  
(without alignments)  
96.217 Million cell updates/sec

Title: US-10-089-500-4  
Perfect score: 89  
Sequence: 1 YISSGSGTYYSDSVK 17

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database : PIR 80:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	74	83.1	111	2 PH1007	Ig heavy chain v r
2	71	79.8	83	2 S21593	Ig heavy chain v r
3	71	79.8	113	2 S26468	Ig heavy chain v r
4	71	79.8	117	1 HVMS34	Ig heavy chain v r
5	68	76.4	83	2 C25913	Ig heavy chain pre
6	68	76.4	94	2 S14580	Ig heavy chain v r
7	68	76.4	102	2 S14581	Ig heavy chain v r
8	68	76.4	106	2 PH1008	Ig heavy chain v r
9	68	76.4	108	2 S24251	Ig heavy chain v r
10	68	76.4	108	2 PH1010	Ig heavy chain v r
11	68	76.4	117	1 HVMS84	Ig heavy chain pre
12	68	76.4	118	2 PH0097	Ig heavy chain v r
13	68	76.4	119	2 F27888	Ig heavy chain v r
14	68	76.4	120	2 S55337	Ig heavy chain v r
15	68	76.4	120	2 S55336	Ig heavy chain v r
16	68	76.4	122	2 S27888	Ig heavy chain v r
17	67	75.3	108	2 FL0248	Ig heavy chain v r
18	67	75.3	118	2 S20641	Ig heavy chain v r
19	67	75.3	138	2 S09258	Ig heavy chain v r
20	66	74.2	97	2 S24252	Ig heavy chain v r
21	66	74.2	98	2 S26891	Ig heavy chain v r
22	66	74.2	98	2 S26930	Ig heavy chain v r
23	66	74.2	110	2 PH1652	Ig heavy chain v r
24	66	74.2	114	2 S31120	Ig heavy chain - h
25	66	74.2	118	2 S31105	Ig heavy chain (eu
26	66	74.2	119	2 D27889	Ig heavy chain v r
27	66	74.2	128	2 S26790	Ig heavy chain v r
28	66	74.2	137	2 I47193	Ig heavy chain var
29	65	73.0	118	2 S00700	Ig heavy chain v r

30	65	73.0	121	2 I27887	Ig heavy chain v r
31	65	73.0	123	2 S63597	Ig heavy chain, v
32	65	73.0	124	2 C27888	Ig heavy chain v r
33	65	73.0	213	2 S68213	Ig heavy chain (Ma
34	65	73.0	548	2 S38864	Ig epsilon chain C
35	64	71.9	97	2 PH0875	Ig heavy chain v r
36	64	71.9	98	1 HVMS96	Ig heavy chain v r
37	64	71.9	101	2 C27889	Ig heavy chain v r
38	64	71.9	119	2 B27889	Ig heavy chain v r
39	64	71.9	121	2 A27888	Ig heavy chain v r
40	64	71.9	121	2 B27888	Ig heavy chain v r
41	64	71.9	152	2 B26471	Ig heavy chain pre
42	63	70.8	102	2 PH1017	Ig heavy chain v r
43	63	70.8	119	1 AHUBR	Ig heavy chain v-l
44	63	70.8	135	2 I37778	Ig variable region
45	63	70.8	140	2 I47204	Ig heavy chain var
46	62	69.7	117	1 HVMS57	Ig heavy chain pre
47	62	69.7	118	2 PH0096	Ig heavy chain v r
48	62	69.7	120	2 S55339	Ig heavy chain v r
49	62	69.7	121	2 H27887	Ig heavy chain v r
50	62	69.7	134	2 S31699	Ig heavy chain v r
51	62	69.7	140	2 S31686	Ig heavy chain v r
52	61	68.5	98	2 PH0874	Ig heavy chain v r
53	61	68.5	119	2 B34353	anti-peptide Fab'
54	61	68.5	146	2 I47196	Ig heavy chain var
55	61	68.5	254	2 B31790	Ig heavy chain v r
56	60.5	68.0	97	1 HVMS91	Ig heavy chain v r
57	60.5	68.0	112	2 S26327	Ig heavy chain v r
58	60	67.4	98	2 S26894	Ig heavy chain v r
59	60	67.4	108	2 PH1006	Ig heavy chain v r
60	60	67.4	110	2 S36282	Ig heavy chain v r
61	60	67.4	117	2 S21980	Ig heavy chain v-g
62	60	67.4	121	2 S55540	Ig heavy chain v r
63	60	67.4	123	2 S26794	Ig heavy chain v r
64	60	67.4	125	2 S30531	Ig heavy chain v r
65	60	67.4	141	2 I47179	Ig heavy chain var
66	60	67.4	143	2 S23624	Ig heavy chain v r
67	60	67.4	145	2 I47203	Ig heavy chain var
68	59	66.3	73	2 G25114	Ig heavy chain v r
69	59	66.3	90	2 S24248	Ig heavy chain v r
70	59	66.3	98	2 S26889	Ig heavy chain v r
71	59	66.3	99	2 S24259	Ig heavy chain v r
72	59	66.3	100	2 S24258	Ig heavy chain v r
73	59	66.3	101	2 S24257	Ig heavy chain v r
74	59	66.3	102	2 S24260	Ig heavy chain v r
75	59	66.3	104	2 S24255	Ig heavy chain v r
76	59	66.3	105	2 S24249	Ig heavy chain v r
77	59	66.3	106	2 S24256	Ig heavy chain v r
78	59	66.3	108	2 PH1648	Ig heavy chain v r
79	59	66.3	108	2 PH1015	Ig heavy chain v r
80	59	66.3	109	2 S24254	Ig heavy chain v r
81	59	66.3	109	2 S24253	Ig heavy chain v r
82	59	66.3	109	2 PH1649	Ig heavy chain v r
83	59	66.3	110	2 S24250	Ig heavy chain v r
84	59	66.3	112	2 PH1647	Ig heavy chain v r
85	59	66.3	113	2 S24247	Ig heavy chain v r
86	59	66.3	115	2 S09382	Ig heavy chain - c
87	59	66.3	117	2 A45953	Ig heavy chain pre
88	59	66.3	117	2 A34964	Ig heavy chain pre
89	59	66.3	118	2 S31121	Ig heavy chain - h
90	59	66.3	119	2 S36005	Ig heavy chain v r
91	59	66.3	119	2 S31107	Ig heavy chain - h
92	59	66.3	119	2 C36005	Ig heavy chain v r
93	59	66.3	119	2 S31108	Ig heavy chain - h
94	59	66.3	120	2 S48798	Ig heavy chain v r
95	59	66.3	120	2 S36278	Ig heavy chain v r
96	59	66.3	120	2 S55338	Ig heavy chain v r
97	59	66.3	121	2 S31113	Ig heavy chain - h
98	59	66.3	121	2 I55673	Ig heavy chain - h
99	59	66.3	121	2 H27888	Ig heavy chain v r
100	59	66.3	123	2 S31114	Ig heavy chain - h
101	59	66.3	124	2 S20762	Ig heavy chain v r
102	59	66.3	124	2 I27888	Ig heavy chain v r

103	59	66.3	127	2	S38489	Ig heavy chain - h	176	54	60.7	117	2	PL0249	Ig heavy chain V r
104	59	66.3	137	2	I47181	Ig heavy chain var	177	54	60.7	118	2	S31677	Ig heavy chain V r
105	59	66.3	138	2	S31666	Ig heavy chain V r	178	54	60.7	118	2	S31116	Ig heavy chain - h
106	59	66.3	140	2	S31588	Ig heavy chain V r	179	54	60.7	119	2	F36005	Ig heavy chain V r
107	59	66.3	140	2	I47182	Ig heavy chain var	180	54	60.7	120	2	S31112	Ig heavy chain - h
108	59	66.3	141	2	I47197	Ig heavy chain var	181	54	60.7	121	2	S19666	Ig heavy chain V r
109	59	66.3	160	2	S05271	Ig heavy chain pre	182	54	60.7	121	2	G36005	Ig heavy chain V r
110	58	65.2	94	2	D25913	Ig heavy chain V r	183	54	60.7	122	2	E36005	Ig heavy chain V r
111	58	65.2	98	2	S54856	Ig heavy chain V r	184	54	60.7	122	2	S31119	Ig heavy chain - h
112	58	65.2	117	1	H3HU26	Ig heavy chain pre	185	54	60.7	123	2	S38493	Ig heavy chain - h
113	58	65.2	120	2	S12953	Ig heavy chain V r	186	54	60.7	125	2	S20785	Ig heavy chain V r
114	58	65.2	121	2	D27888	Ig heavy chain V r	187	54	60.7	128	2	PH0094	Ig heavy chain V r
115	58	65.2	122	1	AlHUTR	Ig heavy chain V-I	188	54	60.7	130	2	PL0098	Ig heavy chain pre
116	58	65.2	128	2	PH0095	Ig kappa chain V r	189	54	60.7	132	2	S31603	Ig heavy chain V r
117	58	65.2	130	2	I37783	Ig variable region	190	54	60.7	133	2	S31510	Ig heavy chain - h
118	58	65.2	136	1	GLMS21	Ig heavy chain pre	191	54	60.7	134	2	S31679	Ig heavy chain V r
119	57.5	64.6	97	2	S26886	Ig heavy chain V r	192	54	60.7	139	2	S31674	Ig heavy chain V r
120	57.5	64.6	97	2	S26886	Ig heavy chain V r	193	53.5	60.1	147	2	I47183	Ig heavy chain var
121	57.5	64.6	116	2	S12557	Ig heavy chain - h	194	53	59.6	98	2	F47624	Ig heavy chain V-I
122	57.5	64.6	146	2	I47184	Ig heavy chain var	195	53	59.6	111	2	S51211	Ig heavy chain V r
123	57	64.0	53	2	I50832	Ig heavy chain - L	196	53	59.6	111	2	PL0199	anti-DNA autoantib
124	57	64.0	110	2	S69897	Ig heavy chain V r	197	53	59.6	117	2	PH1542	Ig H chain V regio
125	57	64.0	111	2	S69911	Ig V-D-J region (R	198	53	59.6	117	2	PH1553	Ig H chain V regio
126	57	64.0	113	2	S25571	Ig heavy chain V r	199	52.5	59.0	139	2	S38808	Ig heavy chain - m
127	57	64.0	119	2	PH0098	Ig heavy chain V r	200	52	58.4	96	2	S20781	Ig heavy chain V r
128	57	64.0	120	2	E49590	Ig heavy chain V r	201	52	58.4	98	2	S29543	Ig heavy chain V r
129	57	64.0	125	2	S72665	Ig heavy chain V r	202	52	58.4	98	2	S26934	Ig heavy chain V r
130	57	64.0	143	2	I47202	Ig heavy chain var	203	52	58.4	98	2	S26940	Ig heavy chain V r
131	57	64.0	145	2	I47186	Ig heavy chain var	204	52	58.4	109	2	PH1653	Ig heavy chain V r
132	56.5	63.5	97	2	S26935	Ig heavy chain V r	205	52	58.4	115	2	S57445	Ig heavy chain V-J
133	56.5	63.5	97	2	S46462	Ig heavy chain V r	206	52	58.4	116	2	S21979	Ig heavy chain V-g
134	56.5	63.5	100	2	D48223	Ig heavy chain V r	207	52	58.4	117	2	S36259	Ig heavy chain V r
135	56.5	63.5	116	2	B28966	Ig heavy chain pre	208	52	58.4	117	2	PH1535	Ig H chain V regio
136	56.5	63.5	116	2	S31110	Ig heavy chain - h	209	52	58.4	117	2	PH1552	Ig H chain V regio
137	56	62.9	96	2	PH0873	Ig heavy chain V r	210	52	58.4	119	2	PH1541	Ig H chain V regio
138	56	62.9	100	2	PH1016	Ig heavy chain V r	211	52	58.4	119	2	PH1546	Ig H chain V regio
139	56	62.9	108	2	PH1656	Ig heavy chain V r	212	52	58.4	119	2	PH1533	Ig H chain V regio
140	56	62.9	121	2	PH1661	Ig heavy chain V r	213	52	58.4	120	2	B49715	Ig heavy chain V r
141	56	62.9	121	2	B34871	Ig heavy chain V r	214	52	58.4	120	2	PH1534	Ig H chain V regio
142	56	62.9	123	2	G27888	Ig heavy chain V r	215	52	58.4	121	1	GLHURL	Ig heavy chain V-I
143	56	62.9	128	2	S26786	Ig heavy chain V r	216	52	58.4	122	2	PH1537	Ig H chain V regio
144	55.5	62.4	137	2	S78054	Ig heavy chain pre	217	52	58.4	134	2	S31688	Ig heavy chain V r
145	55	61.8	98	2	S26929	Ig heavy chain V r	218	52	58.4	135	2	S31598	Ig heavy chain V r
146	55	61.8	112	2	A27889	Ig heavy chain V r	219	52	58.4	137	2	S31701	Ig heavy chain V r
147	55	61.8	113	2	S02717	Ig heavy chain V r	220	52	58.4	140	2	S70442	Ig heavy chain pre
148	55	61.8	115	2	PH1538	Ig H chain V regio	221	52	58.4	141	2	S31669	Ig heavy chain V r
149	55	61.8	117	1	HVMS39	Ig heavy chain pre	222	52	58.4	148	2	I47210	Ig heavy chain var
150	55	61.8	117	1	HVMSRF	Ig heavy chain pre	223	52	58.4	191	2	HL0048	Ig heavy chain V r
151	55	61.8	119	2	PH1548	Ig H chain V regio	224	52	58.4	504	2	S00390	Ig gamma chain (cl
152	55	61.8	119	2	PH1549	Ig H chain V regio	225	51.5	57.9	122	2	A33989	Ig heavy chain V-1
153	55	61.8	120	2	S44111	Ig heavy chain V-D	226	51	57.3	116	2	A38291	Ig heavy chain pre
154	55	61.8	136	2	S31615	hypothetical prote	227	51	57.3	118	2	PH1539	Ig H chain V regio
155	54.5	61.2	92	2	S56009	Ig heavy chain var	228	51	57.3	122	2	PC2398	anti-tetanus toxin
156	54	60.7	70	2	PL0250	Ig heavy chain V r	229	51	57.3	141	2	I47177	Ig H-chain - pig (
157	54	60.7	94	2	PL0120	Ig heavy chain V r	230	50	56.2	118	2	PH1662	Ig heavy chain V r
158	54	60.7	97	2	S44115	Ig heavy chain V-I	231	50	56.2	119	2	PH1554	Ig H chain V regio
159	54	60.7	98	2	PL0116	Ig heavy chain V-I	232	50	56.2	119	2	A43413	Ig heavy chain V r
160	54	60.7	98	2	S29545	Ig heavy chain V r	233	50	56.2	121	2	S26798	Ig heavy chain V r
161	54	60.7	98	2	S29546	Ig heavy chain V r	234	50	56.2	140	2	A30532	Ig heavy chain pre
162	54	60.7	98	2	S26896	Ig heavy chain V r	235	50	56.2	147	2	I37780	Ig variable region
163	54	60.7	109	2	PH1646	Ig heavy chain V r	236	49.5	55.6	98	2	S26933	Ig heavy chain V r
164	54	60.7	109	2	PH1644	Ig heavy chain V r	237	49.5	55.6	117	1	MHDGMO	Ig heavy chain V r
165	54	60.7	110	2	PH1014	Ig heavy chain V r	238	49.5	55.6	152	2	I47198	Ig heavy chain V r
166	54	60.7	111	2	PH1643	Ig heavy chain V r	239	49	55.1	108	2	PH1011	Ig heavy chain V r
167	54	60.7	111	2	PH1645	Ig heavy chain - h	240	49	55.1	108	2	PH1642	Ig heavy chain V r
168	54	60.7	113	2	S38490	Ig heavy chain - h	241	49	55.1	114	2	S46391	Ig heavy chain V r
169	54	60.7	114	1	M3HUME	Ig heavy chain V-I	242	49	55.1	115	1	A2HUBU	Ig heavy chain V-I
170	54	60.7	114	2	S46390	Ig heavy chain V r	243	49	55.1	115	2	S44112	Ig heavy chain V r
171	54	60.7	114	2	S46392	Ig heavy chain V r	244	49	55.1	115	2	PG6026	acetylcoline recep
172	54	60.7	114	2	PH1009	Ig heavy chain V r	245	49	55.1	117	2	S34012	Ig heavy chain V r
173	54	60.7	117	2	B34964	Ig heavy chain pre	246	49	55.1	118	2	PH1532	Ig H chain V regio
174	54	60.7	117	2	S36270	Ig heavy chain V r	247	49	55.1	118	2	PH1550	Ig H chain V regio
175	54	60.7	117	2	PL0252	Ig heavy chain V r	248	49	55.1	119	2	S31111	Ig heavy chain - h

249	49	55.1	119	2	PH1547	Ig H chain V regio	322	45	50.6	190	1	WMV221	21.5K protein - va
250	49	55.1	119	2	PH1531	Ig H chain V regio	323	45	50.6	266	2	E64314	translation initia
251	49	55.1	119	2	PH1551	Ig H chain V regio	324	44.5	50.0	142	2	I47206	Ig heavy chain var
252	49	55.1	122	2	S31117	Ig heavy chain - h	325	44	49.4	35	2	S26887	Ig heavy chain v r
253	49	55.1	124	2	S20784	Ig heavy chain v r	326	44	49.4	86	2	S21595	Ig heavy chain v r
254	49	55.1	128	2	S48797	Ig heavy chain v r	327	44	49.4	95	2	S20777	Ig heavy chain v r
255	49	55.1	133	2	A49028	Ig heavy chain v-I	328	44	49.4	99	2	S20765	Ig heavy chain v r
256	48.5	54.5	92	2	S56008	Ig heavy chain var	329	44	49.4	116	2	S17080	Ig heavy chain v-g
257	48	53.9	111	2	S40090	Ig heavy chain - m	330	44	49.4	118	2	PH1660	Ig heavy chain v r
258	48	53.9	116	2	H29380	Ig heavy chain pre	331	44	49.4	122	2	S20772	Ig heavy chain v r
259	48	53.9	118	2	E27889	Ig heavy chain v r	332	44	49.4	127	2	PT0369	Ig gamma chain pre
260	48	53.9	118	2	A31485	Ig heavy chain v r	333	44	49.4	143	2	I47201	Ig heavy chain var
261	48	53.9	119	2	PH1544	Ig H chain V regio	334	44	49.4	413	2	G69842	3-oxoacyl-lacyl-ca
262	48	53.9	119	2	PH1555	Ig H chain V regio	335	44	49.4	590	2	A29904	keratin 5, type II
263	48	53.9	137	2	B34903	Ig heavy chain pre	336	44	49.4	2723	2	T03221	probable polyketid
264	48	53.9	137	2	A34903	Ig heavy chain pre	337	43.5	48.9	138	2	I47205	Ig heavy chain var
265	48	53.9	137	2	D34903	Ig heavy chain pre	338	43	48.3	98	2	S26928	Ig heavy chain v r
266	48	53.9	137	2	F34903	Ig heavy chain pre	339	43	48.3	113	2	S57441	Ig heavy chain v r
267	48	53.9	139	2	I47207	Ig heavy chain pre	340	43	48.3	119	2	S37453	Ig mu chain - huma
268	48	53.9	140	2	S22657	Ig heavy chain pre	341	43	48.3	126	1	G1HUKL	Ig heavy chain v-I
269	48	53.9	140	2	I47208	Ig heavy chain var	342	43	48.3	137	2	E34903	Ig heavy chain pre
270	48	53.9	145	2	I47185	Ig heavy chain var	343	43	48.3	147	2	PH0124	Ig heavy chain pre
271	48	53.9	147	2	PH0127	Ig heavy chain pre	344	43	48.3	309	2	T08150	Ig delta chain (WI
272	48	53.9	147	2	PH0131	Ig heavy chain pre	345	43	48.3	509	2	S17597	anaerobic dimethyl
273	48	53.9	147	2	PH0135	Ig heavy chain pre	346	43	48.3	814	2	A80612	hypothetical prote
274	48	53.9	147	2	PH0130	Ig heavy chain pre	347	43	48.3	1780	2	T20695	Ig heavy chain var
275	48	53.9	148	2	I47180	Ig heavy chain var	348	42.5	47.8	150	2	I47200	sericin - silkworm
276	48	53.9	151	2	A60943	Ig heavy chain pre	349	42.5	47.8	190	2	A24713	Ig heavy chain v r
277	47.5	53.4	86	2	S26788	Ig heavy chain v r	350	42	47.2	113	2	JL0049	Ig heavy chain pre
278	47.5	53.4	96	2	S54854	Ig heavy chain v r	351	42	47.2	147	2	PH0120	Ig heavy chain pre
279	47.5	53.4	102	2	S14486	Ig heavy chain v r	352	42	47.2	148	2	PH0121	Ig heavy chain pre
280	47	52.8	76	2	S31592	Ig heavy chain v r	353	42	47.2	148	2	PH0116	Ig heavy chain pre
281	47	52.8	97	2	S54855	Ig heavy chain v r	354	42	47.2	148	2	PH0117	Ig heavy chain pre
282	47	52.8	97	2	S26895	Ig heavy chain v r	355	42	47.2	148	2	PH0115	Ig heavy chain pre
283	47	52.8	97	2	PH0872	Ig heavy chain v r	356	42	47.2	148	2	PH0119	Ig heavy chain pre
284	47	52.8	98	2	PL0121	Ig heavy chain v-I	357	42	47.2	355	2	A33821	chromosomal protei
285	47	52.8	98	2	S26932	Ig heavy chain v r	358	42	47.2	445	2	A11418	D-alanyl-D-alanine
286	47	52.8	98	2	PL0123	Ig heavy chain v-I	359	42	47.2	471	2	JC1403	glutamate-ammonia
287	47	52.8	101	2	JT0511	Ig heavy chain v-I	360	42	47.2	472	2	T23534	hypothetical prote
288	47	52.8	105	2	S38488	Ig heavy chain - h	361	42	47.2	481	2	A35628	loricrin - mouse
289	47	52.8	110	2	PH1655	Ig heavy chain v r	362	42	47.2	487	2	F72126	ct339 hypothetical
290	47	52.8	114	2	S36280	Ig heavy chain v r	363	42	47.2	487	2	B86495	Cr339 hypothetical
291	47	52.8	115	2	S36284	Ig heavy chain v r	364	42	47.2	487	2	A81545	conserved hypotet
292	47	52.8	117	2	S17079	Ig heavy chain v-g	365	42	47.2	721	2	F70649	probable Acyl-CoA
293	47	52.8	117	2	S78486	Ig heavy chain v r	366	42	47.2	736	2	T26006	hypothetical prote
294	47	52.8	122	1	M3HUAM	Ig heavy chain v-I	367	42	47.2	781	2	F83884	conserved hypotet
295	47	52.8	122	2	S31675	Ig heavy chain v r	368	42	47.2	1041	2	D82792	Ig heavy chain v r
296	47	52.8	122	2	S69910	Ig V-D-J region (K	369	41.5	46.6	94	2	S26461	Ig heavy chain v r
297	47	52.8	136	2	S31587	Ig heavy chain v r	370	41.5	46.6	100	2	S14485	Ig heavy chain v r
298	47	52.8	139	2	I37781	Ig variable region	371	41.5	46.6	101	2	S14484	Ig heavy chain v r
299	47	52.8	142	2	C34903	Ig heavy chain pre	372	41.5	46.6	113	1	G2MS60	Ig mu chain precu
300	47	52.8	249	2	S69340	Ig heavy chain vH	373	41.5	46.6	115	2	D33932	Ig heavy chain v r
301	47	52.8	313	2	D85855	probable kinase ye	374	41.5	46.6	137	2	S31585	Ig heavy chain v r
302	47	52.8	313	2	B91011	probable kinase fi	375	41	46.1	94	2	S20653	Ig heavy chain v r
303	47	52.8	313	2	E64985	hypothetical 33.6K	376	41	46.1	94	2	S20650	Ig heavy chain v r
304	46	51.7	113	2	PH1018	Ig heavy chain v r	377	41	46.1	100	2	S26462	Ig heavy chain v r
305	46	51.7	115	2	S36267	Ig heavy chain v r	378	41	46.1	110	2	PH1092	Ig heavy chain v r
306	46	51.7	117	2	PH1556	Ig H chain V regio	379	41	46.1	110	2	PH1091	Ig heavy chain v r
307	46	51.7	125	2	S37455	Ig mu chain - huma	380	41	46.1	112	2	PH1654	Ig heavy chain v r
308	46	51.7	132	2	I47191	Ig heavy chain var	381	41	46.1	119	2	A27630	Ig heavy chain pre
309	46	51.7	136	2	S16847	Ig heavy chain v r	382	41	46.1	120	1	M3HUBW	Ig heavy chain v-I
310	46	51.7	136	2	S60296	Ig heavy-chain var	383	41	46.1	120	2	S36273	Ig heavy chain v r
311	46	51.7	155	2	I47199	Ig heavy chain var	384	41	46.1	121	2	A41940	Ig heavy chain v r
312	46	51.7	326	2	D87598	TonB-dependent rec	385	41	46.1	121	2	S09958	Ig heavy chain V-D
313	46	51.7	572	2	B46529	Ig V heavy chain (	386	41	46.1	122	1	M3HUGA	Ig heavy chain v-I
314	45	50.6	60	2	JT0512	Ig heavy chain v-I	387	41	46.1	138	2	B56701	Ig heavy chain v r
315	45	50.6	116	2	PH1540	Ig H chain V regio	388	41	46.1	138	2	S03526	Ig heavy chain pre
316	45	50.6	118	2	PH1530	Ig H chain V regio	389	41	46.1	139	2	PC1213	Ig heavy chain pre
317	45	50.6	118	2	A49026	Ig heavy chain v r	390	41	46.1	139	2	G29380	Ig heavy chain pre
318	45	50.6	118	2	PH1536	Ig H chain V regio	391	41	46.1	141	2	I32513	Ig heavy chain pre
319	45	50.6	127	2	PL0254	Ig heavy chain v r	392	41	46.1	142	2	I47198	Ig heavy chain var
320	45	50.6	127	2	S19878	Ig heavy chain v r	393	41	46.1	148	2	PH0118	Ig heavy chain pre
321	45	50.6	147	2	PH0123	Ig heavy chain pre	394	41	46.1	318	2	A43746	nsain resistance p

395	41	46.1	327	2	S57121	hypothetical prote	468	39	43.8	274	1	A30879	NAD(P)H2 dehydroge
396	41	46.1	333	2	B69853	transcription regu	469	39	43.8	274	1	A34162	NAD(P)H2 dehydroge
397	41	46.1	344	2	C81920	hypothetical prote	470	39	43.8	274	1	A57691	NAD(P)H2 dehydroge
398	41	46.1	344	2	E81183	copper ABC transpo	471	39	43.8	309	2	B87576	hypothetical prote
399	41	46.1	411	2	B84010	3-oxoacyl-(acyl-ca	472	39	43.8	348	2	T04923	hypothetical prote
400	41	46.1	453	2	T44661	nosd protein [impo	473	39	43.8	363	2	AH1880	hypothetical prote
401	41	46.1	488	2	A32235	poly(3-hydroxybuty	474	39	43.8	390	2	JC7162	GoIgi UDP-galactos
402	41	46.1	526	2	E88940	protein C05E4.9 (i	475	39	43.8	396	2	JC5022	UDP-galactose tran
403	41	46.1	608	2	B53295	xyJanase [EC 3.2.1	476	39	43.8	411	2	E97338	3-oxoacyl-(acyl-ca
404	40.5	45.5	111	2	PH1659	Ig heavy chain V r	477	39	43.8	424	2	F70122	flagellar hook-ass
405	40.5	45.5	512	2	F83761	fumarate hydratase	478	39	43.8	430	1	CWUMF	mucorpepsin [EC 3.
406	40	44.9	106	2	S24521	Ig heavy chain V r	479	39	43.8	467	2	S48996	acid phosphatase (
407	40	44.9	106	2	S24521	Ig kappa chain V r	480	39	43.8	467	2	S53476	acid phosphatase (
408	40	44.9	111	1	MWS076	Ig heavy chain V-I	481	39	43.8	478	2	T29174	hypothetical prote
409	40	44.9	115	1	AVMS06	Ig heavy chain V-I	482	39	43.8	499	2	D97000	methyl-accepting c
410	40	44.9	115	2	A25803	Ig heavy chain V r	483	39	43.8	532	2	C97108	penicillin-binding
411	40	44.9	120	1	GLHUBD	Ig heavy chain V-I	484	39	43.8	569	2	S41200	phosphoglucomutase
412	40	44.9	121	1	GVMS11	Ig heavy chain V r	485	39	43.8	585	2	A46507	Ig alpha chain - c
413	40	44.9	125	2	S31509	Ig heavy chain - h	486	39	43.8	608	2	H72292	hypothetical prote
414	40	44.9	125	2	S67945	Ig heavy chain BrE	487	39	43.8	624	2	T04843	hypothetical prote
415	40	44.9	130	2	S31601	Ig heavy chain V r	488	39	43.8	721	2	A51491	hypothetical prote
416	40	44.9	130	2	B32456	Ig kappa chain pre	489	39	43.8	1006	2	S76892	hypothetical prote
417	40	44.9	142	2	I47194	Ig heavy chain var	490	39	43.8	1756	1	BVECAI	DNA helicase I [EC
418	40	44.9	220	2	A95362	Probable inner-mem	491	39	43.8	2342	2	T18200	fatty-acid synthas
419	40	44.9	228	2	S03050	Ig gamma chain (cl	492	38.5	43.3	123	2	S30532	Ig heavy chain V r
420	40	44.9	239	2	E70800	probable transport	493	38.5	43.3	141	2	I47209	Ig heavy chain var
421	40	44.9	312	2	H81432	probable membrane	494	38.5	43.3	172	2	D72372	hypothetical prote
422	40	44.9	332	2	T44437	aminodeoxychromi	495	38.5	43.3	498	1	VGXPLC	surface glycoprote
423	40	44.9	348	2	A70311	hypothetical prote	496	38	42.7	55	2	E84939	S05 ribosomal prot
424	40	44.9	352	2	A97044	uncharacterized co	497	38	42.7	57	2	G81372	probable lipoprote
425	40	44.9	354	2	B69284	sarcosine oxidase,	498	38	42.7	68	2	B43940	lactococcin B prec
426	40	44.9	373	2	A56133	constans protein -	499	38	42.7	75	2	A25155	Ig heavy chain V r
427	40	44.9	387	2	E95933	probable calcium-b	500	38	42.7	97	2	S26890	Ig heavy chain V r
428	40	44.9	417	2	B62554	3-ketoacyl-CoA thi	501	38	42.7	98	2	S31652	Ig kappa chain V r
429	40	44.9	508	2	T22440	hypothetical prote	502	38	42.7	107	2	B48677	Ig kappa chain V-J
430	40	44.9	719	2	AE1131	hypothetical prote	503	38	42.7	107	2	C48677	Ig light chain V-J
431	40	44.9	721	2	B83237	probable TonB-depe	504	38	42.7	107	2	A48677	Ig kappa chain V-J
432	40	44.9	731	2	T04455	hypothetical prote	505	38	42.7	108	2	PH1651	Ig heavy chain V r
433	40	44.9	817	2	T22442	hypothetical prote	506	38	42.7	113	1	AVMS09	Ig heavy chain V-I
434	40	44.9	846	2	A30889	integrin beta chai	507	38	42.7	113	1	AVMS61	Ig heavy chain V-I
435	40	44.9	1029	2	T28956	hypothetical prote	508	38	42.7	113	1	AVMSAB	Ig heavy chain V-I
436	40	44.9	2399	2	H71879	toxin-like outer m	509	38	42.7	113	1	AVMSB7	Ig heavy chain V-I
437	40	44.9	2529	2	B64635	toxin-like outer m	510	38	42.7	115	1	AVMS82	Ig heavy chain V-I
438	40	44.9	4836	2	T14346	hcr2 protein - mo	511	38	42.7	117	1	HVCQ	Ig heavy chain pre
439	39.5	44.4	113	2	A34792	Ig heavy chain pre	512	38	42.7	117	2	A28966	Ig heavy chain pre
440	39.5	44.4	114	2	B34792	Ig heavy chain pre	513	38	42.7	119	1	PSNOA1	phospholipase A2 h
441	39.5	44.4	271	2	C69352	imidazoleglycerol-	514	38	42.7	120	2	PH1650	Ig heavy chain V r
442	39.5	44.4	1217	2	S52714	sericin1B - silkwo	515	38	42.7	133	2	S31590	ataf protein - Rec
443	39.5	44.4	3194	2	D71917	toxin-like outer m	516	38	42.7	147	2	G55545	hypothetical prote
444	39	43.8	35	2	S46473	Ig heavy chain V r	517	38	42.7	151	2	T28264	hypothetical prote
445	39	43.8	88	2	C25155	Ig heavy chain V r	518	38	42.7	201	2	S09887	late competence op
446	39	43.8	88	2	E25155	Ig heavy chain V r	519	38	42.7	205	2	S39863	probable ABC trans
447	39	43.8	88	2	G25155	Ig heavy chain V r	520	38	42.7	221	2	T35856	hypothetical prote
448	39	43.8	88	2	F25155	Ig heavy chain V r	521	38	42.7	238	2	S12259	hypothetical prote
449	39	43.8	96	2	PH1165	Ig heavy chain V r	522	38	42.7	250	2	T10079	expansin S1 precu
450	39	43.8	101	2	S26460	Ig heavy chain V r	523	38	42.7	264	2	AD3353	probable membrane
451	39	43.8	101	2	B42575	Ig heavy chain V r	524	38	42.7	289	2	B25974	phycocyanin-associ
452	39	43.8	102	2	PH1239	Ig heavy chain V r	525	38	42.7	307	2	G68839	phosphate ABC tran
453	39	43.8	106	2	S20774	Ig heavy chain V r	526	38	42.7	325	1	C68805	iron(III) dicitrat
454	39	43.8	107	2	T27713	hypothetical prote	527	38	42.7	326	2	T49966	myo-related protei
455	39	43.8	110	2	PH1093	Ig heavy chain V r	528	38	42.7	347	2	G96700	protein F12A31.7 (
456	39	43.8	110	2	PH1000	Ig heavy chain V r	529	38	42.7	359	2	H96969	aspartate semialde
457	39	43.8	115	2	S38714	Ig heavy chain V r	530	38	42.7	362	2	T45131	DNA-methyltransfer
458	39	43.8	122	2	A49049	Ig heavy chain V r	531	38	42.7	368	2	F64017	hypothetical prote
459	39	43.8	123	2	B30560	Ig heavy chain V r	532	38	42.7	378	2	C81824	3-oxoacyl-(acyl-ca
460	39	43.8	126	2	PH1416	Ig heavy chain V r	533	38	42.7	394	2	S28027	cycochrome-c oxida
461	39	43.8	141	2	I47178	Ig heavy chain var	534	38	42.7	398	2	A37146	probable glycosylt
462	39	43.8	150	2	S39980	hemoglobin II alph	535	38	42.7	412	2	G71922	beta-ketoacyl-acp
463	39	43.8	182	2	A02947	keratin, 60K type	536	38	42.7	412	2	F64589	3-oxoacyl-(acyl-ca
464	39	43.8	214	2	TS1547	hypothetical prote	537	38	42.7	426	2	S72732	B1177 C2 197 prote
465	39	43.8	243	2	F90197	hypothetical prote	538	38	42.7	427	2	A25767	mucorpepsin [EC 3.
466	39	43.8	256	2	E71807	hypothetical prote	539	38	42.7	429	2	S23581	lamb protein precu
467	39	43.8	274	1	I52851	NAD(P)H2 dehydroge	540	38	42.7	438	2	B69023	conserved hypothet



541	38	42.7	444	2	T25413	hypothetical prote	614	37.5	42.1	362	2	JH0539	class I histocompa
542	38	42.7	453	2	D95342	NoSD periplasmic c	615	37.5	42.1	362	2	JH0540	class I histocompa
543	38	42.7	472	2	S62494	probable GTPase-ac	616	37.5	42.1	362	2	I36962	MHC class I protei
544	38	42.7	486	2	T48119	hypothetical prote	617	37.5	42.1	362	2	I56130	HLA-B*5401 - huma
545	38	42.7	503	2	T46852	anthranilate synth	618	37.5	42.1	362	2	I84486	transmembrane glyc
546	38	42.7	508	2	T41345	probable allantost	619	37.5	42.1	362	2	I62042	MHC HLA-B cell sur
547	38	42.7	552	2	AB2361	hypothetical prote	620	37.5	42.1	362	2	I37492	HLA-B alpha-chain
548	38	42.7	553	2	S77623	mannuronan C-5-epi	621	37.5	42.1	362	2	I37120	MHC class I histoc
549	38	42.7	555	2	A86970	probable lipoprote	622	37.5	42.1	362	2	S52486	HLA-B protein alph
550	38	42.7	584	1	QQB3J6	alkaline exonuclea	623	37.5	42.1	362	2	B30345	MHC class I histoc
551	38	42.7	588	2	F70971	hypothetical glyci	624	37.5	42.1	362	2	A45834	MHC class I histoc
552	38	42.7	596	2	E96935	FUSION, methionine	625	37.5	42.1	362	2	I61907	MHC class I histoc
553	38	42.7	603	2	A70770	hypothetical glyci	626	37.5	42.1	362	2	I38421	gene HLA B-1519 pr
554	38	42.7	714	2	C81018	iron-regulated out	627	37.5	42.1	362	2	I37515	MHC class I histoc
555	38	42.7	720	2	S58133	Fe-regulated prote	628	37.5	42.1	362	2	C35997	MHC class I histoc
556	38	42.7	753	2	D81219	NADH dehydrogenase	629	37.5	42.1	362	2	I61861	MHC HLA-B*44.2 cha
557	38	42.7	754	2	A84473	probable serine pr	630	37.5	42.1	362	2	I56149	lymphocyte antigen
558	38	42.7	846	2	F83388	hypothetical prote	631	37.5	42.1	362	2	A45850	MHC class I histoc
559	38	42.7	866	2	F64625	type I restriction	632	37.5	42.1	362	2	I81233	lymphocyte antigen
560	38	42.7	868	2	T31527	hypothetical prote	633	37.5	42.1	362	2	I61864	MHC HLA-B*41 chain
561	38	42.7	875	2	B71890	type I restriction	634	37.5	42.1	362	2	I27255	HLA-B*5602 - huma
562	38	42.7	916	2	F97053	penicillin-binding	635	37.5	42.1	362	2	I84488	lymphocyte antigen
563	38	42.7	934	2	G91198	Gamma intimin [imp	636	37.5	42.1	362	2	I61906	MHC class I histoc
564	38	42.7	934	2	C86045	intimin adherence	637	37.5	42.1	362	2	G01230	MHC class I histoc
565	38	42.7	935	1	I41193	outer membrane pro	638	37.5	42.1	362	2	I37522	MHC class I histoc
566	38	42.7	970	2	T30181	hypothetical prote	639	37.5	42.1	362	2	I59633	MHC HLA-B transmem
567	38	42.7	1002	2	T09438	toxR-activated lip	640	37.5	42.1	362	2	I54505	lymphocyte antigen
568	38	42.7	1013	2	B82276	ToxR-activated gen	641	37.5	42.1	362	2	I61904	MHC class I histoc
569	38	42.7	1046	2	T34566	hypothetical prote	642	37.5	42.1	362	2	I72753	HLA-B*5502 - huma
570	38	42.7	1105	2	T47582	hypothetical prote	643	37.5	42.1	362	2	I59654	major histocompati
571	38	42.7	1158	2	B86241	hypothetical prote	644	37.5	42.1	362	2	I54314	MHC HLA-B39N - hum
572	38	42.7	1585	2	T31611	hypothetical prote	645	37.5	42.1	362	2	I59655	lymphocyte antigen
573	38	42.7	1591	2	A54146	invasion-inducing	646	37.5	42.1	362	2	I72754	HLA-B*5601 - huma
574	38	42.7	3472	2	T31308	hypothetical 367K	647	37.5	42.1	362	2	I62045	gene HLA B-1517 pr
575	37.5	42.1	76	2	H30517	Ig heavy chain V-A	648	37.5	42.1	362	2	I61863	MHC HLA-B*46 - hum
576	37.5	42.1	96	2	A26555	Ig heavy chain V r	649	37.5	42.1	362	2	S77966	MHC class I histoc
577	37.5	42.1	99	2	C48223	Ig heavy chain v r	650	37.5	42.1	362	2	I37519	MHC class I histoc
578	37.5	42.1	117	2	G34792	Ig heavy chain pre	651	37.5	42.1	362	2	I54457	MHC class I lympho
579	37.5	42.1	118	2	E34792	Ig heavy chain pre	652	37.5	42.1	362	2	I72752	HLA-B*5501 - huma
580	37.5	42.1	145	2	S07450	hypothetical prote	653	37.5	42.1	362	2	I56133	MHC class I protei
581	37.5	42.1	305	2	T05115	class I histocompa	654	37.5	42.1	362	2	I68724	MHC class I histoc
582	37.5	42.1	308	2	I36956	MHC CHla chain - c	655	37.5	42.1	362	2	I84490	lymphocyte antigen
583	37.5	42.1	328	2	A82087	phosphoserine phos	656	37.5	42.1	362	2	S60601	HLA-B*POT (classI)
584	37.5	42.1	338	2	I56116	MHC HLA-B27-HS - h	657	37.5	42.1	362	2	I59645	HLA-B*6701 - huma
585	37.5	42.1	348	2	I68747	MHC class I lympho	658	37.5	42.1	362	2	I54298	gene HLA-B protein
586	37.5	42.1	350	2	I68747	MHC class I lympho	659	37.5	42.1	362	2	I68850	MHC class I histoc
587	37.5	42.1	354	2	S24433	class I histocompa	660	37.5	42.1	362	2	A30345	MHC class I histoc
588	37.5	42.1	354	2	I59308	class I histocompa	661	37.5	42.1	362	2	I61903	MHC class I histoc
589	37.5	42.1	354	2	I80166	class I histocompa	662	37.5	42.1	362	2	A45880	MHC class I histoc
590	37.5	42.1	354	2	I80167	class I histocompa	663	37.5	42.1	362	2	I61859	MHC HLA-B*14 chain
591	37.5	42.1	354	2	I80165	class I histocompa	664	37.5	42.1	362	2	I84431	MHC HLA-B*8 chain -
592	37.5	42.1	354	2	I80170	class I histocompa	665	37.5	42.1	362	2	I61905	MHC class I histoc
593	37.5	42.1	354	2	I80168	class I histocompa	666	37.5	42.1	362	2	I62043	MHC HLA-B cell sur
594	37.5	42.1	354	2	S24438	class I histocompa	667	37.5	42.1	362	2	I54442	MHC class I histoc
595	37.5	42.1	354	2	S24436	class I histocompa	668	37.5	42.1	362	2	I59651	lymphocyte antigen
596	37.5	42.1	354	2	S24440	class I histocompa	669	37.5	42.1	362	2	I37520	MHC class I histoc
597	37.5	42.1	354	2	S24437	class I histocompa	670	37.5	42.1	362	2	I62041	MHC HLA-B cell sur
598	37.5	42.1	355	2	I80171	class I histocompa	671	37.5	42.1	362	2	I62044	MHC class I histoc
599	37.5	42.1	355	2	I80169	class I histocompa	672	37.5	42.1	362	2	I61865	MHC HLA-B*42, HLA-
600	37.5	42.1	355	2	I37516	HLA-B alpha-chain	673	37.5	42.1	362	2	I61860	MHC HLA-B*18 chain
601	37.5	42.1	356	2	A27797	class I histocompa	674	37.5	42.1	362	2	S16789	class I histocompa
602	37.5	42.1	356	2	B64009	hypothetical prote	675	37.5	42.1	362	2	S25415	class I histocompa
603	37.5	42.1	358	2	S03538	class I histocompa	676	37.5	42.1	362	2	S24435	class I histocompa
604	37.5	42.1	358	2	A28834	MHC class I histoc	677	37.5	42.1	362	2	S24434	class I histocompa
605	37.5	42.1	359	1	HLHUB3	MHC class I histoc	678	37.5	42.1	363	1	S42102	MHC class I histoc
606	37.5	42.1	359	2	I61867	MHC class I protei	679	37.5	42.1	363	2	JH0542	class I histocompa
607	37.5	42.1	361	2	I54418	MHC class I histoc	680	37.5	42.1	363	2	S07113	class I histocompa
608	37.5	42.1	361	2	F90174	sugar phosphate nu	681	37.5	42.1	363	2	S03537	class I histocompa
609	37.5	42.1	362	1	HLHUB8	MHC class I histoc	682	37.5	42.1	364	2	D35997	MHC class I histoc
610	37.5	42.1	362	1	HLHU40	MHC class I histoc	683	37.5	42.1	419	2	S22136	endothiapepsin (EC
611	37.5	42.1	362	1	HLHUB2	MHC class I histoc	684	37.5	42.1	470	2	S22080	Ig heavy chain pre
612	37.5	42.1	362	1	HLHUB7	MHC class I histoc	685	37.5	42.1	497	2	C72213	conserved hypothet
613	37.5	42.1	362	2	JH0541	class I histocompa	686	37.5	42.1	635	1	A29358	cerevisin (EC 3.4.

687	37	41.6	59	2	S11812	opacity protein (c	760	404	1	VHVNS	nucleoprotein - he
688	37	41.6	64	2	I77394	Ig heavy chain v r	761	404	2	S34562	nucleoside prot
689	37	41.6	94	2	PH0996	Ig heavy chain v r	762	409	2	S10485	licheninase (EC 3.
690	37	41.6	97	2	S17603	Ig heavy chain v r	763	422	2	AH1614	weakly pyrophospha
691	37	41.6	98	2	S26927	Ig heavy chain v r	764	429	2	AC3303	isocitrate lyase (
692	37	41.6	98	2	A28572	Ig heavy chain v r	765	431	2	B97277	probable O-antigen
693	37	41.6	98	2	S26313	Ig heavy chain v r	766	434	2	AB2651	isocitrate lyase (
694	37	41.6	98	2	S26312	Ig heavy chain v r	767	434	2	A97433	icl containing pro
695	37	41.6	101	2	S26311	Ig heavy chain v r	768	437	2	A23330	preprotein translo
696	37	41.6	101	2	S28310	Ig heavy chain v r	769	437	2	B98074	hypothetical prote
697	37	41.6	104	2	PH0991	Ig heavy chain v r	770	441	2	F96519	hypothetical prote
698	37	41.6	106	2	F32513	Ig heavy chain v r	771	448	2	A26190	glucuronate permease
699	37	41.6	109	2	PH0989	Ig heavy chain v r	772	450	2	A54429	paired box transcr
700	37	41.6	109	2	PH1094	Ig heavy chain v r	773	455	2	C83494	probable 2-isoprop
701	37	41.6	109	2	PH1096	Ig heavy chain v r	774	457	2	A56925	paired box transcr
702	37	41.6	110	2	PH0995	Ig heavy chain v r	775	459	2	S22250	paired box transcr
703	37	41.6	111	2	PH0990	Ig heavy chain v r	776	461	2	H84099	cell wall-binding
704	37	41.6	111	2	PH0993	Ig heavy chain v r	777	469	2	A10187	phosphoglucuronate d
705	37	41.6	111	2	PH0994	Ig heavy chain v r	778	470	1	S14628	phosphoglucuronate d
706	37	41.6	111	2	PH0992	Ig heavy chain v r	779	473	2	S04113	nitrogenase (EC 1.
707	37	41.6	112	2	A30502	Ig heavy chain v r	780	473	2	A47050	nitrogenase (EC 1.
708	37	41.6	112	2	S41546	faeB protein - Esc	781	474	2	C35405	glutamate-ammonia
709	37	41.6	114	2	PH1523	Ig heavy chain v r	782	475	2	S49886	probable membrane
710	37	41.6	114	2	PH1522	Ig heavy chain v r	783	486	2	S57786	phosphoglucuronate d
711	37	41.6	116	1	M3HUGL	Ig heavy chain v-I	784	519	2	S36471	L2 protein - human
712	37	41.6	117	2	S25176	Ig heavy chain v r	785	520	2	S36489	L2 protein - human
713	37	41.6	118	2	S38565	Ig heavy chain v r	786	530	2	T43089	transfer complex p
714	37	41.6	119	2	PH1505	Ig heavy chain v r	787	549	2	A80987	alpha,alpha-trehal
715	37	41.6	119	2	PH1517	Ig heavy chain v r	788	549	2	G91178	cytoplasmic trehal
716	37	41.6	119	2	PH1502	Ig heavy chain v r	789	549	2	H86024	cytoplasmic trehal
717	37	41.6	119	2	PH1521	Ig heavy chain v r	790	549	2	S47739	probable alpha,alp
718	37	41.6	119	2	PH1500	Ig heavy chain v r	791	553	1	QRECM4	aspartate chemorec
719	37	41.6	119	2	PH1504	Ig heavy chain v r	792	553	2	H85801	hypothetical prote
720	37	41.6	119	2	PH1520	Ig heavy chain v r	793	553	2	D90953	mechyl-accepting c
721	37	41.6	119	2	PH1512	Ig heavy chain v r	794	568	2	A34891	Ig heavy chain pre
722	37	41.6	121	2	S31104	Ig heavy chain (su	795	570	2	A83637	hypothetical prote
723	37	41.6	121	2	A26405	Ig heavy chain v r	796	583	2	S29622	hydroxymethylgluta
724	37	41.6	125	2	S20639	Ig heavy chain v r	797	594	2	C96638	hypothetical prote
725	37	41.6	128	2	S31595	Ig heavy chain v r	798	642	2	A11827	cyclomaltodextrin
726	37	41.6	131	2	S66537	Ig heavy chain v r	799	643	2	I50539	intermediate filam
727	37	41.6	135	2	PH1493	Ig heavy chain v r	800	684	2	A56154	Ab1 substrate ena
728	37	41.6	137	2	T46904	hypothetical prote	801	694	2	F70868	hypothetical glyci
729	37	41.6	138	2	S74831	protein par-1 (imp	802	695	2	A38314	L-amino-acid oxida
730	37	41.6	139	2	H89287	hypothetical prote	803	735	1	PC4225	replication licens
731	37	41.6	140	2	PH1482	Ig heavy chain v r	804	738	2	T40035	hypothetical prote
732	37	41.6	142	2	I47190	Ig heavy chain var	805	759	2	T24130	hypothetical prote
733	37	41.6	144	2	S01391	phospholipase A2 (	806	803	2	A86655	hypothetical prote
734	37	41.6	144	2	B30502	Ig heavy chain v r	807	835	2	JC6140	cell surface-assoc
735	37	41.6	145	2	S11239	Ig heavy chain v r	808	837	2	D82796	conserved hypother
736	37	41.6	202	2	A97082	proline/glycine be	809	907	2	A86460	99.9K hypotherical
737	37	41.6	206	2	B69938	hypothetical prote	810	921	2	T19694	hypothetical prote
738	37	41.6	218	2	A36040	Ig heavy chain v-I	811	949	2	T08658	mixed-lineage prot
739	37	41.6	224	2	T37825	serine /proline ri	812	954	1	S68178	protein kinase hom
740	37	41.6	224	2	T36291	probable glycine-r	813	976	2	T05897	ATP citrate (pro-S
741	37	41.6	234	2	C90837	hypothetical prote	814	1100	2	A35007	virG protein - Shi
742	37	41.6	250	2	E97797	hypothetical prote	815	1102	2	A32247	ATP citrate (pro-S
743	37	41.6	264	2	B71362	probable exodoxyr	816	1105	2	S21173	probable outer mem
744	37	41.6	265	2	A59141	silaffin sllp pre	817	1112	2	H59664	tonS-dependent rec
745	37	41.6	270	2	G86633	conserved hypother	818	1125	2	H87644	ice nucleation pro
746	37	41.6	272	2	E84478	hypothetical prote	819	1176	2	T18042	probable serine/th
747	37	41.6	287	2	T21222	hypothetical prote	820	1192	2	T18611	DNA-directed RNA p
748	37	41.6	303	2	B84744	hypothetical prote	821	1194	2	S70415	autolysin (importe
749	37	41.6	316	1	A38743	loricrin - human	822	1248	2	C98874	hypothetical prote
750	37	41.6	317	2	E84434	probable phloem-ep	823	1353	2	T19691	receptor-adenylate
751	37	41.6	319	2	A70340	conserved hypother	824	1380	2	T18309	translation initia
752	37	41.6	331	2	F86633	fatty acid/phospho	825	1396	2	A44453	polyketide synthas
753	37	41.6	359	2	S52650	omega-3 fatty acid	826	1446	2	S73013	polyketide synthas
754	37	41.6	369	2	H87633	threonine aldolase	827	1528	2	D85912	polyketide synthas
755	37	41.6	384	2	D69809	spore germination	828	1540	2	H87203	hypothetical prote
756	37	41.6	384	2	I40867	hypothetical prote	829	1569	2	A65044	hypothetical prote
757	37	41.6	387	2	E95995	hypothetical calci	830	1571	2	C91068	hypothetical prote
758	37	41.6	389	2	S73942	oligopeptide trans	831	1795	2	T30332	avirulence protein
759	37	41.6	404	1	JQ1531	nucleoprotein - he	832	1955	2	T41170	probable 1,3-beta-

833	37	41.6	2064	2	G82562	bacteriocin XP2407	906	36	40.4	293	2	G97555	hypothetical prote
834	37	41.6	2214	2	T16305	hypothetical prote	907	36	40.4	294	2	AB0772	hypothetical prote
835	37	41.6	5147	1	IJFPTM	cadherin-related t	908	36	40.4	296	2	P95380	probable hydrolase
836	36.5	41.0	97	2	PL0118	Ig heavy chain V-I	909	36	40.4	299	2	T05494	glycine-rich prote
837	36.5	41.0	99	2	S28699	Ig heavy chain V r	910	36	40.4	302	2	D96625	hypothetical prote
838	36.5	41.0	123	2	T24281	anti-SS-A/Ro 60K p	911	36	40.4	306	2	S60906	hrpr protein - Pae
839	36.5	41.0	281	2	PC22670	hypothetical prote	912	36	40.4	307	2	C86494	sulphohydrolase/gl
840	36.5	41.0	308	2	JC5468	leukocidin chain 1	913	36	40.4	307	2	H72127	probable sulfatase
841	36.5	41.0	319	2	G83279	probable hydrolase	914	36	40.4	316	2	D83362	probable 2-ketogl
842	36.5	41.0	327	2	H83659	serine/threonine-p	915	36	40.4	317	2	G84776	hypothetical prote
843	36.5	41.0	355	2	AB1041	Vi polysaccharide	916	36	40.4	333	1	A23438	probable DNA-bind
844	36.5	41.0	355	2	F36892	Vi polysaccharide	917	36	40.4	338	2	G64862	hypothetical prote
845	36.5	41.0	363	2	E65104	hypothetical 38.5	918	36	40.4	339	2	S02880	homeotic protein H
846	36.5	41.0	498	1	VGXPLA	surface glycoprote	919	36	40.4	340	1	PEIKL	polycopropagin (C
847	36.5	41.0	498	1	VGXPLM	surface glycoprote	920	36	40.4	341	2	T16296	hypothetical prote
848	36.5	41.0	498	2	F83329	probable outer mem	921	36	40.4	342	2	S18649	homeotic protein H
849	36.5	41.0	514	1	A47692	fumarate hydratase	922	36	40.4	347	2	T06584	probable DNA-bind
850	36.5	41.0	515	2	T03070	hypothetical prote	923	36	40.4	362	1	ZP8OC1	ubiquinol-cytochro
851	36.5	41.0	609	2	T16135	hypothetical prote	924	36	40.4	366	1	W3WLR1	E2 protein - rhesu
852	36.5	41.0	678	2	C86495	hypothetical prote	925	36	40.4	374	2	E72595	hypothetical prote
853	36.5	41.0	678	2	H72128	3-methyl-2-oxobuta	926	36	40.4	379	2	D86744	amino acid aminohy
854	36.5	41.0	770	2	C87316	alpha-N-acetylgluc	927	36	40.4	380	2	S70964	pkns protein - Myx
855	36.5	41.0	2554	2	AB3528	extracellular seri	928	36	40.4	384	1	SUTIKA	endopeptidase K (S
856	36	40.4	47	2	JT0518	Ig heavy chain V-I	929	36	40.4	386	2	S52718	coat protein - car
857	36	40.4	56	2	T29940	hypothetical prote	930	36	40.4	398	2	T46475	hypothetical prote
858	36	40.4	79	2	A28840	Ig kappa chain V r	931	36	40.4	402	1	JU0332	alkaline proteinase
859	36	40.4	84	2	PH1487	Ig heavy chain V r	932	36	40.4	406	2	D97147	3-oxoacyl-(acyl-ca
860	36	40.4	87	2	S78490	Ig kappa chain V r	933	36	40.4	407	2	A97149	molybdopterin bios
861	36	40.4	98	2	PH1145	Ig heavy chain V r	934	36	40.4	419	2	D82408	conserved hypotet
862	36	40.4	106	2	PH1002	Ig heavy chain V r	935	36	40.4	420	1	S25076	3-oxoacyl-(acyl-ca
863	36	40.4	106	2	S20652	Ig kappa chain V r	936	36	40.4	422	1	JN0825	polyketide beta-ke
864	36	40.4	107	2	A45722	anti-glycoprotein	937	36	40.4	422	2	S35197	hypothetical prote
865	36	40.4	109	2	PH1001	Ig heavy chain V r	938	36	40.4	423	2	S11974	polyketide beta-ke
866	36	40.4	113	1	AVMS57	Ig heavy chain V-I	939	36	40.4	424	2	S25840	beta-ketoacyl synt
867	36	40.4	115	2	S60066	Ig kappa chain V r	940	36	40.4	425	2	JC5850	polyketide synthas
868	36	40.4	118	2	S38491	Ig heavy chain - h	941	36	40.4	426	1	S05973	tetracenomycin C p
869	36	40.4	119	1	G1HUNI	Ig heavy chain V-I	942	36	40.4	429	2	G87636	conserved hypotet
870	36	40.4	121	2	A21854	Ig heavy chain V r	943	36	40.4	430	2	A81214	conserved hypotet
871	36	40.4	121	2	PT0378	Ig heavy chain V r	944	36	40.4	438	2	S25260	porin precursor, p
872	36	40.4	126	2	PH1417	Ig heavy chain V r	945	36	40.4	446	2	A27810	tubulin beta-2 cha
873	36	40.4	126	2	PH1418	Ig heavy chain V r	946	36	40.4	449	2	B25072	tubulin alpha-2 ch
874	36	40.4	126	2	PH1419	Ig heavy chain V r	947	36	40.4	454	2	C70100	hypothetical prote
875	36	40.4	133	2	PC1155	Ig heavy chain pre	948	36	40.4	467	1	PABYC	acid phosphatase (
876	36	40.4	135	2	H64344	hypothetical prote	949	36	40.4	474	1	AJAIQ	glutamate-ammonia
877	36	40.4	137	2	S34149	Ig mu chain - axol	950	36	40.4	474	2	A12096	glutamate-ammonia
878	36	40.4	138	2	A35676	Ig heavy chain pre	951	36	40.4	476	2	AC2465	6-phosphogluconate
879	36	40.4	140	2	S14179	hypothetical prote	952	36	40.4	482	2	T01659	phosphogluconate d
880	36	40.4	140	2	S04165	hypothetical prote	953	36	40.4	484	2	T01658	phosphogluconate d
881	36	40.4	152	2	B84409	hypothetical prote	954	36	40.4	491	2	H97088	protein containing
882	36	40.4	158	2	H82688	hypothetical prote	955	36	40.4	495	1	WMECTC	export system oute
883	36	40.4	159	2	S57630	hypothetical prote	956	36	40.4	495	2	B85964	hypothetical prote
884	36	40.4	180	2	A33791	PBDX protein - hum	957	36	40.4	495	2	C91119	outer membrane cha
885	36	40.4	187	2	A65007	hypothetical prote	958	36	40.4	511	2	T05363	phosphogluconate d
886	36	40.4	198	2	S56510	hypothetical prote	959	36	40.4	513	2	T14194	extensin homolog T
887	36	40.4	206	2	F98172	protocatechuate 3,	960	36	40.4	519	1	WXXRWN	core protein P6 -
888	36	40.4	206	2	AG3114	protocatechuate 3,	961	36	40.4	519	1	WXXRWT	core protein P6 -
889	36	40.4	209	2	B95189	conserved hypotet	962	36	40.4	520	2	J50291	intermediate filam
890	36	40.4	209	2	C98055	conserved hypotet	963	36	40.4	541	2	T15299	hypothetical prote
891	36	40.4	220	2	T20366	hypothetical prote	964	36	40.4	552	2	AD0242	hypothetical prote
892	36	40.4	239	2	T01599	hypothetical prote	965	36	40.4	559	1	KBMSE1	keratin, 59K type
893	36	40.4	240	2	AC2748	LexA repressor [im	966	36	40.4	570	2	S07330	keratin, epidermal
894	36	40.4	240	2	B97529	LexA repressor [im	967	36	40.4	577	2	C89059	acetylactate synth
895	36	40.4	245	2	A84289	hypothetical prote	968	36	40.4	591	2	S74999	iron-regulated pro
896	36	40.4	248	2	D71826	hypothetical prote	969	36	40.4	594	2	A49804	cellular Hsp70 hom
897	36	40.4	248	2	C84444	probable expansin	970	36	40.4	604	2	A39369	homeotic protein B
898	36	40.4	252	2	F86335	hypothetical prote	971	36	40.4	629	2	C96149	TiNS-18 protein -
899	36	40.4	255	2	T50655	expansin Exps [imp	972	36	40.4	638	2	A33505	sonatotropin recep
900	36	40.4	278	2	C96785	hypothetical prote	973	36	40.4	641	2	C69943	AtP-dependent heli
901	36	40.4	279	2	B32985	sonatotropin-bind	974	36	40.4	653	2	T34356	hypothetical prote
902	36	40.4	279	2	A89920	conserved hypotet	975	36	40.4	662	2	I38400	melanoma-associate
903	36	40.4	287	2	AE2309	hypothetical prote	976	36	40.4	668	2	A41234	melanocyte-specifi
904	36	40.4	290	2	D82545	succinyl-CoA synth	977	36	40.4	707	2	T14195	extensin homolog T
905	36	40.4	293	2	A12775	conserved hypotet	978	36	40.4	714	2	T35770	hypothetical prote

979 36 40.4 797 2 T46737 X-Pro dipeptidyl-p  
980 36 40.4 835 2 T47521 respiratory burst  
981 36 40.4 848 2 E86443 probable G-protein  
982 36 40.4 886 2 A59223 nitrate reductase  
983 36 40.4 890 2 T35237 probable secreted  
984 36 40.4 898 1 RDBJNH nitrate reductase  
985 36 40.4 900 2 S47029 nitrate reductase  
986 36 40.4 900 2 AC1852 hypothetrical prote  
987 36 40.4 926 1 RDSPNH nitrate reductase  
988 36 40.4 929 2 C96623 hypothetrical prote  
989 36 40.4 958 2 A82583 conserved hypotet  
990 36 40.4 1045 2 S55253 sucrose-phosphate  
991 36 40.4 1052 2 F97268 superfamily II DNA  
992 36 40.4 1128 1 QQBE47 DNA-binding protei  
993 36 40.4 1290 2 S76853 hypothetrical prote  
994 36 40.4 1363 1 VGHQU E2 glycoprotein pr  
995 36 40.4 1363 1 VGHVA E2 glycoprotein pr  
996 36 40.4 1363 1 VGHFI E2 glycoprotein pr  
997 36 40.4 1363 1 VGHIL9 E2 glycoprotein pr  
998 36 40.4 1363 1 VGHLY E2 glycoprotein pr  
999 36 40.4 1363 1 VGHNM E2 glycoprotein -  
1000 36 40.4 1363 2 S44240 surface protein -

## ALIGNMENTS

RESULT 1  
PH1007  
Ig heavy chain V region (clone 163-cl) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C>Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996  
C:Accession: PH1007  
R:Fillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.  
J. Exp. Med. 176, 761-779, 1992  
A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B c  
A:Reference number: PH0971; MUID:92381444; PMID:1512540  
A:Accession: PH1007  
A:Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-111 <TIL>  
A:Cross-references: UNIPARC:UPI0000176D17  
A:Experimental source: B cell, strain [NZB x NZW]F1  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 83.1%; Score 74; DB 2; Length 111;  
Best Local Similarity 82.4%; Pred. No. 0.0007;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 YISGGSGTYYSDSVKG 17  
||||| ||| |||||  
Db 50 YISGGSGTYYPDIVKG 66

RESULT 2  
S21593  
Ig heavy chain V region (10C5) - mouse  
C:Species: Mus musculus (house mouse)  
C>Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 23-Jul-1999  
C:Accession: S21593  
R:Kaartinen, M.  
submitted to the EMBL Data Library, May 1992  
A:Reference number: S21591  
A:Accession: S21593  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-83 <KAA>  
A:Cross-references: UNIPARC:UPI0000116053; EMBL:X66457; NID:G51598; PIDN:CAA47072.1; PID  
C25913  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin

Query Match 79.8%; Score 71; DB 2; Length 83;  
Best Local Similarity 76.5%; Pred. No. 0.0015;  
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
QY 1 YISGGSGTYYSDSVKG 17  
||||| ||| |||||  
Db 20 YITGGVSTYYSDIVKG 36  
RESULT 3  
S26468  
Ig heavy chain V region - mouse  
C:Species: Mus musculus (house mouse)  
C>Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 23-Jul-1999  
C:Accession: S26468  
R:Kavaler, J.  
submitted to the EMBL Data Library, April 1991  
A:Reference number: S26459  
A:Accession: S26468  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-113 <KAV>  
A:Cross-references: UNIPARC:UPI0000115F61; EMBL:X59107; NID:G51944; PIDN:CAA41833.1; PID  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:11-94/Domain: immunoglobulin homology <IMM>

Query Match 79.8%; Score 71; DB 2; Length 113;  
Best Local Similarity 76.5%; Pred. No. 0.002;  
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 YISGGSGTYYSDSVKG 17  
||||| ||| |||||  
Db 46 YISGGSGTYYPDIVKG 62

RESULT 4  
HVMS34  
Ig heavy chain precursor V region (345) - mouse  
C:Species: Mus musculus (house mouse)  
C>Date: 30-Jun-1990 #sequence\_revision 30-Jun-1990 #text\_change 09-Jul-2004  
C:Accession: JT0502  
R:Levy, N.S.; Malipiero, U.V.; Lebecque, S.G.; Gearhart, P.J.  
J. Exp. Med. 169, 2007-2019, 1989  
A:Title: Early onset of somatic mutation in immunoglobulin VH genes during the primary  
A:Reference number: JT0501; MUID:89279149; PMID:2499654  
A:Accession: JT0502  
A:Status: translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-117 <LEV>  
A:Cross-references: UNIPROT:P18526; UNIPARC:UPI00000278D9  
A:Experimental source: strain BALB/cJ  
A:Note: this sequence belongs to the VH7183 subfamily  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:1-19/Domain: signal sequence #status predicted <SIG>  
F:20-117/Product: Ig heavy chain V region (345) #status predicted <MAT>  
F:34-117/Domain: immunoglobulin homology <IMM>  
F:41-115/Disulfide bonds: #status predicted

Query Match 79.8%; Score 71; DB 1; Length 117;  
Best Local Similarity 76.5%; Pred. No. 0.002;  
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 YISGGSGTYYSDSVKG 17  
||||| ||| |||||  
Db 69 YISGGSGTYYPDIVKG 85

RESULT 5  
C25913  
Ig heavy chain V region (BFL14) - mouse (fragment)  
C:Species: Mus musculus (house mouse)

CjDate: 16-Aug-1988 #sequence\_revision 16-Aug-1988 #text\_change 31-Dec-2004  
 CjAccession: C25913  
 RjLawler, A.M.; Lin, P.S.; Gearhart, P.J.  
 Proc. Natl. Acad. Sci. U.S.A. 84, 2454-2458, 1987  
 A>Title: Adult B-cell repertoire is biased toward two heavy-chain variable-region genes  
 A;Reference number: A94148; MUID:87175692; PMID:3104915  
 A;Accession: C25913  
 A;Molecule type: DNA  
 A;Residues: 1-83 <LAW>  
 A;Cross-references: UNIPROT:Q920E7; UNIPARC:UPI0000176983  
 C;Superfamily: immunoglobulin homology  
 C;Keywords: heterotetramer; immunoglobulin

Query Match 76.4%; Score 68; DB 2; Length 83;  
 Best Local Similarity 87.5%; Pred. No. 0.004; 2; Indels 0; Gaps 0;  
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 ISSGGSGTYSDSVK 17  
 ||||| |||||  
 DB 36 ISSGGSYTYPDVK 51

RESULT 6  
 S14580  
 Ig heavy chain V region - mouse  
 C;Species: Mus musculus (house mouse)  
 CjDate: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 23-Jul-1999  
 CjAccession: S14580  
 R;Chen, Q.; Stenzel-Poore, M.; Rittenberg, M.B.  
 submitted to the EMBL Data Library, March 1991  
 A;Description: Natural polyreactive antibodies differ from Ag-induced antibodies in VH C  
 A;Reference number: S14484  
 A;Accession: S14580  
 A;Status: preliminary  
 A;Molecule type: mRNA  
 A;Residues: 1-94 <CHE>  
 A;Cross-references: UNIPARC:UPI0000115F39; EMBL:X58652; NID:G51293; PIDN:CAA41509.1; PID  
 C;Superfamily: immunoglobulin V region; immunoglobulin homology  
 C;Keywords: heterotetramer; immunoglobulin  
 F;7-90/Domain: immunoglobulin homology <IMM>

Query Match 76.4%; Score 68; DB 2; Length 94;  
 Best Local Similarity 87.5%; Pred. No. 0.0045; 2; Indels 0; Gaps 0;  
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 ISSGGSGTYSDSVK 17  
 ||||| |||||  
 DB 43 ISSGGSYTYPDVK 58

RESULT 7  
 S14581  
 Ig heavy chain V region - mouse  
 C;Species: Mus musculus (house mouse)  
 CjDate: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 23-Jul-1999  
 CjAccession: S14581  
 R;Chen, Q.; Stenzel-Poore, M.; Rittenberg, M.B.  
 submitted to the EMBL Data Library, March 1991  
 A;Description: Natural polyreactive antibodies differ from Ag-induced antibodies in VH C  
 A;Reference number: S14484  
 A;Accession: S14581  
 A;Status: preliminary  
 A;Molecule type: mRNA  
 A;Residues: 1-102 <CHE>  
 A;Cross-references: UNIPARC:UPI0000115F3A; EMBL:X58653; NID:G51295; PIDN:CAA41510.1; PID  
 C;Superfamily: immunoglobulin V region; immunoglobulin homology  
 C;Keywords: heterotetramer; immunoglobulin  
 F;7-90/Domain: immunoglobulin homology <IMM>

Query Match 76.4%; Score 68; DB 2; Length 102;  
 Best Local Similarity 87.5%; Pred. No. 0.0049; 2; Indels 0; Gaps 0;  
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 ISSGGSGTYSDSVK 17  
 ||||| |||||  
 DB 43 ISSGGSYTYPDVK 58

RESULT 8  
 PH1008  
 Ig heavy chain V region (clone 83-cl) - mouse (fragment)  
 C;Species: Mus musculus (house mouse)  
 CjDate: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996  
 CjAccession: PH1008  
 R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.  
 J. Exp. Med. 176, 761-779, 1992  
 A>Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B c  
 A;Reference number: PH0971; MUID:92381444; PMID:1512540  
 A;Accession: PH1008  
 A;Status: nucleic acid sequence not shown  
 A;Molecule type: mRNA  
 A;Residues: 1-106 <TIL>  
 A;Cross-references: UNIPARC:UPI0000176D18  
 A;Experimental source: B cell, strain (NZB x NZW)F1  
 C;Superfamily: immunoglobulin V region; immunoglobulin homology  
 C;Keywords: heterotetramer; immunoglobulin  
 F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 76.4%; Score 68; DB 2; Length 106;  
 Best Local Similarity 70.6%; Pred. No. 0.0051; 3; Indels 0; Gaps 0;  
 Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 YISSGGSGTYSDSVK 17  
 ||||| |||||  
 DB 50 YISSGGSDTYPDNKG 66

RESULT 9  
 S24251  
 Ig heavy chain V region (NS4P3-D-JH4) - human  
 C;Species: Homo sapiens (man)  
 CjDate: 19-Feb-1994 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999  
 CjAccession: S24251  
 R;Stewart, A.K.; Huang, C.; Stollar, B.D.; Schwartz, R.S.  
 submitted to the EMBL Data Library, June 1992  
 A;Description: A single VH gene predominates in the rearranged and expressed human B cel  
 A;Reference number: S24247  
 A;Accession: S24251  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-108 <STE>  
 A;Cross-references: UNIPARC:UPI0000116090; EMBL:X67072; NID:G38401; PIDN:CAA47457.1; PID  
 C;Superfamily: immunoglobulin V region; immunoglobulin homology  
 C;Keywords: heterotetramer; immunoglobulin  
 F;11-94/Domain: immunoglobulin homology <IMM>

Query Match 76.4%; Score 68; DB 2; Length 108;  
 Best Local Similarity 76.5%; Pred. No. 0.0052; 3; Indels 0; Gaps 0;  
 Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 YISSGGSGTYSDSVK 17  
 ||||| |||||  
 DB 46 YISSGSAIYYADSVK 62

RESULT 10  
 PH1010  
 Ig heavy chain V region (clone 17s.93) - mouse (fragment)  
 C;Species: Mus musculus (house mouse)  
 CjDate: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996  
 CjAccession: PH1010  
 R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.  
 J. Exp. Med. 176, 761-779, 1992  
 A>Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B c  
 A;Reference number: PH0971; MUID:92381444; PMID:1512540  
 A;Accession: PH1010

A>Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-108 <TIL>  
A:Cross-references: UNIPARC:UPI0000176D1A  
A:Experimental source: B cell, strain [NZB x NZW]F1  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:15-97/Domain: immunoglobulin homology <IMM>

Query Match 76.4%; Score 68; DB 2; Length 108;  
Best Local Similarity 87.5%; Pred. No. 0.0052;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 ISSGGSGTYYSDSVKG 17  
||||| ||||| |||||  
Db 51 ISSGGSYTYPPDSVKG 66

RESULT 11  
HVMS84  
Ig heavy chain precursor V region (5-84) - mouse  
C:Species: Mus musculus (house mouse)  
C>Date: 30-Jun-1990 #sequence\_revision 30-Jun-1990 #text\_change 09-Jul-2004  
C:Accession: JTO505  
R:Levy, N.S.; Malipiero, U.V.; Lebecque, S.G.; Gearhart, P.J.  
J. Exp. Med. 169, 2007-2019, 1989  
A>Title: Early onset of somatic mutation in immunoglobulin VH genes during the primary  
A:Reference number: JTO501; MUID:89279149; PMID:2499654  
A:Accession: JTO505  
A>Status: translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-117 <LEV>  
A:Cross-references: UNIPROT:P18525; UNIPARC:UPI00000278D7  
A:Experimental source: strain BALB/cJ  
A>Note: This sequence belongs to the VH7183 subfamily  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:1-19/Domain: signal sequence #status predicted <SIG>  
F:20-117/Product: Ig heavy chain V region (5-84) #status predicted <MAT>  
F:34-117/Domain: immunoglobulin homology <IMM>  
F:41-115/Disulfide bonds: #status predicted

Query Match 76.4%; Score 68; DB 1; Length 117;  
Best Local Similarity 70.6%; Pred. No. 0.0056;  
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 YISGGSGTYYSDSVKG 17  
||||| ||||| |||||  
Db 69 YISGGGSGTYYPDSVKG 85

RESULT 12  
PH0097  
Ig heavy chain V region (anti-cyclosporin B) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C>Date: 15-Jan-1993 #sequence\_revision 15-Jan-1993 #text\_change 16-Aug-1996  
C:Accession: PH0097  
R:Schmitter, D.; Poch, O.; Zeder, G.; Heinrich, G.F.; Kocher, H.P.; Quesniaux, V.F.J.; V  
Mol. Immunol. 27, 1029-1038, 1990  
A>Title: Analysis of the structural diversity of monoclonal antibodies to cyclosporine.  
A:Reference number: PH0087; MUID:91042649; PMID:2122240  
A:Accession: PH0097  
A:Molecule type: mRNA  
A:Residues: 1-118 <SCH>  
A:Cross-references: UNIPARC:UPI0000176C71  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:15-98/Domain: immunoglobulin homology <IMM>  
F:31-35/Region: complementarity-determining 1  
F:50-66/Region: complementarity-determining 2  
F:99-105/Region: complementarity-determining 3

Query Match 76.4%; Score 68; DB 2; Length 118;

Best Local Similarity 87.5%; Pred. No. 0.0057;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 ISSGGSGTYYSDSVKG 17  
||||| ||||| |||||  
Db 51 ISSGGRYTYYSDSVKG 66

RESULT 13  
F27888  
Ig heavy chain V region (H158-89H4) - mouse  
C:Species: Mus musculus (house mouse)  
C>Date: 15-Dec-1988 #sequence\_revision 15-Dec-1988 #text\_change 16-Aug-1996  
C:Accession: F27888  
R:Caton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.  
EMBO J. 5, 1577-1587, 1986  
A>Title: Structural and functional implications of a restricted antibody response to a d  
A:Reference number: A91043; MUID:86300658; PMID:2427335  
A:Accession: F27888  
A:Molecule type: DNA  
A:Residues: 1-119 <CAT>  
A:Cross-references: UNIPARC:UPI0000176868  
A:Experimental source: strain Balb/c  
A>Note: This sequence was determined from the germline gene  
C:Comment: This chain was isolated from a hybridoma protein that binds influenza virus h  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 76.4%; Score 68; DB 2; Length 119;  
Best Local Similarity 87.5%; Pred. No. 0.0057;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 ISSGGSGTYYSDSVKG 17  
||||| ||||| |||||  
Db 51 ISSGGSYTYPPDSVKG 66

RESULT 14  
S55537  
Ig heavy chain V region pe21 - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C>Date: 27-Oct-1995 #sequence\_revision 03-Nov-1995 #text\_change 23-Jul-1999  
C:Accession: S55537  
R:Boettger, V.; Boettger, A.; Lane, E.B.; Spruce, B.A.  
J. Mol. Biol. 247, 932-946, 1995  
A>Title: Comprehensive epitope analysis of monoclonal anti-proenkephalin antibodies usin  
A:Reference number: S55528; MUID:95239763; PMID:7536850  
A:Accession: S55537  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-120 <BOE>  
A:Cross-references: UNIPARC:UPI0000116201; EMBL:X82590; NID:9854306; PIDN:CAAS7926.1; PI  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:14-97/Domain: immunoglobulin homology <IMM>

Query Match 76.4%; Score 68; DB 2; Length 120;  
Best Local Similarity 87.5%; Pred. No. 0.0058;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 ISSGGSGTYYSDSVKG 17  
||||| ||||| |||||  
Db 50 ISSGGSYTYPPDSVKG 65

RESULT 15  
S55536  
Ig heavy chain V region pe20 - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C>Date: 27-Oct-1995 #sequence\_revision 03-Nov-1995 #text\_change 23-Jul-1999  
C:Accession: S55536

R;Boettger, V.; Boettger, A.; Lane, E.B.; Spruce, B.A.  
 J. Mol. Biol. 247, 932-946, 1995  
 A;Title: Comprehensive epitope analysis of monoclonal anti-proenkephalin antibodies using  
 uations in the variable region genes.  
 A;Reference number: S55528; MUID:95239763; PMID:7536850  
 A;Accession: S55536  
 A;Status: preliminary  
 A;Molecule type: mRNA  
 A;Residues: 1-120 <BOE>  
 A;Cross-references: UNIPARC:UPI0000116200; EMBL:X82589; NID:G854304; PIDN:CAA57925.1; PI  
 C;Superfamily: immunoglobulin V region; immunoglobulin homology  
 C;Keywords: heterotetramer; immunoglobulin  
 F;14-97/Domain: immunoglobulin homology <IMM>

Query Match 76.4%; Score 68; DB 2; Length 120;  
 Best Local Similarity 87.5%; Pred. No. 0.0058;  
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 ISSGGSGTYSDSVKG 17  
 ||||| |||||  
 Db 50 ISSGGSYTPDSVKG 65

RESULT 16  
 E27888  
 Ig heavy chain V region (H35-C6) - mouse  
 C;Species: Mus musculus (house mouse)  
 C;Date: 15-Dec-1988 #sequence\_revision 15-Dec-1988 #text\_change 16-Aug-1996  
 C;Accession: E27888  
 R;Caton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.  
 EMBO J. 5, 1577-1587, 1986  
 A;Title: Structural and functional implications of a restricted antibody response to a d  
 A;Reference number: A91043; MUID:86300658; PMID:2427335  
 A;Accession: E27888  
 A;Molecule type: DNA  
 A;Residues: 1-122 <CAT>  
 A;Experimental source: strain Balb/c  
 A;Cross-references: UNIPARC:UPI000017686B  
 A;Note: This sequence was determined from the germline gene  
 C;Comment: This chain was isolated from a hybridoma protein that binds influenza virus h  
 C;Superfamily: immunoglobulin V region; immunoglobulin homology  
 C;Keywords: heterotetramer; immunoglobulin  
 F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 76.4%; Score 68; DB 2; Length 122;  
 Best Local Similarity 87.5%; Pred. No. 0.0058;  
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 ISSGGSGTYSDSVKG 17  
 ||||| |||||  
 Db 51 ISSGGSYTPDSVKG 66

RESULT 17  
 PL0248  
 Ig heavy chain V region (anti-DNA, DP12VH) - mouse (fragment)  
 C;Species: Mus musculus (house mouse)  
 C;Date: 16-Sep-1992 #sequence\_revision 16-Sep-1992 #text\_change 16-Aug-1996  
 C;Accession: PL0248  
 R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A  
 J. Exp. Med. 171, 265-297, 1990  
 A;Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic  
 A;Reference number: PL0231; MUID:90111618; PMID:2104919  
 A;Accession: PL0248  
 A;Molecule type: mRNA  
 A;Residues: 1-108 <SHL>  
 A;Cross-references: UNIPARC:UPI0000176C39  
 C;Superfamily: immunoglobulin V region; immunoglobulin homology  
 C;Keywords: heterotetramer; immunoglobulin  
 F;1-24/Region: framework 1  
 F;9-92/Domain: immunoglobulin homology <IMM>  
 F;25-29/Region: complementarity-determining 1  
 F;30-43/Region: framework 2

F;44-60/Region: complementarity-determining 2  
 F;61-92/Region: framework 3  
 F;93-99/Region: complementarity-determining 3  
 F;100-108/Region: framework 4

Query Match 75.3%; Score 67; DB 2; Length 108;  
 Best Local Similarity 81.2%; Pred. No. 0.0073;  
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 ISSGGSGTYSDSVKG 17  
 ||||| |||||  
 Db 45 ISSGGSGTYTPDSVKG 60

RESULT 18  
 S20641  
 Ig heavy chain V region - mouse  
 C;Species: Mus musculus (house mouse)  
 C;Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 23-Jul-1999  
 C;Accession: S20641  
 R;Lozman, M.; Fasy, T.M.; Novick, K.E.; Monestier, M.  
 submitted to the EMBL Data Library, February 1992  
 A;Description: Relationships among antinuclear antibodies from autoimmune MRL mice react  
 A;Reference number: S20639  
 A;Accession: S20641  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-118 <LOS>  
 A;Cross-references: UNIPARC:UPI0000116021; EMBL:X65003; NID:G52602; PIDN:CAA46136.1; PID  
 C;Superfamily: immunoglobulin V region; immunoglobulin homology  
 C;Keywords: heterotetramer; immunoglobulin  
 F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 75.3%; Score 67; DB 2; Length 110;  
 Best Local Similarity 81.2%; Pred. No. 0.0079;  
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 ISSGGSGTYSDSVKG 17  
 ||||| |||||  
 Db 51 ISSGGGNTYTPDSVKG 66

RESULT 19  
 S09258  
 Ig heavy chain V region precursor - mouse (fragment)  
 C;Species: Mus musculus (house mouse)  
 C;Date: 29-Jan-1993 #sequence\_revision 29-Jan-1993 #text\_change 23-Jul-1999  
 C;Accession: S09258  
 R;Hamada, H.; Maezawa, K.; Tsuruo, T.  
 Nucleic Acids Res. 18, 1900, 1990  
 A;Title: Nucleotide sequences of the variable regions of a mouse monoclonal antibody MRK  
 A;Reference number: S09258; MUID:90245594; PMID:2110659  
 A;Accession: S09258  
 A;Molecule type: DNA  
 A;Residues: 1-138 <HAM>  
 A;Cross-references: UNIPARC:UPI0000115E49; EMBL:X51719; NID:G53207; PIDN:CAA36012.1; PID  
 C;Genetics: 16/1  
 C;Superfamily: immunoglobulin V region; immunoglobulin homology  
 C;Keywords: heterotetramer; immunoglobulin  
 F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 75.3%; Score 67; DB 2; Length 138;  
 Best Local Similarity 81.2%; Pred. No. 0.0093;  
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 ISSGGSGTYSDSVKG 17  
 ||||| |||||  
 Db 70 ISSGGGNTYTPDSVKG 85

RESULT 20  
 S24252



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Best Local Similarity 76.5%; Pred.No. 0.0093;
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 YISSGGSGTYIVSDSVKG 17
    ||||| || ||:|||||
Db 50 YISSGGSTIYYADSVKG 66

RESULT 23
PH1652
IG heavy chain V region (clone 5D4) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 16-Aug-1996
C;Accession: PH1652
R;Hillson, J.L.; Karr, N.S.; Opplinger, I.R.; Mannik, M.; Sasso, E.H.
J. Exp. Med. 178, 331-336, 1993
A;Title: The structural basis of germline-encoded VH3 immunoglobulin binding to
A;Reference number: PH1642; MUID:93301610; PMID:8315398
A;Accession: PH1652
A;Molecule type: mRNA
A;Residues: 1-110 <HIL>
A;Cross-references: UNIPARC:UPI0000176BD9
A;Experimental source: B cell
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;7-90/Domain: immunoglobulin homology <IMM>

Query Match 74.2%; Score 66; DB 2; Length 110;
Best Local Similarity 76.5%; Pred.No. 0.01;
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 YISSGGSGTYIVSDSVKG 17
    ||||| || ||:|||||
Db 42 YISSGGSTIYYADSVKG 58

RESULT 24
S31120
IG heavy chain - human
C;Species: Homo sapiens (man)
C;Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C;Accession: S31120
R;Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.;
Eur. J. Immunol. 22, 247-251, 1992
A;Title: Restricted utilization of germ-line V(H)3 genes and short diverse third
A;Reference number: S31104; MUID:92111633; PMID:1730252
A;Accession: S31120
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Residues: 1-114 <RAA>
A;Cross-references: UNIPARC:UPI0000176DC9; EMBL:X62972
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 74.2%; Score 66; DB 2; Length 114;
Best Local Similarity 76.5%; Pred.No. 0.011;
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 YISSGGSGTYIVSDSVKG 17
    ||||| || ||:|||||
Db 50 YISSGGSTIYYADSVKG 66

RESULT 25
S31105
IG heavy chain (subclass IgM) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 23-Jul-1999
C;Accession: S31105
R;Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.;
Eur. J. Immunol. 22, 247-251, 1992

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A:Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complement  
A:Reference number: S31104; MUID:92111633; PMID:1730252  
A:Accession: S31105  
A>Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-118 <RAA>  
A:Cross-references: UNIPARC:UPI000011600C; EMBL:X63081; NID:G32648; PIDN:CAA44803.1; PID  
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:15-98/Domain: immunoglobulin homology <IMM>  
Query Match 74.2%; Score 66; DB 2; Length 118;  
Best Local Similarity 76.5%; Pred. No. 0.011; 3; Indels 0; Gaps 0;  
Matches 13; Conservative 1; Mismatches 3;  
QY 1 YISSGGSGTYYSDSVKG 17  
DB 50 YISSGGSTYYADSVKG 66  
RESULT 26  
D27889  
IG heavy chain V region (H36-2) - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 15-Dec-1988 #sequence\_revision 15-Dec-1988 #text\_change 16-Aug-1996  
C:Accession: D27889  
R:Caton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.  
EMBO J. 5, 1577-1587, 1986  
A:Title: Structural and functional implications of a restricted antibody response to a d  
A:Reference number: A91043; MUID:86300658; PMID:2427335  
A:Accession: D27889  
A:Molecule type: DNA  
A:Residues: 1-119 <CAT>  
A:Cross-references: UNIPARC:UPI000017686C  
A:Experimental source: strain Balb/c  
A>Note: this sequence was determined from the germline gene  
C:Comment: This chain was isolated from a hybridoma protein that binds influenza virus H  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:15-98/Domain: immunoglobulin homology <IMM>  
Query Match 74.2%; Score 66; DB 2; Length 119;  
Best Local Similarity 81.2%; Pred. No. 0.011;  
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 2 ISSGGSGTYYSDSVKG 17  
DB 51 ISDGSFTYYSDTVKG 66  
RESULT 27  
S26790  
IG heavy chain V region - human  
C:Species: Homo sapiens (man)  
C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 20-Jun-2000  
C:Accession: S26790  
R:Mortari, F.; Newton, J.A.; Wang, J.Y.; Schroeder Jr., H.W.  
Eur. J. Immunol. 22, 241-245, 1992  
A:Title: The human cord blood antibody repertoire. Frequent usage of the V(H)7 gene fami  
A:Reference number: S26786; MUID:92111632; PMID:1730251  
A:Accession: S26790  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-128 <MOR>  
A:Cross-references: UNIPARC:UPI0000115FC4; EMBL:X61013; NID:G32798; PIDN:CAA43347.1; PID  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:15-98/Domain: immunoglobulin homology <IMM>  
Query Match 74.2%; Score 66; DB 2; Length 128;  
Best Local Similarity 76.5%; Pred. No. 0.012; 3; Indels 0; Gaps 0;  
Matches 13; Conservative 1; Mismatches 3;

QY 1 YISSGGSGTYYSDSVKG 17  
DB 50 YISSGGSTYYADSVKG 66

RESULT 28  
I47193  
IG heavy chain variable VDJ region - pig (fragment)  
C:Species: Sus scrofa domestica (domestic pig)  
C:Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 21-Jan-2000  
C:Accession: I47193  
R:Sun, J.; Kaczkovics, I.; Brown, W.R.; Butler, J.E.  
J. Immunol. 153, 5618-5627, 1994  
A:Title: Expressed swine VH genes belong to a small VH gene family homologous to human v  
A:Reference number: I47177; MUID:95081609; PMID:7989761  
A:Accession: I47193  
A>Status: preliminary; translated from GB/EMBL/DBDJ  
A:Molecule type: mRNA  
A:Residues: 1-137 <SUN>  
A:Cross-references: UNIPARC:UPI0000115SE2; EMBL:U15452; NID:G571390; PIDN:AAA67018.1; PI  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 74.2%; Score 66; DB 2; Length 137;  
Best Local Similarity 75.0%; Pred. No. 0.013; 2; Indels 0; Gaps 0;  
Matches 12; Conservative 2; Mismatches 2;

QY 2 ISSGGSGTYYSDSVKG 17  
DB 70 ISTSGGTYADSVKG 85

RESULT 29  
S00700  
IG heavy chain V region - African clawed frog  
C:Species: Xenopus laevis (African clawed frog)  
C:Date: 31-Dec-1988 #sequence\_revision 31-Dec-1988 #text\_change 23-Jul-1999  
C:Accession: S00700  
R:Yamawaki-Kataoka, Y.; Honjo, T.  
Nucleic Acids Res. 15, 5888, 1987  
A:Title: Nucleotide sequences of variable region segments of the immunoglobulin heavy ch  
A:Reference number: S00700; MUID:87289054; PMID:3112743  
A:Accession: S00700  
A:Molecule type: DNA  
A:Residues: 1-118 <YAM>  
A:Cross-references: UNIPARC:UPI00001162E9; EMBL:Y00380; NID:G64810; PIDN:CAA68452.1; PID  
A>Note: the sequence was determined from the germline gene  
C:Genetics:  
A:Introns: 15/3  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 73.0%; Score 65; DB 2; Length 118;  
Best Local Similarity 75.0%; Pred. No. 0.016; 3; Indels 0; Gaps 0;  
Matches 12; Conservative 1; Mismatches 1;

QY 2 ISSGGSGTYYSDSVKG 17  
DB 70 ISDGSFTYYADSVKG 85

RESULT 30  
I27887  
IG heavy chain V region (H37-45) - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 15-Dec-1988 #sequence\_revision 15-Dec-1988 #text\_change 16-Aug-1996  
C:Accession: I27887  
R:Caton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.  
EMBO J. 5, 1577-1587, 1986  
A:Title: Structural and functional implications of a restricted antibody response to a d  
A:Reference number: A91043; MUID:86300658; PMID:2427335

A:Accession: I27887  
A:Molecule type: DNA  
A:Residues: 1-121 <CAT>  
A:Cross-references: UNIPARC:UPI0000176B6F  
A:Experimental source: strain Balb/c  
A:Note: This sequence was determined from the germline gene  
C:Comment: This chain was isolated from a hybridoma protein that binds influenza virus H  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 73.0%; Score 65; DB 2; Length 121;  
Best Local Similarity 81.2%; Pred. No. 0.016;  
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 ISSGGSGTYTSDSVK 17  
|||||: ||| |||||  
Db 51 ISSGGTYTYPDSVK 66

RESULT 31  
S63597  
Ig heavy chain, V region - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 28-Oct-1996 #sequence\_revision 13-Mar-1997 #text\_change 21-Jan-2000  
C:Accession: S63597  
R:Verdaguer, N.; Mateu, M.G.; Bravo, J.; Domingo, E.; Fita, I.  
J. Mol. Biol. 256, 364-376, 1996  
A:Title: Induced pocket to accommodate the cell attachment Arg-Gly-Asp motif in a neutra  
A:Reference number: S63596; MUID:96174482; PMID:8594203  
A:Superfamily: immunoglobulin V region; immunoglobulin homology  
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 73.0%; Score 65; DB 2; Length 123;  
Best Local Similarity 81.2%; Pred. No. 0.016;  
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 ISSGGSGTYTSDSVK 17  
|||||: ||| |||||  
Db 51 ISSGGTYTYPDSVK 66

RESULT 32  
C27888  
Ig heavy chain V region (H37-62) - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 15-Dec-1988 #sequence\_revision 15-Dec-1988 #text\_change 16-Aug-1996  
C:Accession: C27888  
R:Caton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.  
EMBO J. 5, 1577-1587, 1986  
A:Title: Structural and functional implications of a restricted antibody response to a d  
A:Reference number: A91043; MUID:86300658; PMID:2427335  
A:Superfamily: immunoglobulin V region; immunoglobulin homology  
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 73.0%; Score 65; DB 2; Length 124;  
Best Local Similarity 81.2%; Pred. No. 0.016;  
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 ISSGGSGTYTSDSVK 17

Db 51 ISSGGTYTYPDSVK 66  
|||||: ||| |||||

RESULT 33  
S68213  
Ig heavy chain (Mab03-1) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 29-Jul-1997 #sequence\_revision 17-Sep-1997 #text\_change 31-Dec-2004  
C:Accession: S68213  
R:Takagi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Kamachi, M.; Inanaka, T.  
FEBS Lett. 375, 273-276, 1995  
A:Title: Thermostable peroxidase activity with a recombinant antibody L chain-porphyrin  
A:Reference number: S68211; MUID:96085223; PMID:7498516  
A:Accession: S68213  
A:Status: preliminary; nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-213 <TAK>  
A:Cross-references: UNIPROT:Q91Z05; UNIPARC:UPI0000176F3F; EMBL:D29667  
C:Superfamily: immunoglobulin homology  
F:137-201/Domain: immunoglobulin homology <IMM>

Query Match 73.0%; Score 65; DB 2; Length 213;  
Best Local Similarity 70.6%; Pred. No. 0.028;  
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 YISSGGSGTYTSDSVK 17  
|||||: ||| |||||  
Db 50 YISSGSSIIYADIVK 66

RESULT 34  
S38864  
Ig epsilon chain C region - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 24-May-2001  
C:Accession: S38864  
R:Kipp, B.; Becker, W.; Schlaak, M.  
submitted to the EMBL Data Library, November 1993  
A:Description: Combination of a defined specificity and desired isotype by cloning of an  
A:Reference number: S38864  
A:Accession: S38864  
A:Molecule type: mRNA  
A:Residues: 1-548 <KIP>  
A:Cross-references: UNIPARC:UPI00001165CC; EMBL:227397; NID:9416537; PIDN:CAA81788.1; PI  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
F:353-421/Domain: immunoglobulin homology <IMM>

Query Match 73.0%; Score 65; DB 2; Length 548;  
Best Local Similarity 81.2%; Pred. No. 0.07;  
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 ISSGGSGTYTSDSVK 17  
|||||: ||| |||||  
Db 51 ISSGGTYTYPDSVK 66

RESULT 35  
PH0875  
Ig heavy chain V region (anti-DNA, H2F) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 09-Oct-1992 #sequence\_revision 09-Oct-1992 #text\_change 31-Dec-2004  
C:Accession: PH0875  
R:Manheimer-Lory, A.; Katz, J.B.; Pillinger, M.; Ghosssein, C.; Smith, A.; Diamond, B.  
J. Exp. Med. 174, 1639-1652, 1991  
A:Title: Molecular characteristics of antibodies bearing an anti-DNA-associated idiotype  
A:Reference number: PH0862; MUID:92078875; PMID:1660528  
A:Accession: PH0875  
A:Molecule type: DNA  
A:Residues: 1-97 <MAN>  
A:Cross-references: UNIPROT:Q9UL91; UNIPARC:UPI0000176C03  
C:Comment: This antibody is produced by Epstein-Barr virus-transformed B cell that bears

C;Superfamily: immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;14-97/Domain: immunoglobulin homology <IMM>  
F;30-35/Region: complementarity-determining 1  
F;49-66/Region: complementarity-determining 2

Query Match 71.9%; Score 64; DB 2; Length 97;  
Best Local Similarity 76.5%; Pred. No. 0.018;  
Matches 13; Conservative 1; Mismatches 0; Indels 3; Gaps 0;

QY 1 YISSGGSGTYSDSVK 17  
||||| :||:|||||  
DB 49 YISSRGSTIYADSVK 65

RESULT 36  
HVN596  
Ig heavy chain V region (6.96) - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 30-Jun-1990 #sequence\_revision 30-Jun-1990 #text\_change 09-Jul-2004  
C;Accession: JT0501  
R;Levy, N.S.; Malipiero, U.V.; Lebecque, S.G.; Gearhart, P.J.  
J. Exp. Med. 169, 2007-2019, 1989  
A;Title: Early onset of somatic mutation in immunoglobulin VH genes during the primary  
A;Reference number: JT0501; MUID:89279149; PMID:2499654  
A;Accession: JT0501  
A;Status: translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-98 <LEV>  
A;Cross-references: UNIPROT:P18528; UNIPARC:UPI00000278DB  
A;Experimental source: strain BALB/cJ  
A;Note: this sequence belongs to the VH7183 subfamily  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;15-98/Domain: immunoglobulin homology <IMM>  
F;22-96/Diulfide bonds: #status predicted

Query Match 71.9%; Score 64; DB 1; Length 98;  
Best Local Similarity 81.2%; Pred. No. 0.018;  
Matches 13; Conservative 0; Mismatches 3; Indels 3; Gaps 0;

QY 2 ISSGGSGTYSDSVK 17  
||||| :||:|||||  
DB 51 ISDGGSTIYDPSVK 66

RESULT 37  
C27889  
Ig heavy chain V region (H220-25) - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 15-Dec-1988 #sequence\_revision 15-Dec-1988 #text\_change 16-Aug-1996  
C;Accession: C27889  
R;Caton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhardt, W.  
EMBO J. 5, 1577-1587, 1986  
A;Title: Structural and functional implications of a restricted antibody response to a  
A;Reference number: A91043; MUID:86300658; PMID:2427335  
A;Accession: C27889  
A;Molecule type: DNA  
A;Residues: 1-101 <CAT>  
A;Cross-references: UNIPARC:UPI0000176AOC  
A;Experimental source: strain Balb/c  
A;Note: this sequence was determined from the germline gene  
C;Comment: This chain was isolated from a hybridoma protein that binds influenza virus  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin

Query Match 71.9%; Score 64; DB 2; Length 101;  
Best Local Similarity 81.2%; Pred. No. 0.019;  
Matches 13; Conservative 0; Mismatches 3; Indels 3; Gaps 0;

QY 2 ISSGGSGTYSDSVK 17  
||||| :||:|||||  
DB 33 ISDGGSTIYDPSVK 48

RESULT 38  
B27889  
Ig heavy chain V region (H146-24B3) - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 15-Dec-1988 #sequence\_revision 15-Dec-1988 #text\_change 16-Aug-1996  
C;Accession: B27889  
R;Caton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhardt, W.  
EMBO J. 5, 1577-1587, 1986  
A;Title: Structural and functional implications of a restricted antibody response to a  
A;Reference number: A91043; MUID:86300658; PMID:2427335  
A;Accession: B27889  
A;Molecule type: DNA  
A;Residues: 1-119 <CAT>  
A;Cross-references: UNIPARC:UPI0000176B67  
A;Experimental source: strain Balb/c  
A;Note: this sequence was determined from the germline gene  
C;Comment: This chain was isolated from a hybridoma protein that binds influenza virus  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 71.9%; Score 64; DB 2; Length 119;  
Best Local Similarity 81.2%; Pred. No. 0.022;  
Matches 13; Conservative 0; Mismatches 3; Indels 3; Gaps 0;

QY 2 ISSGGSGTYSDSVK 17  
||||| :||:|||||  
DB 51 ISDGGSTIYDPSVK 66

RESULT 39  
A27888  
Ig heavy chain V region (H37-84) - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 15-Dec-1988 #sequence\_revision 15-Dec-1988 #text\_change 16-Aug-1996  
C;Accession: A27888  
R;Caton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhardt, W.  
EMBO J. 5, 1577-1587, 1986  
A;Title: Structural and functional implications of a restricted antibody response to a  
A;Reference number: A91043; MUID:86300658; PMID:2427335  
A;Accession: A27888  
A;Molecule type: DNA  
A;Residues: 1-121 <CAT>  
A;Cross-references: UNIPARC:UPI0000176B73  
A;Experimental source: strain Balb/c  
A;Note: this sequence was determined from the germline gene  
C;Comment: This chain was isolated from a hybridoma protein that binds influenza virus  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 71.9%; Score 64; DB 2; Length 121;  
Best Local Similarity 81.2%; Pred. No. 0.023;  
Matches 13; Conservative 1; Mismatches 2; Indels 3; Gaps 0;

QY 2 ISSGGSGTYSDSVK 17  
||||| :||:|||||  
DB 51 ISSGGSTIYDPSVK 66

RESULT 40  
B27888  
Ig heavy chain V region (H37-311) - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 15-Dec-1988 #sequence\_revision 15-Dec-1988 #text\_change 16-Aug-1996  
C;Accession: B27888  
R;Caton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhardt, W.  
EMBO J. 5, 1577-1587, 1986  
A;Title: Structural and functional implications of a restricted antibody response to a  
A;Reference number: A91043; MUID:86300658; PMID:2427335  
A;Accession: B27888

A:Molecule type: DNA  
A:Residues: 1-121 <CAT>  
A:Cross-references: UNIPARC:UPI0000176B6D  
A:Experimental source: strain Balb/c  
A>Note: This sequence was determined from the germline gene  
C:Comment: This chain was isolated from a hybridoma protein that binds influenza virus H  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 71.9%; Score 64; DB 2; Length 121;  
Best Local Similarity 81.2%; Pred. No. 0.023;  
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 ISSGGSGTYSDSVKVG 17  
|||||:|:|||||  
Db 51 ISSGGSYTFPDSVKVG 66

RESULT 41  
B26471  
Ig heavy chain precursor V region (MAK33) - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 05-Jun-1988 #sequence\_revision 05-Jun-1988 #text\_change 23-Jul-1999  
C:Accession: B26471; S70410  
R:Buckel, P.; Hubner-Parajez, C.; Mattee, R.; Lenz, H.; Haug, H.; Beaucamp, K.  
Gene 51, 13-19, 1987  
A:Title: Cloning and nucleotide sequence of heavy- and light-chain cDNAs from a creatine  
A:Reference number: A91572; MUID:87248058; PMID:3110009  
A:Accession: B26471  
A:Molecule type: mRNA  
A:Residues: 1-152 <BUC>  
A:Cross-references: UNIPARC:UPI000011677B; GB:M16163; NID:g195405; PIDN:AAA38292.1; PID:  
R:Juebecque, S.G.; Gearhart, P.J.  
J. Exp. Med. 172, 1717-1727, 1990  
A:Title: Boundaries of somatic mutation in rearranged immunoglobulin genes: 5' boundary  
A:Reference number: S70410; MUID:91079775; PMID:2258702  
A:Accession: S70410  
A>Status: translation not shown  
A:Molecule type: DNA  
A:Residues: 1-19 <LEB>  
A:Cross-references: UNIPARC:UPI0000115881; EMBL:X53776; NID:g52475; PIDN:CAA37792.1; PID:  
C:Genetics:  
A:Introns: 16/1  
A:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:1-19/Domain: signal sequence #status predicted <SIG>  
F:20-152/Product: Ig heavy chain V region MAK33 #status predicted <MAT>  
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 71.9%; Score 64; DB 2; Length 152;  
Best Local Similarity 81.2%; Pred. No. 0.028;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 ISSGGSGTYSDSVKVG 17  
|||||:|:|||||  
Db 70 ISSGGSYTFPDSVKVG 85

RESULT 42  
PH1017  
Ig heavy chain V region (clone 163-c4) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996  
C:Accession: PH1017  
R:Tillman, D.M.; Jow, N.T.; Hill, R.J.; Marion, T.N.  
J. Exp. Med. 176, 761-779, 1992  
A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B c  
A:Reference number: PH0971; MUID:92381444; PMID:1512540  
A:Accession: PH1017  
A>Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-102 <TIL>

A:Cross-references: UNIPARC:UPI0000176CE9  
A:Experimental source: B cell, strain [N2B x NZW]F1  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:6-89/Domain: immunoglobulin homology <IMM>

Query Match 70.8%; Score 63; DB 2; Length 102;  
Best Local Similarity 70.6%; Pred. No. 0.027;  
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 YISSGSGTYSDSVKVG 17  
|||||:|:|||||  
Db 41 YISSGSSTIYYADTVKG 57

RESULT 43  
AIHUBR  
Ig heavy chain V-III region (Bur) - human  
C:Species: Homo sapiens (man)  
C:Date: 22-May-1981 #sequence\_revision 22-May-1981 #text\_change 09-Jul-2004  
C:Accession: A02056  
R:Putnam, F.W.; Liu, Y.S.V.; Low, T.L.K.  
J. Biol. Chem. 254, 2865-2874, 1979  
A:Title: Primary structure of a human IgA1 immunoglobulin. IV. Streptococcal IgA1 protea  
A:Reference number: A92249; MUID:79151016; PMID:107164  
A:Contents: myeloma protein Bur  
A:Accession: A02056  
A:Molecule type: protein  
A:Residues: 1-119 <PUT>  
A:Cross-references: UNIPROT:P01773; UNIPARC:UPI000012CBFC  
A>Note: this is the final paper in a series  
A>Note: the sequence of the C region is also given  
C:Genetics:  
A:Gene: GDB:IGHV@  
A:Cross-references: GDB:128528; OMTM:147070  
A:Map position: 14q32.33-14q32.33  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: glycoprotein; heterotetramer; immunoglobulin; pyroglutamic acid  
F:15-98/Domain: immunoglobulin homology <IMM>  
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F:22-96/Disulfide bonds: #status experimental  
F:28/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 70.8%; Score 63; DB 1; Length 119;  
Best Local Similarity 75.0%; Pred. No. 0.031;  
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 ISSGGSGTYSDSVKVG 17  
|||||:|:|||||  
Db 51 ISYGGSBTYADSVRG 66

RESULT 44  
I37778  
Ig variable region (VDJ) (clone T34-1) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 16-Feb-1996 #sequence\_revision 16-Feb-1996 #text\_change 23-Jul-1999  
C:Accession: I37778; S25472  
R:Demaision, C.; Chastagner, P.; Theze, J.; Zouali, M.  
Proc. Natl. Acad. Sci. U.S.A. 91, 514-518, 1994  
A:Title: Somatic diversification in the heavy chain variable region genes expressed by h  
A:Reference number: A36876; MUID:94119917; PMID:8290556  
A:Accession: I37778  
A>Status: Preliminary  
A:Molecule type: mRNA  
A:Residues: 1-135 <RES>  
A:Cross-references: UNIPARC:UPI00001160E5; EMBL:X67909; NID:g33574; PIDN:CAA48107.1; PID:  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
F:28-111/Domain: immunoglobulin homology <IMM>

Query Match 70.8%; Score 63; DB 2; Length 135;  
Best Local Similarity 70.6%; Pred. No. 0.035;  
Matches 12; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 YISGSGSGTYYSDSVKG 17  
:|||||  
Db 63 FISESGSNTYYVDSVKG 79

## RESULT 45

I47204  
Ig heavy chain variable VDJ region - pig (fragment)  
C:Species: Sus scrofa domestica (domestic pig)  
C:Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 21-Jan-2000  
C:Accession: I47204  
R:Sun, J.; Kacskovics, I.; Brown, W.R.; Butler, J.E.  
J. Immunol. 153, 5618-5627, 1994  
A:Title: Expressed swine VH genes belong to a small VH gene family homologous to human V  
A:Reference number: I47177; MUID:95081609; PMID:7989761  
A:Accession: I47204  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-140 <SUN>  
A:Cross-references: UNIPARC:UPI00001155ED; EMBL:U15520; NID:G571412; PIDN:AAA67029.1; PI  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 70.8%; Score 63; DB 2; Length 140;  
Best Local Similarity 75.0%; Pred. No. 0.036; Mismatches 1; Indels 0; Gaps 0;  
Matches 12; Conservative 1;

QY 2 ISSGSGSGTYYSDSVKG 17  
|||||  
Db 70 ISGSGSNTYYADSVKG 85

## RESULT 46

HW557  
Ig heavy chain precursor V region (5-76) - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 30-Jun-1990 #sequence\_revision 30-Jun-1990 #text\_change 09-Jul-2004  
C:Accession: J70506  
R:Levy, N.S.; Malipiero, U.V.; Lebecque, S.G.; Gearhart, P.J.  
J. Exp. Med. 169, 2007-2019, 1999  
A:Title: Early onset of somatic mutation in immunoglobulin VH genes during the primary  
A:Reference number: J70501; MUID:89279149; PMID:2499654  
A:Accession: J70506  
A:Status: translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-117 <LEV>  
A:Cross-references: UNIPROT:P18529; UNIPARC:UPI00000278DC  
A:Experimental source: strain BALB/cJ  
A:Note: this sequence belongs to the VH7183 subfamily  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:1-19/Domain: signal sequence #status predicted <SIG>  
F:20-117/Product: Ig heavy chain V region (5-76) #status predicted <MAT>  
F:34-117/Domain: immunoglobulin homology <IMM>  
F:41-115/Disulfide bonds: #status predicted

Query Match 69.7%; Score 62; DB 1; Length 117;  
Best Local Similarity 81.2%; Pred. No. 0.043; Mismatches 0; Indels 0; Gaps 0;  
Matches 13; Conservative 0;

QY 2 ISSGSGSGTYYSDSVKG 17  
|||||  
Db 70 ISSGGLXTYYPDSVKG 85

## RESULT 47

PH0096  
Ig heavy chain V region (anti-cyclosporin A) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 15-Jan-1993 #sequence\_revision 15-Jan-1993 #text\_change 16-Aug-1996  
C:Accession: PH0096  
R:Schmitter, D.; Poch, O.; Zeder, G.; Heinrich, G.F.; Koehler, H.P.; Quesniaux, V.F.J.;

Mol. Immunol. 27, 1029-1038, 1990  
A:Title: Analysis of the structural diversity of monoclonal antibodies to cyclosporine.  
A:Reference number: PH0087; MUID:91042649; PMID:2122240  
A:Accession: PH0096  
A:Molecule type: mRNA  
A:Residues: 1-118 <SCH>  
A:Cross-references: UNIPARC:UPI0000176C70  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:15-98/Domain: immunoglobulin homology <IMM>  
F:31-35/Region: complementarity-determining 1  
F:50-66/Region: complementarity-determining 2  
F:99-105/Region: complementarity-determining 3

Query Match 69.7%; Score 62; DB 2; Length 118;  
Best Local Similarity 75.0%; Pred. No. 0.043; Mismatches 2; Indels 0; Gaps 0;  
Matches 12; Conservative 2;

QY 2 ISSGSGSGTYYSDSVKG 17  
|||||  
Db 51 ISSGSGSYTYPDNMKG 66

## RESULT 48

S55539  
Ig heavy chain V region pe24 - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 27-Oct-1995 #sequence\_revision 03-Nov-1995 #text\_change 23-Jul-1999  
C:Accession: S55539  
R:Boettger, V.; Boettger, A.; Lane, E.B.; Spruce, B.A.  
J. Mol. Biol. 247, 932-946, 1995

A:Title: Comprehensive epitope analysis of monoclonal anti-proenkephalin antibodies using  
utations in the variable region genes.

A:Reference number: S55528; MUID:95239763; PMID:7536850  
A:Accession: S55539  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-120 <BOE>  
A:Cross-references: UNIPARC:UPI0000116204; EMBL:X82593; NID:G854312; PIDN:CAA57929.1; PI

C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:14-97/Domain: immunoglobulin homology <IMM>

Query Match 69.7%; Score 62; DB 2; Length 120;  
Best Local Similarity 81.2%; Pred. No. 0.044; Mismatches 0; Indels 0; Gaps 0;  
Matches 13; Conservative 0;

QY 2 ISSGSGSGTYYSDSVKG 17  
|||||  
Db 50 ISSGSGSYTYPDPSVKG 65

## RESULT 49

H27887  
Ig heavy chain V regions (H37-80, H37-43) - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 15-Dec-1988 #sequence\_revision 15-Dec-1988 #text\_change 16-Aug-1996  
C:Accession: H27887  
R:Caton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhardt, W.  
EMBO J. 5, 1577-1587, 1986

A:Title: Structural and functional implications of a restricted antibody response to a d  
A:Reference number: A91043; MUID:86300658; PMID:2427335  
A:Accession: H27887  
A:Molecule type: DNA  
A:Residues: 1-121 <CAT>

A:Cross-references: UNIPARC:UPI0000176875  
A:Experimental source: strain Balb/c  
A:Note: This sequence was determined from the germline gene  
C:Comment: These chains were isolated from hybridoma proteins that bind influenza virus  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:15-98/Domain: immunoglobulin homology <IMM>

```

Query Match          69.7%; Score 62; DB 2; Length 121;
Best Local Similarity 75.0%; Pred. No. 0.044;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 ISSGGSGTYYSDSVKG 17
   |||||: ||| |||
Db 51 ISSGGTYTYPDSLKG 66

RESULT 50
S31699
Ig heavy chain V region - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S31699
R:Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelles, C.
submitted to the EMBL Data Library, June 1992
A:Description: Mechanisms that generate human immunoglobulin diversity operate from the
A:Reference number: S31585
A:Accession: S31699
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-134 <CUI>
A:Cross-references: UNIPARC:UPI0000116473; EMBL:Z14201; NID:g30961; PIDN:CAA78570.1; PID
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match          69.7%; Score 62; DB 2; Length 134;
Best Local Similarity 75.0%; Pred. No. 0.049;
Matches 12; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 ISSGGSGTYYSDSVKG 17
   ||| ||| ||| |||
Db 70 ISSGGSGTYYSDSVKG 85

Search completed: April 6, 2006, 08:58:34
Job time : 21 secs

```

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 6, 2006, 08:55:21 ; Search time 112.949 Seconds

(without alignments)  
106.189 Million cell updates/sec

Title: US-10-089-500-4

Perfect score: 89

Sequence: 1 YISSGSGSYYSVSKG 17

Scoring table: BLOSUMP62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : UniProt 05.80.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	71	79.8	117	1 HV55_MOUSE	P18526 mus musculus
2	69	77.5	99	2 Q4T5M5_TETNG	Q4T5M5 tetraodon n
3	68	76.4	117	1 HV34_MOUSE	P18525 mus musculus
4	68	76.4	119	2 Q920E7_MOUSE	Q920E7 mus musculus
5	68	76.4	196	2 Q65ZL8_MOUSE	Q65ZL8 mus musculus
6	66	74.2	367	2 Q5M8X4_XENTR	Q5M8X4 xenopus tro
7	66	74.2	479	2 Q5BK12_RAT	Q5BK12 rattus norv
8	65	73.0	255	2 Q6KB05_MOUSE	Q6KB05 mus musculus
9	65	73.0	589	2 Q5XHD5_XENLA	Q5XHD5 xenopus lae
10	64	71.9	97	2 Q4SZF9_TETNG	Q4SZF9 tetraodon n
11	64	71.9	98	1 HV57_MOUSE	P18528 mus musculus
12	63	70.8	96	2 Q4T5S4_TETNG	Q4T5S4 tetraodon n
13	63	70.8	98	2 Q4TJ56_TETNG	Q4TJ56 tetraodon n
14	63	70.8	119	1 HV3L_HUMAN	P01773 homo sapien
15	62	69.7	117	1 HV58_MOUSE	P18529 mus musculus
16	62	69.7	614	2 Q6DDQ7_XENLA	Q6DDQ7 xenopus lae
17	61.5	69.1	96	2 Q4SK92_TETNG	Q4SK92 tetraodon n
18	61	68.5	119	2 Q5F218_MOUSE	Q5F218 mus musculus
19	61	68.5	475	2 Q6WZQ6_HUMAN	Q6WZQ6 homo sapien
20	61	68.5	487	2 Q99KA4_MOUSE	Q99KA4 mus musculus
21	60.5	68.0	97	1 HV56_MOUSE	P18527 mus musculus
22	59	66.3	597	2 Q6B8B9_HUMAN	Q6B8B9 homo sapien
23	58	65.2	117	1 HV3C_HUMAN	P01764 homo sapien
24	58	65.2	121	2 Q9UL71_HUMAN	Q9UL71 homo sapien
25	58	65.2	122	1 HV3A_HUMAN	P01762 homo sapien
26	58	65.2	136	1 HV16_MOUSE	P01783 mus musculus
27	57	64.0	473	2 Q91Z05_MOUSE	Q91Z05 mus musculus
28	57	64.0	479	2 Q91WP5_MOUSE	Q91WP5 mus musculus
29	57	64.0	584	2 Q6INK3_XENLA	Q6INK3 xenopus lae
30	57	64.0	591	2 Q4QQW0_RAT	Q4QQW0 rattus norv
31	56.5	63.5	116	1 HV05_CARAU	P19181 carassius a

32	56	62.9	367	2 Q6DFE5_XENLA	Q6DFE5 xenopus lae
33	56	62.9	379	2 Q8K210_MOUSE	Q8K210 mus musculus
34	56	62.9	464	2 Q6MZU5_HUMAN	Q6MZU5 homo sapien
35	56	62.9	606	2 Q6GMY2_HUMAN	Q6GMY2 mus musculus
36	55	61.8	117	1 HV53_MOUSE	P18524 mus musculus
37	55	61.8	117	1 HV59_MOUSE	P18530 mus musculus
38	55	61.8	469	2 Q569F4_MOUSE	Q569F4 homo sapien
39	54	60.7	114	1 HV3B_HUMAN	P01763 homo sapien
40	54	60.7	116	2 Q9UL93_HUMAN	Q9UL93 homo sapien
41	54	60.7	240	2 Q6SZC9_HUMAN	Q6SZC9 homo sapien
42	54	60.7	467	2 Q4VBH1_RAT	Q4VBH1 rattus norv
43	54	60.7	493	2 Q6GMX2_HUMAN	Q6GMX2 homo sapien
44	54	60.7	593	2 Q6INM5_XENLA	Q6INM5 xenopus lae
45	54	60.7	613	2 Q8WUK1_HUMAN	Q8WUK1 homo sapien
46	53	59.6	122	2 Q9UL84_HUMAN	Q9UL84 homo sapien
47	53	59.6	465	2 Q510J0_RAT	Q510J0 rattus norv
48	53	59.6	475	2 Q6GMW7_HUMAN	Q6GMW7 homo sapien
49	53	59.6	493	2 Q8NCL6_HUMAN	Q8NCL6 homo sapien
50	52	58.4	113	2 Q9UL90_HUMAN	Q9UL90 homo sapien
51	52	58.4	121	1 HV3J_HUMAN	P01771 homo sapien
52	51.5	57.9	486	2 Q91Z07_MOUSE	Q91Z07 mus musculus
53	51	57.3	383	2 Q4FRX0_9GAMM	Q4FRX0 psychrobact
54	51	57.3	387	2 Q8GRC8_PARDE	Q8GRC8 paracoccus
55	51	57.3	458	2 Q5BK05_RAT	Q5BK05 rattus norv
56	51	57.3	461	2 Q5M7V3_RAT	Q5M7V3 rattus norv
57	51	57.3	466	2 Q6IN78_HUMAN	Q6IN78 homo sapien
58	51	57.3	479	2 Q5PQK9_RAT	Q5PQK9 rattus norv
59	50.5	56.7	118	2 Q9UL72_HUMAN	Q9UL72 homo sapien
60	50	56.2	380	2 Q8WV03_HUMAN	Q8WV03 homo sapien
61	50	56.2	393	2 Q8NBI6_HUMAN	Q8NBI6 homo sapien
62	50	56.2	465	2 Q6P6C4_HUMAN	Q6P6C4 homo sapien
63	50	56.2	519	2 Q8N092_HUMAN	Q8N092 homo sapien
64	50	56.2	590	2 Q6P171_HUMAN	Q6P171 homo sapien
65	49.5	55.6	117	1 HV02_CANFA	P01785 canis faml
66	49	55.1	115	1 HV3F_HUMAN	Q65ZQ7 mus sp. b3
67	49	55.1	248	2 Q65ZQ7_9MURI	Q65ZQ7 xenopus lae
68	49	55.1	323	1 PIM3_XENLA	Q55M77 cryptococcu
69	49	55.1	424	2 Q55M77_CRYNE	Q55M77 cryptococcu
70	49	55.1	425	2 Q5K8J2_CRYNE	Q5K8J2 cryptococcu
71	49	55.1	473	2 Q6MZV7_HUMAN	Q6MZV7 homo sapien
72	49	55.1	480	2 Q6N094_HUMAN	Q6N094 homo sapien
73	49	55.1	485	2 Q6PDB8_MOUSE	Q6PDB8 mus musculus
74	49	55.1	724	2 Q926C6_RHIME	Q926C6 rhizobium m
75	49	55.1	987	2 Q89CB5_BRAJA	Q89CB5 bradyrhizob
76	49	53.9	105	2 Q8B6Z3_RABIT	Q8B6Z3 oryctolagus
77	48	53.9	118	2 Q9UL91_HUMAN	Q9UL91 homo sapien
78	48	53.9	226	2 Q4SDV2_TETNG	Q4SDV2 tetraodon n
79	48	53.9	475	2 Q5FVP3_RAT	Q5FVP3 rattus norv
80	48	53.9	479	2 Q7TMK4_MOUSE	Q7TMK4 mus musculus
81	48	53.9	480	2 Q91XEL_MOUSE	Q91XEL mus musculus
82	48	53.9	618	2 Q7N6X3_PHOLL	Q7N6X3 photorhabdu
83	48	53.9	779	2 Q54HJ7_DICDI	Q54HJ7 dictyostell
84	47.5	53.4	105	2 Q4T1Z2_TETNG	Q4T1Z2 tetraodon n
85	47.5	53.4	424	2 Q69972_9HIV1	Q69972 human immun
86	47.5	53.4	855	2 Q8AC90_9HIV1	Q8AC90 human immun
87	47.5	53.4	858	2 Q9DKZ2_9HIV1	Q9DKZ2 human immun
88	47.5	53.4	864	2 Q9DKP8_9HIV1	Q9DKP8 human immun
89	47.5	53.4	95	2 Q9ULB6_HUMAN	P01768 homo sapien
90	47	52.8	122	1 HV3G_HUMAN	Q62P85 homo sapien
91	47	52.8	236	2 Q6ZPB5_HUMAN	Q6ZPB5 escherichia
92	47	52.8	313	1 Y8IC_ECOLI	P30235 escherichia
93	47	52.8	313	2 Q3KX99_SHIFL	Q3KX99 shigella fl
94	47	52.8	313	2 Q8XE92_ECO57	Q8XE92 escherichia
95	47	52.8	351	2 Q8FFT5_ECOL6	Q8FFT5 escherichia
96	47	52.8	470	2 Q6PJA4_HUMAN	Q6PJA4 homo sapien
97	47	52.8	478	2 Q6P181_HUMAN	Q6P181 homo sapien
98	47	52.8	888	2 Q5TTP4_ANOGA	Q5TTP4 anophales g
99	47	52.8	1173	2 Q86KTO_DICDI	Q86KTO dictyostell
100	47	52.8	1766	2 Q6Z7D0_CAEBR	Q6Z7D0 caenorhabd
101	46.5	52.2	863	2 Q8AC98_9HIV1	Q8AC98 human immun
102	46	51.7	102	2 Q6B6S8_RABIT	Q6B6S8 oryctolagus
103	46	51.7	297	2 Q73GV7_WOLPM	Q73GV7 wolbachia p
104	46	51.7	326	2 Q9A4L1_CAUCR	Q9A4L1 caulobacter





251	42	47.2	525	2	Q7QVT2_GIALA	Q7QVT2 Giardia lam	324	41	46.1	417	2	Q4YJB2_PLABE	Q4YJB2 plasmodium
252	42	47.2	531	2	Q4UAF1_THEAN	Q4UAF1 theileria a	325	41	46.1	418	2	Q4XH7_GIBZE	Q4XH7 gibberella
253	42	47.2	549	2	Q6CTB8_YARLI	Q6CTB8 yarowia li	326	41	46.1	422	2	Q81IH3_DROER	Q81IH3 drosophila
254	42	47.2	600	2	Q7YXC4_MYCBO	Q7YXC4 mycobacteri	327	41	46.1	433	2	Q8ZIC4_LISMO	Q8ZIC4 listeria mo
255	42	47.2	602	2	Q7Q2P2_ANOGA	Q7Q2P2 anopheles g	328	41	46.1	435	2	Q854B3_9CAUD	Q854B3 mycobacteri
256	42	47.2	704	2	Q6D916_ERWCT	Q6D916 erwina car	329	41	46.1	445	2	Q71W09_LIFSMF	Q71W09 listeria mo
257	42	47.2	721	2	P95097_MYCTU	P95097 mycobacteri	330	41	46.1	453	2	Q31383_BRAJA	Q31383 bradyrhizob
258	42	47.2	729	2	Q17803_CABEL	Q17803 caenorhabdi	331	41	46.1	453	2	Q89XJ5_BRAJA	Q89XJ5 bradyrhizob
259	42	47.2	781	2	Q9KBP7_BACHD	Q9KBP7 bacillus ha	332	41	46.1	458	2	Q85ZQ1_HUMAN	Q85ZQ1 homo sapien
260	42	47.2	837	2	Q5BEY8_EMENI	Q5BEY8 aspergillus	333	41	46.1	467	2	Q8D1W7_WIGBR	Q8D1W7 wigglewort
261	42	47.2	866	2	Q87TA2_VIBPA	Q87TA2 vibrio para	334	41	46.1	468	2	Q5LMX0_SILPO	Q5LMX0 silicibacte
262	42	47.2	867	2	Q7RW65_NEUCR	Q7RW65 neurospora	335	41	46.1	471	2	Q8D1J7_SYNEL	Q8D1J7 synecococ
263	42	47.2	1038	2	Q4USM6_XANCP	Q4USM6 xanthomonas	336	41	46.1	471	2	Q66K04_MOUSE	Q66K04 mus musculu
264	42	47.2	941	2	Q81AL6_BACCR	Q81AL6 bacillus ce	337	41	46.1	472	2	Q6NA08_RHOPA	Q6NA08 rhodopseudo
265	42	47.2	1006	2	Q4UI86_THEAN	Q4UI86 theileria a	338	41	46.1	473	2	Q9D8L4_MOUSE	Q9D8L4 mus musculu
266	42	47.2	1010	2	Q7NY07_CHRVO	Q7NY07 chromobacte	339	41	46.1	475	2	Q5EF85_HUMAN	Q5EF85 homo sapien
267	42	47.2	1017	2	Q4SCA2_TETNG	Q4SCA2 tetraodon n	340	41	46.1	488	1	PHB_ALCFEA	PHB2625 alcaligenes
268	42	47.2	1038	2	Q4USM6_XANCP	Q4USM6 xanthomonas	341	41	46.1	492	2	Q52155_BURPI	Q52155 burkholderi
269	42	47.2	1038	2	Q8PAY6_XANCP	Q8PAY6 xanthomonas	342	41	46.1	492	2	Q62L43_BURMA	Q62L43 burkholderi
270	42	47.2	1041	2	Q87B69_XYLFT	Q87B69 xyliella fas	343	41	46.1	492	2	Q63T94_BURPS	Q63T94 burkholderi
271	42	47.2	1041	2	Q9PFV7_XYLFA	Q9PFV7 xyliella fas	344	41	46.1	494	2	Q6GSK2_WOLTR	Q6GSK2 wolbachia s
272	42	47.2	1123	2	Q81811_DICDI	Q81811 dictyosteli	345	41	46.1	495	2	Q6DCQ8_XENLA	Q6DCQ8 xenopus lae
273	42	47.2	1125	2	Q54XQ2_DICDI	Q54XQ2 dictyosteli	346	41	46.1	514	2	Q4WIN3_ASFPF	Q4WIN3 aspergillus
274	42	47.2	1522	2	Q4FX48_LEIMA	Q4FX48 leishmania	347	41	46.1	525	2	Q8KNU9_BACTI	Q8KNU9 bacillus th
275	42	47.2	2358	2	Q6HVP1_BACAN	Q6HVP1 bacillus an	348	41	46.1	527	2	Q5M7F9_XENLA	Q5M7F9 xenopus lae
276	42	47.2	2358	2	Q81VE8_BACAN	Q81VE8 bacillus an	349	41	46.1	552	2	Q7UM91_RHOBA	Q7UM91 rhodopirell
277	42	47.2	2490	2	Q4MKP9_BACCE	Q4MKP9 bacillus ce	350	41	46.1	567	2	Q5UWGI_HALMA	Q5UWGI haloarcula
278	42	47.2	2490	2	Q6HFP9_BACHK	Q6HFP9 bacillus th	351	41	46.1	608	1	XINC_FIBSU	XINC11 fibrobacter
279	42	47.2	2490	2	Q733U8_BACCK	Q733U8 bacillus th	352	41	46.1	608	2	Q416S9_GIBZE	Q416S9 gibberella
280	42	47.2	2490	2	Q637S6_BACCA	Q637S6 bacillus ce	353	41	46.1	623	2	Q6C053_YARLI	Q6C053 yarowia li
281	42	47.2	4254	2	Q7YU38_RHOBA	Q7YU38 rhodopirell	354	41	46.1	661	2	Q6BPG9_DEBHA	Q6BPG9 debaryomyce
282	41.5	46.6	113	1	HV47_MOUSE	P01823 mus musculu	355	41	46.1	697	2	Q5B517_EMENI	Q5B517 aspergillus
283	41.5	46.6	142	2	Q4WK93_ASFPF	Q4WK93 aspergillus	356	41	46.1	701	2	Q6FTV7_CANGA	Q6FTV7 candida gla
284	41.5	46.6	307	2	Q5BU41_9VIRU	Q5BU41 groundnut b	357	41	46.1	706	2	Q7XKV8_ORISA	Q7XKV8 oryza sativ
285	41.5	46.6	307	2	Q5RL15_9VIRU	Q5RL15 groundnut b	358	41	46.1	715	1	AECBA_MOUSE	Q5142P7_MOUSE
286	41.5	46.6	307	2	Q5RL17_9VIRU	Q5RL17 groundnut b	359	41	46.1	715	2	Q9C7V1_ARATH	Q9C7V1 arabidopsis
287	41.5	46.6	307	2	Q80BA6_9VIRU	Q80BA6 groundnut b	360	41	46.1	719	2	Q4UTU0_XANCP	Q4UTU0 xanthomonas
288	41.5	46.6	307	2	Q80BA7_9VIRU	Q80BA7 groundnut b	361	41	46.1	751	2	Q8P9U5_XANCP	Q8P9U5 xanthomonas
289	41.5	46.6	307	2	Q80BA8_9VIRU	Q80BA8 groundnut b	362	41	46.1	751	2	Q8P9U5_XANCP	Q8P9U5 xanthomonas
290	41.5	46.6	307	2	Q80P92_9VIRU	Q80P92 groundnut b	363	41	46.1	751	2	Q8P9U5_XANCP	Q8P9U5 xanthomonas
291	41.5	46.6	307	2	Q80P93_9VIRU	Q80P93 groundnut b	364	41	46.1	833	2	Q9K3N6_STRCO	Q9K3N6 streptomyce
292	41.5	46.6	307	2	Q80PB4_9VIRU	Q80PB4 groundnut b	365	41	46.1	857	2	Q5RKL4_RAT	Q5RKL4 rattus norv
293	41.5	46.6	307	2	Q80PB5_9VIRU	Q80PB5 groundnut b	366	41	46.1	863	2	Q81A71_CAEEL	Q81A71 caenorhabdi
294	41.5	46.6	307	2	Q84404_9VIRU	Q84404 peanut bud	367	41	46.1	902	2	Q61S36_CAEER	Q61S36 caenorhabdi
295	41.5	46.6	351	2	Q95430_PONPY	Q95430 pongo pygma	368	41	46.1	910	2	Q5QWH2_IDILO	Q5QWH2 idiomarina
296	41.5	46.6	364	2	Q9TPL1_PONPY	Q9TPL1 pongo pygma	369	41	46.1	968	1	GCP_CAEEL	Q10663 caenorhabdi
297	41.5	46.6	449	1	TBB_CICAR	Q39445 cicar ariet	370	41	46.1	989	2	Q9XD84_ECOLI	Q9XD84 escherichia
298	41	46.1	120	1	HV3E_HUMAN	P01766 homo sapien	371	41	46.1	1000	2	Q5CII8_CRYHO	Q5CII8 cryptospori
299	41	46.1	122	1	HV3H_HUMAN	P01769 homo sapien	372	41	46.1	1037	2	Q54NG5_DICDI	Q54NG5 dictyosteli
300	41	46.1	124	2	Q95TE1_DROME	Q95TE1 drosophila	373	41	46.1	1200	2	Q4YPA6_PLABE	Q4YPA6 plasmodium
301	41	46.1	147	2	Q9M7Y1_ARATH	Q9M7Y1 arabidopsis	374	41	46.1	1250	2	Q6L315_SOLDE	Q6L315 solanum dem
302	41	46.1	196	2	Q5LLN8_SILPO	Q5LLN8 silicibacte	375	41	46.1	1274	2	Q8L155_ORISA	Q8L155 oryza sativ
303	41	46.1	230	2	Q88YV7_LACPL	Q88YV7 lactobacilli	376	41	46.1	1291	2	Q5CY24_CRYPV	Q5CY24 cryptospori
304	41	46.1	238	2	Q745R3_MYCPA	Q745R3 mycobacteri	377	41	46.1	1338	2	Q6CHT2_YARLI	Q6CHT2 yarowia li
305	41	46.1	244	2	Q4J7G3_SULAC	Q4J7G3 sulfolobus	378	41	46.1	1402	2	Q7Q9V5_ANOGA	Q7Q9V5 anopheles g
306	41	46.1	246	2	Q4TR54_9SPHN	Q4TR54 erythrobact	379	41	46.1	1407	2	Q5ULM4_9CAUD	Q5ULM4 lactobacilli
307	41	46.1	246	2	Q6LKJ3_PHOPR	Q6LKJ3 photobacteri	380	41	46.1	1505	2	Q5S3N1_SALSA	Q5S3N1 salmo salar
308	41	46.1	269	2	Q7YVY3_CRYPV	Q7YVY3 cryptospori	381	41	46.1	1604	2	Q4YT32_PLABE	Q4YT32 plasmodium
309	41	46.1	286	2	Q55G31_DICDI	Q55G31 dictyosteli	382	41	46.1	1743	2	Q4N570_THEPA	Q4N570 theileria p
310	41	46.1	290	2	Q416V6_GIBZE	Q416V6 gibberella	383	41	46.1	1772	2	Q4Q8V1_LEIMA	Q4Q8V1 leishmania
311	41	46.1	318	1	NSR_LACLA	P23648 lactococcus	384	41	46.1	1801	1	INADL_HUMAN	Q8ni35 homo sapien
312	41	46.1	318	2	Q48609_9LACT	Q48609 lactococcus	385	41	46.1	1834	1	INADL_MOUSE	Q632W7 mus musculu
313	41	46.1	318	2	Q847A1_9LACT	Q847A1 lactococcus	386	41	46.1	2141	2	Q5LV53_SILPO	Q5LV53 silicibacte
314	41	46.1	319	2	Q5AWM1_EMENI	Q5AWM1 aspergillus	387	41	46.1	2258	2	Q7TN96_RAT	Q7TN96 rattus norv
315	41	46.1	327	1	YJ70_YEAST	P47140 saccharomyc	388	41	46.1	3290	2	Q9SH73_ARATH	Q9SH73 arabidopsis
316	41	46.1	333	2	Q9JMQ1_BACSU	Q9JMQ1 bacillus su	389	41	46.1	4212	2	Q4V218_BURMA	Q4V218 burkholderi
317	41	46.1	344	2	Q9JVN9_NEIMA	Q9JVN9 neisseria m	390	41	46.1	5835	2	Q63LX8_BURPS	Q63LX8 burkholderi
318	41	46.1	344	2	Q9KOL5_NEIMB	Q9KOL5 neisseria m	391	40.5	45.5	255	2	Q81294_PLAF7	Q81294 plasmodium
319	41	46.1	347	2	Q7Q0X8_ANOGA	Q7Q0X8 anopheles g	392	40.5	45.5	273	1	EXOS3_MOUSE	Q7Tqk4 mus musculu
320	41	46.1	365	2	Q8A6T9_BACTN	Q8A6T9 bacteroides	393	40.5	45.5	338	2	Q89Z17_BACTN	Q89Z17 bacteroides
321	41	46.1	402	2	Q6EX55_SINSB	Q6EX55 sinorhizobi	394	40.5	45.5	367	2	Q6D2H6_ERWCT	Q6D2H6 erwina car
322	41	46.1	411	2	Q9K8X0_BACHD	Q9K8X0 bacillus ha	395	40.5	45.5	410	1	HXA3A_BRARE	Q8awz2 brachydanio
323	41	46.1	414	2	Q899N9_CLOTE	Q899N9 clostridium	396	40.5	45.5	512	2	Q9KFE8_BACHD	Q9KFE8 bacillus ha



543	40	44.9	1871	2	Q5DU32_MOUSE	Q5du32 mus musculus	616	39	43.8	253	2	Q6IGN8_DROME	Q6ign8 drosophila
544	40	44.9	1933	2	Q5AZ08_EMENI	Q5az08 aspergillus	617	39	43.8	253	2	Q84L77_PYRGO	Q84l77 pyrco commu
545	40	44.9	2260	2	Q4ZND0_PSESI	Q4znd0 pseudomonas	618	39	43.8	253	2	Q8KX25_HELPU	Q8kx25 helicobacte
546	40	44.9	2399	2	Q9ZKS9_HELPU	Q9zks9 helicobacte	619	39	43.8	255	2	Q8KX26_HELPU	Q8kx26 helicobacte
547	40	44.9	2529	2	Q2S579_HELPU	Q2s579 helicobacte	620	39	43.8	255	2	Q8LE68_ARATH	Q8le68 arabidopsis
548	40	44.9	4628	2	Q4SD98_TETNG	Q4sd98 tetraodon n	621	39	43.8	256	2	Q9J777_HELPU	Q9j777 helicobacte
549	40	44.9	4834	2	Q9S714_HUMAN	Q9s714 homo sapien	622	39	43.8	258	2	Q8LKK3_GOSHI	Q8lkk3 gosyplum h
550	40	44.9	4836	2	Q4U2R1_MOUSE	Q4u2r1 mus musculus	623	39	43.8	261	2	Q6ZE10_ORYSA	Q6ze10 oryza sativ
551	40	44.9	4836	2	Q8U473_MOUSE	Q8u473 mus musculus	624	39	43.8	267	2	Q8E6N4_ORYSA	Q8e6n4 mycoplasma
552	40	44.9	5017	2	Q81FJ0_BACRC	Q81fj0 bacillus ce	625	39	43.8	271	2	Q8LSD2_ARATH	Q8lsd2 arabidopsis
553	39.5	44.4	96	2	Q4SZG1_TETNG	Q4szg1 tetraodon n	626	39	43.8	273	1	Q8LSD2_ARATH	Q8lsd2 mus musculus
554	39.5	44.4	271	1	HIS6_ARCFU	Q29439 archaeoglob	627	39	43.8	273	1	Q8LSD2_ARATH	Q8lsd2 mus musculus
555	39.5	44.4	326	2	Q87M27_VIBPA	Q87m27 vibrio para	628	39	43.8	274	1	Q8LSD2_ARATH	Q8lsd2 mus musculus
556	39.5	44.4	428	2	Q58G55_CYPCA	Q58g55 cyprinus ca	629	39	43.8	274	1	Q8LSD2_ARATH	Q8lsd2 mus musculus
557	39.5	44.4	458	2	Q9LKO3_ARATH	Q9lko3 arabidopsis	630	39	43.8	274	2	Q8RD31_PONPY	Q8rd31 pongo pygma
558	39.5	44.4	461	2	Q8A5M1_BACTN	Q8a5m1 bacteroides	631	39	43.8	274	2	Q8RD31_PONPY	Q8rd31 pongo pygma
559	39.5	44.4	463	2	Q6JUX8_BURPS	Q6jux8 burkholderi	632	39	43.8	274	2	Q8RD31_PONPY	Q8rd31 pongo pygma
560	39.5	44.4	467	2	Q7NU87_CHRVO	Q7nu87 chromobacte	633	39	43.8	278	2	Q8RD31_PONPY	Q8rd31 pongo pygma
561	39.5	44.4	467	2	Q4RLX8_TETNG	Q4rlx8 tetraodon n	634	39	43.8	279	2	Q8RD31_PONPY	Q8rd31 pongo pygma
562	39.5	44.4	473	1	6PGD_BUCAP	Q9zhd9 buchnera ap	635	39	43.8	287	2	Q8RD31_PONPY	Q8rd31 pongo pygma
563	39.5	44.4	507	2	Q9K3F2_STRCO	Q9k3f2 streptomyce	636	39	43.8	287	2	Q8RD31_PONPY	Q8rd31 pongo pygma
564	39.5	44.4	572	2	Q8XZS9_RALSO	Q8xzs9 ralstonia s	637	39	43.8	292	2	Q8RD31_PONPY	Q8rd31 pongo pygma
565	39.5	44.4	597	2	Q6JUR7_BURMA	Q6jur7 burkholderi	638	39	43.8	300	2	Q8RD31_PONPY	Q8rd31 pongo pygma
566	39.5	44.4	600	2	Q4LXC7_9BURK	Q4lxc7 burkholderi	639	39	43.8	300	2	Q8RD31_PONPY	Q8rd31 pongo pygma
567	39.5	44.4	632	2	Q5OT77_ENTHI	Q5ot77 entamoeba h	640	39	43.8	301	2	Q8RD31_PONPY	Q8rd31 pongo pygma
568	39.5	44.4	1217	2	Q17240_BOMMO	Q17240 bombyx mori	641	39	43.8	303	2	Q8RD31_PONPY	Q8rd31 pongo pygma
569	39.5	44.4	3194	2	Q9ZLM3_HELPU	Q9zlm3 helicobacte	642	39	43.8	309	2	Q8RD31_PONPY	Q8rd31 pongo pygma
570	39	43.8	50	1	P8BM_PROMP	Q7vdl9 prochloroco	643	39	43.8	310	2	Q8RD31_PONPY	Q8rd31 pongo pygma
571	39	43.8	50	1	P8BM_PROMP	Q7vdl9 prochloroco	644	39	43.8	310	2	Q8RD31_PONPY	Q8rd31 pongo pygma
572	39	43.8	106	2	Q6B6X9_RABIT	Q6b6x9 ocyctolagus	645	39	43.8	316	2	Q8RD31_PONPY	Q8rd31 pongo pygma
573	39	43.8	107	2	Q9XXL3_CAEEL	Q9xxl3 caenorhadi	646	39	43.8	321	2	Q8RD31_PONPY	Q8rd31 pongo pygma
574	39	43.8	109	2	Q59K63_CANAL	Q59k63 candida alb	647	39	43.8	325	2	Q8RD31_PONPY	Q8rd31 pongo pygma
575	39	43.8	109	2	Q59K66_CANAL	Q59k66 candida alb	648	39	43.8	325	2	Q8RD31_PONPY	Q8rd31 pongo pygma
576	39	43.8	110	2	Q5C6Q5_SCHJA	Q5c6q5 schistosoma	649	39	43.8	325	2	Q8RD31_PONPY	Q8rd31 pongo pygma
577	39	43.8	113	2	Q6CCA0_YARLI	Q6cca0 yarrowia li	650	39	43.8	325	2	Q8RD31_PONPY	Q8rd31 pongo pygma
578	39	43.8	118	2	Q6DR87_ARATH	Q6dr87 arabidopsis	651	39	43.8	325	2	Q8RD31_PONPY	Q8rd31 pongo pygma
579	39	43.8	120	2	Q59KC9_CANAL	Q59kc9 candida alb	652	39	43.8	325	2	Q8RD31_PONPY	Q8rd31 pongo pygma
580	39	43.8	130	2	Q59KLC_CANAL	Q59klc candida alb	653	39	43.8	325	2	Q8RD31_PONPY	Q8rd31 pongo pygma
581	39	43.8	131	2	Q5ACN5_CANAL	Q5acn5 candida alb	654	39	43.8	325	2	Q8RD31_PONPY	Q8rd31 pongo pygma
582	39	43.8	149	1	GLB2A_SCAIN	Q5g7p2 listonella	655	39	43.8	326	2	Q8RD31_PONPY	Q8rd31 pongo pygma
583	39	43.8	158	2	Q5G7P2_9CAUD	Q5g7p2 listonella	656	39	43.8	327	2	Q8RD31_PONPY	Q8rd31 pongo pygma
584	39	43.8	162	2	Q91XH8_FRAAN	Q91xh8 fragaria an	657	39	43.8	336	2	Q8RD31_PONPY	Q8rd31 pongo pygma
585	39	43.8	163	2	Q4XDT8_PLACH	Q4xdt8 plasmodium	658	39	43.8	341	2	Q8RD31_PONPY	Q8rd31 pongo pygma
586	39	43.8	167	2	Q946W4_PRUPE	Q946w4 prunus pers	659	39	43.8	347	2	Q8RD31_PONPY	Q8rd31 pongo pygma
587	39	43.8	174	2	Q7WSK7_HELPU	Q7wsk7 helicobacte	660	39	43.8	348	2	Q8RD31_PONPY	Q8rd31 pongo pygma
588	39	43.8	176	2	Q4FU36_9GAMM	Q4fu36 psychrobact	661	39	43.8	350	2	Q8RD31_PONPY	Q8rd31 pongo pygma
589	39	43.8	177	2	Q6KC30_ECCHIC	Q6kc30 escherichia	662	39	43.8	351	2	Q8RD31_PONPY	Q8rd31 pongo pygma
590	39	43.8	178	2	Q7QW7_LEPIC	Q7qw7 leptospira	663	39	43.8	353	2	Q8RD31_PONPY	Q8rd31 pongo pygma
591	39	43.8	178	2	Q8F4X6_LEPIN	Q8f4x6 leptospira	664	39	43.8	355	2	Q8RD31_PONPY	Q8rd31 pongo pygma
592	39	43.8	182	1	K2C3_BOVIN	Q04261 bos taurus	665	39	43.8	357	2	Q8RD31_PONPY	Q8rd31 pongo pygma
593	39	43.8	183	2	Q50FK6_9BACT	Q50fk6 uncultured	666	39	43.8	362	2	Q8RD31_PONPY	Q8rd31 pongo pygma
594	39	43.8	184	2	Q6KBS9_ECCHIC	Q6kbs9 escherichia	667	39	43.8	363	2	Q8RD31_PONPY	Q8rd31 pongo pygma
595	39	43.8	184	2	Q7WSM0_HELPU	Q7wsm0 helicobacte	668	39	43.8	366	2	Q8RD31_PONPY	Q8rd31 pongo pygma
596	39	43.8	184	2	Q7WSM3_HELPU	Q7wsm3 helicobacte	669	39	43.8	367	2	Q8RD31_PONPY	Q8rd31 pongo pygma
597	39	43.8	186	2	Q7WSM6_HELPU	Q7wsm6 helicobacte	670	39	43.8	368	2	Q8RD31_PONPY	Q8rd31 pongo pygma
598	39	43.8	187	2	Q7WSL8_HELPU	Q7wsl8 helicobacte	671	39	43.8	369	2	Q8RD31_PONPY	Q8rd31 pongo pygma
599	39	43.8	187	2	Q7WSL9_HELPU	Q7wsl9 helicobacte	672	39	43.8	371	2	Q8RD31_PONPY	Q8rd31 pongo pygma
600	39	43.8	190	2	Q5JZW6_ECCHIC	Q5jzw6 escherichia	673	39	43.8	371	2	Q8RD31_PONPY	Q8rd31 pongo pygma
601	39	43.8	194	2	Q5TS55_ANOGA	Q5ts55 anopheles g	674	39	43.8	377	2	Q8RD31_PONPY	Q8rd31 pongo pygma
602	39	43.8	207	2	Q4F8K1_EUOGL	Q4f8k1 eucalyptus	675	39	43.8	385	2	Q8RD31_PONPY	Q8rd31 pongo pygma
603	39	43.8	207	2	Q7WVC2_ECCHIC	Q7wvc2 escherichia	676	39	43.8	389	2	Q8RD31_PONPY	Q8rd31 pongo pygma
604	39	43.8	208	2	Q7WSM2_HELPU	Q7wsm2 helicobacte	677	39	43.8	390	1	Q8RD31_PONPY	Q8rd31 pongo pygma
605	39	43.8	212	2	Q7WSM5_HELPU	Q7wsm5 helicobacte	678	39	43.8	392	2	Q8RD31_PONPY	Q8rd31 pongo pygma
606	39	43.8	214	2	Q91FK9_ARATH	Q91fk9 arabidopsis	679	39	43.8	393	2	Q8RD31_PONPY	Q8rd31 pongo pygma
607	39	43.8	216	2	Q5JZJ5_ECCHIC	Q5jzj5 escherichia	680	39	43.8	393	2	Q8RD31_PONPY	Q8rd31 pongo pygma
608	39	43.8	230	2	Q8L5Z9_ARATH	Q8l5z9 arabidopsis	681	39	43.8	396	1	Q8RD31_PONPY	Q8rd31 pongo pygma
609	39	43.8	234	2	Q5R8J8_RAT	Q5r8j8 rattus norv	682	39	43.8	396	2	Q8RD31_PONPY	Q8rd31 pongo pygma
610	39	43.8	242	2	Q7XA66_ARATH	Q7xa66 arabidopsis	683	39	43.8	396	2	Q8RD31_PONPY	Q8rd31 pongo pygma
611	39	43.8	243	2	Q9UWS5_SULSO	Q9uws5 sulfolobus	684	39	43.8	397	2	Q8RD31_PONPY	Q8rd31 pongo pygma
612	39	43.8	246	2	Q5TUC7_9TRYP	Q5tuc7 trypanosoma	685	39	43.8	397	2	Q8RD31_PONPY	Q8rd31 pongo pygma
613	39	43.8	252	2	Q84UK5_PRUPE	Q84uks prunus pers	686	39	43.8	397	2	Q8RD31_PONPY	Q8rd31 pongo pygma
614	39	43.8	252	2	Q8VWV2_PROSA	Q8vwv2 prunus cera	687	39	43.8	398	2	Q8RD31_PONPY	Q8rd31 pongo pygma
615	39	43.8	252	2	Q8FUM2_PRUAV	Q8fum2 prunus aviu	688	39	43.8	400	2	Q8RD31_PONPY	Q8rd31 pongo pygma





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981 38 42.7 238 2 Q5TNT5 ANOGA
982 38 42.7 239 2 Q9NKC5 DROME
983 38 42.7 239 2 Q82HK1 STRAW
984 38 42.7 244 2 Q8LKK1 GOSHI
985 38 42.7 245 2 Q9LLB2 ZINEL
986 38 42.7 246 1 PDXJ1 RHILLO
987 38 42.7 246 2 Q8GI04 PSBRE
988 38 42.7 249 2 Q651Z5 ORYSA
989 38 42.7 249 2 Q7X9Q1 SAMNI
990 38 42.7 249 2 Q6T5H5 GRSI
991 38 42.7 250 2 Q6T5H6 GRSI
992 38 42.7 250 2 Q396Z5 CUCSA
993 38 42.7 252 2 Q81L33 PRUAR
994 38 42.7 252 2 Q84L78 PYRCO
995 38 42.7 252 2 Q8L5S6 9CARY
996 38 42.7 252 2 Q9FS30 PRUPE
997 38 42.7 253 2 Q84L80 PYRCO
998 38 42.7 253 2 Q8L5S7 9CARY
999 38 42.7 253 2 Q93XP2 9ROSA
1000 38 42.7 253 2 Q9SWD4 9CARY

Q5tns5 anopheles g
Q9nkc5 drosophila
Q82hk1 streptomyce
Q8lkk1 gosyplum h
Q9llb2 zinnia eleg
Q98k16 rhizobium l
Q8gi04 pseudomonas
Q651z5 oryza sativ
Q7x9q1 sambucus ni
Q6t5h5 populus tre
Q6t5h6 populus tre
Q396z5 cucumis sat
Q81l33 prunus arne
Q84l78 pyrus commu
Q8l5s6 rumex palus
Q9fs30 prunus pers
Q84l80 pyrus commu
Q8l5s7 rumex palus
Q93xp2 prunus cera
Q9swd4 rumex palus

ALIGNMENTS

RESULT 1
HV55_MOUSE STANDARD; PRT; 117 AA.
AC P18526;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig heavy chain V region 345 precursor.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BALE/cu;
RX MEDLINE=89279149; PubMed=2499654; DOI=10.1084/jem.169.6.2007;
RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during the
RT primary immune response.";
RL J. Exp. Med. 169:2007-2019(1989).
CC -!- MISCELLANEOUS: This sequence belongs to the VH7183 subfamily.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC PIR; JT0502; HVMS34.
CC HSSP; P01783; 1IGC.
DR SMR; P18526; 20-117.
DR Ensembl; ENSMUSG00000062386; Mus musculus.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_V.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin domain; Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117
FT REGION 20 49
FT REGION 50 54
FT REGION 55 68
FT REGION 69 85
FT REGION 86 117
FT DISULFID 41 115
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12902 MW; 49380E4627ACA99A CRC64;

Query Match 79.8%; Score 71; DB 1; Length 117;
Best Local Similarity 76.5%; Pred. No. 0.0033;
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 YISGGSGTYYSDSVKG 17
Db 69 YISGGSGTYYSDSVKG 85
||||| ||||| |||||

RESULT 2
Q4TSM5 TETNG PRELIMINARY; PRT; 99 AA.
AC Q4TSM5;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Chromosome undetermined SCAF9197, whole genome shotgun sequence.
DE (Fragment).
GN ORFNames=GSTENG00006732001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Jallou O., Aubry J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA Bionnet C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA Craud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Wincker P., Lander E.S., Weissenbach J., Roest Crolius H.;
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT the early vertebrate proto-karyotype.";
RL Nature 431:946-957(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RG Genoscope, Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAAB01009197; CAF91807.1; -; Genomic_DNA.
FT NON_TER 1 1
FT NON_TER 99 99
SQ SEQUENCE 99 AA; 10975 MW; 1EC40587BBD4BAF5 CRC64;

Query Match 77.5%; Score 69; DB 2; Length 99;
Best Local Similarity 81.2%; Pred. No. 0.0057;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 ISSGGSGTYYSDSVKG 17
Db 49 ISTGSGSTYYSDSVKG 64
||||| ||||| |||||

RESULT 3
HV54_MOUSE STANDARD; PRT; 117 AA.
ID HV54_MOUSE
AC P18525;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig heavy chain V region 5-84 precursor.
OS Mus musculus (Mouse).

```



OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RN NUCLEOTIDE SEQUENCE.  
 RC STRAIN=BALB/cJ;  
 RX MEDLINE=89279149; PubMed=2499654; DOI=10.1084/jem.169.6.2007;  
 RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;  
 RT "Early onset of somatic mutation in immunoglobulin VH genes during the  
 primary immune response.";  
 RL J. Exp. Med. 169:2007-2019(1989).  
 CC -!- MISCELLANEOUS: This sequence belongs to the VH183 subfamily.  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 between the Swiss Institute of Bioinformatics and the EMBL Outstation -  
 the European Bioinformatics Institute. There are no restrictions on its  
 use as long as its content is in no way modified and this statement is not  
 removed.  
 CC -----  
 DR PIR; JT0505; HVMS84.  
 DR FDB; IARI; X-ray; D=-.  
 DR Ensembl; ENSMUSG00000062386; Mus musculus.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003596; Ig\_v.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 KW 3D-structure; Immunoglobulin domain; Immunoglobulin V region; Signal.  
 FT SIGNAL 1 19  
 FT CHAIN 20 117 Ig heavy chain V region 5-84.  
 FT REGION 20 49 Framework-1.  
 FT REGION 50 54 Complementarity-determining-1.  
 FT REGION 55 68 Framework-2.  
 FT REGION 69 85 Complementarity-determining-2.  
 FT REGION 86 117 Framework-3.  
 FT DISULFID 41 115 By similarity.  
 FT NON\_TER 117 117  
 SQ SEQUENCE 117 AA; 12872 MW; 234055CB6A469861 CRC64;  
 Query Match 76.4%; Score 68; DB 1; Length 117;  
 Best Local Similarity 70.6%; Pred. No. 0.0098;  
 Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 YISNGSGSTYYSDSVK 17  
 DB 69 YISNGSGSTYYPDVTKG 85  
 RESULT 4  
 Q920E7\_MOUSE  
 ID Q920E7\_MOUSE PRELIMINARY; PRT; 119 AA.  
 AC Q920E7;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Pterin-mimicking anti-idiotypic heavy chain variable region  
 DE (fragment).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RN NUCLEOTIDE SEQUENCE.  
 RP Atkin J.D., Iape A., Jennings I.G., Horaitis O., Cotton R.G.H.;  
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RN NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=87175692; PubMed=3104915;  
 RA Lawler A.M., Lin P.S., Gearhart P.J.;  
 RT "Adult B-cell repertoire is biased toward two heavy-chain variable-  
 region genes that rearrange frequently in fetal pre-B cells.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 84:2454-2458(1987).

DR EMBL; AF307937; AAL09421.1; -; Genomic\_DNA.  
 DR PIR; C25913; C25913.  
 DR HSSP; P01783; IIGC.  
 DR SMR; Q920E7; 1-119.  
 DR Ensembl; ENSMUSG000000021155; Mus musculus.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003596; Ig\_v.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 FT NON\_TER 1 119  
 FT NON\_TER 119 119  
 SQ SEQUENCE 119 AA; 13026 MW; F6B90404381CA7C CRC64;  
 Query Match 76.4%; Score 68; DB 2; Length 119;  
 Best Local Similarity 87.5%; Pred. No. 0.01;  
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 2 ISSGGSGTYSDSVK 17  
 DB 51 ISSGGSGTYYPDSVK 66  
 RESULT 5  
 Q65ZL8\_MOUSE  
 ID Q65ZL8\_MOUSE PRELIMINARY; PRT; 196 AA.  
 AC Q65ZL8;  
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
 DE VH7183-DSP2-JH3-CH1 protein (Fragment).  
 GN Name=VH7183-DSP2-JH3-CH1;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RN NUCLEOTIDE SEQUENCE.  
 RC STRAIN=BALB/c;  
 RX MEDLINE=95362300; PubMed=7635518;  
 RA Komori T., Sugiyama H.;  
 RT "An aberrant splicing using a 3' cryptic splice site within the CH1  
 exon induces truncated mu-chain production.";  
 RL Immunology 85:166-170(1995).  
 DR EMBL; S79401; AAB35023.2; -; mRNA.  
 DR SMR; Q65ZL8; 20-195.  
 DR InterPro; IPR003599; Ig.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003596; Ig\_v.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 FT NON\_TER 196 196  
 SQ SEQUENCE 196 AA; 21429 MW; 12A381018944B268 CRC64;  
 Query Match 76.4%; Score 68; DB 2; Length 196;  
 Best Local Similarity 87.5%; Pred. No. 0.017;  
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 2 ISSGGSGTYSDSVK 17  
 DB 70 ISSGGSGTYYPDSVK 85  
 RESULT 6  
 Q5M8X4\_XENTR  
 ID Q5M8X4\_XENTR PRELIMINARY; PRT; 367 AA.  
 AC Q5M8X4;  
 DT 01-FEB-2005 (TrEMBLrel. 29, Created)  
 DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)  
 DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)  
 DE Hypothetical protein.  
 OS Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).

```

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus; Silurana.
OX NCBI_TaxID=8364;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalon D.K., Muzny K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX NIH MGC Project;
RG Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
RL EMBL; BC091247; AAH91247.1; -; mRNA.
DR GO; GO:0003823; P:antigen binding; IEA.
DR InterPro; IPR003599; IG-like.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG.MHC.
DR InterPro; IPR003596; IG.v.
DR Pfam; PF07654; CI-set; 2.
DR SMART; SM00409; IG; 3.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00290; IG.MHC; UNKNOWN_2.
DR PROSITE; PS00290; IG.MHC; UNKNOWN_2.
SQ SEQUENCE 367 AA; 40058 MW; 66DE2E25CDF0CB34 CRC64;

Query Match 74.2%; Score 66; DB 2; Length 367;
Best Local Similarity 70.6%; Pred. No. 0.07;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 YISSGGSGTYSDSVKG 17
Db 69 YISSDGGSTYADSVRG 85

RESULT 7
Q5BK12 RAT
ID Q5BK12_RAT PRELIMINARY; PRT; 479 AA.
AC Q5BK12;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE Igha protein.
GN Name=Igha;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.

Query Match 74.2%; Score 66; DB 2; Length 367;
Best Local Similarity 70.6%; Pred. No. 0.07;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 YISSGGSGTYSDSVKG 17
Db 69 YISSDGGSTYADSVRG 85

RESULT 7
Q5BK12 RAT
ID Q5BK12_RAT PRELIMINARY; PRT; 479 AA.
AC Q5BK12;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE Igha protein.
GN Name=Igha;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.

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OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Sodergren E.J., Lu X., Gibbs R.A.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX NIH MGC Project;
RG Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
RL EMBL; BC091247; AAH91247.1; -; mRNA.
DR GO; GO:0003823; P:antigen binding; IEA.
DR InterPro; IPR003599; IG-like.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG.MHC.
DR InterPro; IPR003596; IG.v.
DR Pfam; PF07654; CI-set; 2.
DR SMART; SM00409; IG; 3.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00290; IG.MHC; UNKNOWN_2.
DR PROSITE; PS00290; IG.MHC; UNKNOWN_2.
SQ SEQUENCE 479 AA; 52329 MW; 8B146164AE8437C5 CRC64;

Query Match 74.2%; Score 66; DB 2; Length 479;
Best Local Similarity 75.0%; Pred. No. 0.093;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 ISSGGSGTYSDSVKG 17
Db 70 VTSGSNTYLDVSKG 85

RESULT 8
Q5KB05 MOUSE
ID Q5KB05_MOUSE PRELIMINARY; PRT; 255 AA.
AC Q5KB05;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE ScFv B8E5 protein (Fragment).
GN Name=scFv B8E5;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Balb/c;
RA Peter J.C., Wallukat G., Tugler J., Maurice D., Roegel J.C.,

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RA Briand J.P., Hoebeke J.;  
RT "Modulation of the M2 muscarinic acetylcholine receptor activity with  
monoclonal anti-M2 receptor antibody fragments."; J. Biol. Chem. 279:55697-55706(2004).  
RL EMBL; AF746180; CAG34081.1; -; Other\_DNA.  
DR HSP; P01837; 1KCR.  
DR InterPro; IPR003599; IG.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003596; IG\_v.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00406; IGV; 2.  
DR PROSITE; PS00835; IG LIKE; 2.  
FT NON TER 1  
SQ SEQUENCE 255 AA; 27445 MW; B68BD38395DF713B CRC64;  
Query Match 73.0%; Score 65; DB 2; Length 255;  
Best Local Similarity 81.2%; Pred. No. 0.069;  
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 2 ISSGGSGTYSDSVK 17  
DB 51 ITSGGSYTPDSVK 66  
RESULT 9  
OSXHD5\_XENLA  
ID Q5XHD5\_XENLA PRELIMINARY; PRT; 589 AA.  
AC Q5XHD5;  
DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
DE Hypothetical protein.  
OS Xenopus laevis (African clawed frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;  
OC Xenopodinae; Xenopus; Xenopus.  
OX NCBI\_TaxID=8355;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Whole;  
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;  
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,  
RA Richardson P.;  
RA "Genetic and genomic tools for Xenopus research: The NIH Xenopus  
RT initiative."; Dev. Dyn. 225:384-391 (2002).  
RL Dev. Dyn. 225:384-391 (2002).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Whole;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H.A., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Datschenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,  
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield V.S.N., Krzywicki M.I., Skalska U., Smalios D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Whole;

RA Klein S., Gerhard D.S.;  
RL Submitted (OCT-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC084123; AAH84123.1; -; mRNA.  
DR GO; GO:0030106; P:MHC class I receptor activity; IEA.  
DR GO; GO:0019883; P:antigen presentation, endogenous antigen; IEA.  
DR GO; GO:0019885; P:antigen processing, endogenous antigen via . . .; IEA.  
DR InterPro; IPR003599; IG.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003597; IG-cl.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_v.  
DR Pfam; PF07654; CI-set; 3.  
DR SMART; SM00409; IG; 4.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00835; IG LIKE; 5.  
DR PROSITE; PS00290; IG MHC; UNKNOWN\_4.  
KW Hypothetical protein.  
SQ SEQUENCE 589 AA; 65361 MW; DIA212699D6E9FCE CRC64;  
Query Match 73.0%; Score 65; DB 2; Length 589;  
Best Local Similarity 75.0%; Pred. No. 0.17;  
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
QY 2 ISSGGSGTYSDSVK 17  
DB 68 ISDGGGTYADSVK 83  
RESULT 10  
Q4SZF9\_TETNG  
ID Q4SZF9\_TETNG PRELIMINARY; PRT; 97 AA.  
AC Q4SZF9;  
DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
DE Chromosome undetermined SCAF11639, whole genome shotgun sequence.  
DE (Fragment).  
GN ORFNames=GSTENG0009860001;  
OS Tetraodon nigroviridis (Green puffer).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthopterygii; Acanthopterygii; Percomorpha; Tetraodontiformes;  
OC Tetraodontidae; Tetraodontidae; Tetraodon.  
OX NCBI\_TaxID=99883;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,  
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,  
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,  
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,  
RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,  
RA Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,  
RA Craud C., Duprat S., Brostier P., Coutanceau J.P., Guzy J.,  
RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,  
RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,  
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,  
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,  
RA Winkler P., Lander E.S., Weissenbach J., Roest Crollius H.;  
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals  
the early vertebrate proto-karyotype."; Nature 431:946-957(2004).  
RL Nature 431:946-957(2004).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RG Genoscope; Whitehead Institute Centre for Genome Research;  
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.  
CC !- CAUTION: The sequence shown here is derived from an  
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
CC preliminary data.  
DR EMBL; CAAB01011639; CAF93973.1; -; Genomic\_DNA.  
FT NON TER 1  
FT NON TER 97  
SQ SEQUENCE 97 AA; 10838 MW; CC9D9956817183C9 CRC64;

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Query Match          71.9%; Score 64; DB 2; Length 97;
Best Local Similarity 70.6%; Pred. No. 0.035;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 YISGGSGTYSDSVK 17
  ||||| |||||
Db 47 YIYTGSSKYYSESVK 63

RESULT 11
HV57 MOUSE
ID HV57 MOUSE STANDARD; PRT; 98 AA.
AC P18528;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig heavy chain V region 6.96.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BALB/cJ;
RX MEDLINE=89279149; PubMed=2499654; DOI=10.1084/jem.169.6.2007;
RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during the
primary immune response."
RL J. Exp. Med. 169:2007-2019(1989).
CC -!- MISCELLANEOUS: This sequence belongs to the VH7183 subfamily.
CC -!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC -----
CC This Swiss-Prot entry is copyrighted. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR J05001; HVM96.
DR HSP; P01783; IIGC.
DR SMR; P18528; 1-98.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin domain; Immunoglobulin V region.
FT DOMAIN 1 >98
FT NON_TER 98 98
SQ SEQUENCE 98 AA; 11007 MW; B8644F7F92FBF95B CRC64;

Query Match          71.9%; Score 64; DB 1; Length 98;
Best Local Similarity 81.2%; Pred. No. 0.035;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 ISSGGSGTYSDSVK 17
  ||||| |||||
Db 51 ISDGGSYTYPSVK 66

RESULT 12
Q4T554 TETNG
ID Q4T554_TETNG PRELIMINARY; PRT; 96 AA.
AC Q4T554;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Chromosome 3 SCAP9141, whole genome shotgun sequence. (Fragment).
GN ORFNames=GSTENG0000665001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Tetraodontidae; Tetraodontiformes; Tetraodon.
OX NCBI_TaxID=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA Blemont C., Skalli Z., Catolico L., Poulain J., De Berardinis V.,
RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Guzy J.,
RA Parra G., Lardier G., Chapelle C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Wolff J.N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Winkler P., Lander E.S., Weissenbach J., Roest Crolius H.;
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
the early vertebrate proto-karyotype."
RL Nature 431:946-957(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RG Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAAB01009141; CAP91758.1; -; Genomic_DNA.
FT NON_TER 1 96
FT NON_TER 96 96
SQ SEQUENCE 96 AA; 10733 MW; 473C4C407BB3E1F0 CRC64;

Query Match          70.8%; Score 63; DB 2; Length 96;
Best Local Similarity 76.5%; Pred. No. 0.049;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 YISGGSGTYSDSVK 17
  ||||| |||||
Db 47 YISTGGSYTDSVK 63

RESULT 13
Q4TJ56 TETNG
ID Q4TJ56_TETNG PRELIMINARY; PRT; 98 AA.
AC Q4TJ56;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Chromosome undetermined SCAF649, whole genome shotgun sequence.
DE (Fragment).
GN ORFNames=GSTENG00004372001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA Blemont C., Skalli Z., Catolico L., Poulain J., De Berardinis V.,
RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Guzy J.,
RA Parra G., Lardier G., Chapelle C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Wolff J.N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Winkler P., Lander E.S., Weissenbach J., Roest Crolius H.;
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
the early vertebrate proto-karyotype."
RL Nature 431:946-957(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RG Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAAB01009141; CAP91758.1; -; Genomic_DNA.
FT NON_TER 1 96
FT NON_TER 96 96
SQ SEQUENCE 96 AA; 10733 MW; 473C4C407BB3E1F0 CRC64;
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```

RL Nature 431:946-957(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RG Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (Feb-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAAE01000649; CAF87076.1; -; Genomic_DNA.
FT NON_TER 1
SQ SEQUENCE 98 AA; 10882 MW; 0EB7F34D9BC4648D CRC64;

Query Match 70.8%; Score 63; DB 2; Length 98;
Best Local Similarity 81.2%; Pred. No. 0.05;
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 ISSGSGTYYSDSVK 17
Db ||||| ||||| |||||
48 ISSGSGTYYSDSVK 63

RESULT 14
HV3L_HUMAN
ID HV3L_HUMAN STANDARD; PRT; 119 AA.
AC P01773;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-JUL-2005 (Rel. 47, Last annotation update)
DE Ig heavy chain V-II region BUR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;

PROTEIN SEQUENCE (MYELOMA PROTEIN BUR).
MEDLINE=79151016; PubMed=107164;
Putnam F.W.; Liu Y.-S.V.; Low T.L.K.;
"Primary structure of a human IgA1 immunoglobulin. IV. Streptococcal
IgA1 protease, digestion, Fab and Fc fragments, and the complete amino
acid sequence of the alpha 1 heavy chain.";
J. Biol. Chem. 254:2865-2874(1979).
CC -!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC PIR; A02056; AIHUBR.
DR HSP; P01772; 2FB4.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; P:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Pyridoxine carboxylic acid.
FT DOMAIN 1 112
FT MOD_RES 1 1 Pyridoxine carboxylic acid.
FT CARBOHYD 28 28 N-linked (GlcNAc...).
FT DISULFID 22 96
FT NON_TER 119 119
SQ SEQUENCE 119 AA; 12981 MW; 12A709A75344D024 CRC64;

Query Match 70.8%; Score 63; DB 1; Length 119;
Best Local Similarity 75.0%; Pred. No. 0.062;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 ISSGSGTYYSDSVK 17
Db ||||| ||||| |||||

RESULT 15
HV58_MOUSE
ID HV58_MOUSE STANDARD; PRT; 117 AA.
AC P18529;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig heavy chain V region 5-76 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BALB/cJ;
RX MEDLINE=89279149; PubMed=2499654; DOI=10.1084/jem.169.6.2007;
RA Levy N.S.; Malipiero U.V.; Lebecque S.G.; Gearhart P.J.;
"Early onset of somatic mutation in immunoglobulin VH genes during the
primary immune response.";
J. Exp. Med. 169:2007-2019(1989).
CC -!- MISCELLANEOUS: This sequence belongs to the VH7183 subfamily.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC PIR; JTO506; HVMS57.
DR PDB; 1I8K; X-ray; B=26-115.
DR PDB; 1I8K; X-ray; B=26-115.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW 3D-structure; Immunoglobulin domain; Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 Ig heavy chain V region 5-76.
FT REGION 20 49 Framework-1.
FT REGION 50 54 Complementarity-determining-1.
FT REGION 55 68 Framework-2.
FT REGION 66 85 Complementarity-determining-2.
FT REGION 86 117 Framework-3.
FT DISULFID 41 115 By similarity.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12991 MW; 93A04782B7888FA0 CRC64;

Query Match 69.7%; Score 62; DB 1; Length 117;
Best Local Similarity 81.2%; Pred. No. 0.088;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 ISSGSGTYYSDSVK 17
Db ||||| ||||| |||||
70 ISSGSGTYYSDSVK 85

RESULT 16
Q6DDQ7_XENLA
ID Q6DDQ7_XENLA PRELIMINARY; PRT; 614 AA.
AC Q6DDQ7;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE MGC69066 protein.
GN Name=MGC69066;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;

```



DR EMBL; AJ880390; CA154294.1; -; mRNA.

DR InterPro; IPR003599; IG.

DR InterPro; IPR007110; IG-like.

DR InterPro; IPR003596; IG\_v.

DR Pfam; PF07686; V-set; 1.

DR SMART; SM00409; IG; 1.

DR SMART; SM00406; IG; 1.

DR PROSITE; PS50835; IG LIKE; 1.

FT NON\_TER 1

FT NON\_TER 119 119

SQ SEQUENCE 119 AA; 13330 MW; 7A3A880833BAB11F CRC64;

Query Match 68.5%; Score 61; DB 2; Length 119;

Best Local Similarity 64.7%; Pred. No. 0.13;

Matches 11; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 YISSGGSGTYSDSVK 17

Db 50 YISTGNGTYTPDVK 66

RESULT 19

Q6MZQ6 HUMAN

ID Q6MZQ6 HUMAN PRELIMINARY; PRT; 475 AA.

AC Q6MZQ6;

DT 05-JUL-2004 (TrEMBLrel. 27, Created)

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DE Hypothetical protein DKFZp686G11190.

GN Name=DKFZp686G11190;

OS Homo sapiens (Human)

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Cactarrhini; Hominidae;

OC Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Esophagus tumor;

RG The German cDNA Consortium;

RA Bahr A., Lauber J., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G.,

RA Han M., Wiemann S.;

RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.

DR EMBL; BX640947; CAE45972.1; -; mRNA.

DR HSP; P01861; 1A0Q.

DR SMR; Q6MZQ6; 20-475.

DR InterPro; IPR003599; IG.

DR InterPro; IPR007110; IG-like.

DR InterPro; IPR003597; IG cl.

DR InterPro; IPR003006; IG\_MHC.

DR InterPro; IPR003596; IG\_v.

DR Pfam; PF07654; Cl-set; 3.

DR SMART; SM00409; IG; 2.

DR SMART; SM00407; IGcl; 3.

DR SMART; SM00406; IG; 1.

DR PROSITE; PS50835; IG LIKE; 4.

DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.

KW Hypothetical protein.

SQ SEQUENCE 475 AA; 52043 MW; B7BAE255A26F4B8E CRC64;

Query Match 68.5%; Score 61; DB 2; Length 475;

Best Local Similarity 75.0%; Pred. No. 0.57;

Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 ISSGGSGTYSDSVK 17

Db 70 ISSSGVNTYADSVK 85

RESULT 20

Q99KA4 MOUSE

ID Q99KA4 MOUSE PRELIMINARY; PRT; 487 AA.

AC Q99KA4;

DT 01-JUN-2001 (TrEMBLrel. 17, Created)

DT

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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)

01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

Igh-VJ558 protein.

Name=Igh-VJ558;

Mus musculus (Mouse).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

Muridae; Murinae; Mus.

NCBI\_TaxID=10090;

[1]

NUCLEOTIDE SEQUENCE.

STRAIN=CZECH II;

TISSUE=Mammary tumor metastatized to lung. Tumor arose spontaneously;

MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullah S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,

Schneerch A., Schein J.E., Jones S.J.M., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length human

and mouse cDNA sequences.";

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

[2]

NUCLEOTIDE SEQUENCE.

STRAIN=CZECH II;

TISSUE=Mammary tumor metastatized to lung. Tumor arose spontaneously;

Director MGC Project;

Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.

EMBL; BC004786; AA04786.1; -; mRNA.

HSP; P01810; 2PBJ.

Ensembl; ENSMUSG0000021155; Mus musculus.

MGI; MGI:96486; Igh-VJ558.

GO; GO:0003823; F-antigen binding; IEA.

InterPro; IPR007110; IG-like.

InterPro; IPR003597; IG cl.

InterPro; IPR003006; IG\_MHC.

InterPro; IPR003596; IG\_v.

Pfam; PF07654; Cl-set; 3.

SMART; SM00406; IG; 1.

PROSITE; PS50835; IG LIKE; 4.

PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.

Immunoglobulin domain.

SEQUENCE 487 AA; 52555 MW; 7DC8E96DB333077B CRC64;

Query Match 68.5%; Score 61; DB 2; Length 487;

Best Local Similarity 75.0%; Pred. No. 0.59;

Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 ISSGGSGTYSDSVK 17

Db 70 ISDGGSYTYPDNVK 85

RESULT 21

HV56\_MOUSE

ID HV56\_MOUSE STANDARD; PRT; 97 AA.

AC P18527;

DT 01-NOV-1990 (Rel. 16, Created)

DT 01-NOV-1990 (Rel. 16, Last sequence update)

DT 10-MAY-2005 (Rel. 47, Last annotation update)

DE Ig heavy chain V region 914.

OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=BA1B/CJ;  
RX MEDLINE=89279149; PubMed=2499654; DOI=10.1084/jem.169.6.2007;  
RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;  
RT "Early onset of somatic mutation in immunoglobulin V genes during the primary immune response.";  
RL J. Exp. Med. 169:2007-2019(1989).  
CC 1- MISCELLANEOUS; This sequence belongs to the VH7183 subfamily.  
CC 1- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.  
CC -----  
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CC -----  
DR PIR; J70504; HVM591.  
DR HSSP; P01783; 1IGC.  
DR SMR; P18527; 1-97.  
DR Ensembl; ENSMUSG0000062386; Mus musculus.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG LIKE; 1.  
KW Immunoglobulin domain; Immunoglobulin V region.  
FT DOMAIN 1 >97  
FT NON\_TER 97  
FT SEQUENCE 97 AA; 10661 MW; C23CB33FF55DA893 CRC64;  
Query Match 68.0%; Score 60.5; DB 1; Length 97;  
Best Local Similarity 87.5%; Pred. No. 0.12;  
Matches 14; Conservative 0; Mismatches 1; Indels 1; Gaps 1;  
QY 2 ISSGSGTGYSDSVKG 17  
||||| ||| |||||  
Db 51 ISSGGS-TYYPDSVKG 65  
RESULT 22  
Q96BB9 HUMAN PRELIMINARY; PRT; 597 AA.  
AC Q96BB9;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE IGHM protein.  
GN Name=IGHM;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Primary B-Cells;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan B., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaney P.H., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalusz D.E., Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Primary B-Cells;  
RG NIH MGC Project;  
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RX PubMed=2500644;  
RX Kishimoto T., Okajima H., Okumoto T., Taniguchi M.;  
RT "Nucleotide sequences of the cDNAs encoding the V-regions of H- and L-chains of a human monoclonal antibody with broad reactivity to malignant tumor cells.";  
RT Nucleic Acids Res. 17:4385-0(1989).  
DR EMBL; BC015760; AAL15760.1; -; mRNA.  
DR PIR; S05271; S05271.  
DR PIR; S24260; S24260.  
DR HSSP; P01861; 1ADQ.  
DR Ensembl; ENSG00000130076; Homo sapiens.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig\_cl.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF07654; C1-set; 4.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG LIKE; 5.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_3.  
KW Immunoglobulin domain.  
SQ SEQUENCE 597 AA; 65039 MW; 4FCA3AD8ECE263D9 CRC64;  
Query Match 66.3%; Score 59; DB 2; Length 597;  
Best Local Similarity 68.8%; Pred. No. 1.5;  
Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
QY 2 ISSGSGTGYSDSVKG 17  
||||| ||| |||||  
Db 70 ISSGSGTGYADSVKG 85  
RESULT 23  
HV3C HUMAN STANDARD; PRT; 117 AA.  
AC P01764;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 13-SEP-2005 (Rel. 48, Last annotation update)  
DE Ig heavy chain V-III region VH26 precursor.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=81101090; PubMed=6450418;  
RA Mathysesens G., Rabbitts T.H.;  
RT "Structure and multiplicity of genes for the human immunoglobulin heavy chain variable region.";  
RL Proc. Natl. Acad. Sci. U.S.A. 77:6561-6565(1980).  
RN [2]  
RP NUCLEOTIDE SEQUENCE OF 20-117.  
RX MEDLINE=93209281; PubMed=7681398;  
RA Mariette X., Tsapis A., Brouet J.C.;  
RT "Nucleotide sequence analysis of the variable domains of four human monoclonal IgM with an antibody activity to myelin-associated

RT glycoprotein.";  
RL Eur. J. Immunol. 23:846-851(1993).  
RN [3]  
RP 3D-STRUCTURE MODELING OF 20-117.  
RX MEDLINE=86094276; PubMed=3866244;  
RA Toyonaga B., Yoshikai Y., Vadaez V., Chin B., Mak T.W.;  
RT "Organization and sequences of the diversity, joining, and constant  
RT region genes of the human T-cell receptor beta chain.";  
RT Proc. Natl. Acad. Sci. U.S.A. 82:8624-8628(1985).  
CC -!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.  
CC -----  
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.  
CC -----  
CC EMBL; J00236; AAA53516.1; -; Unassigned DNA.  
DR EMBL; M35415; AAA58735.1; -; Genomic DNA.  
DR PIR; A02047; H3HU26.  
DR PDB; 1HQJ; Model; H=20-117.  
DR HGNC; HGNC:5545;IGHV@.  
DR GO; GO:0005576; C:extracellular region; NAS.  
DR GO; GO:0003823; F:antigen binding; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW 3D-structure; Immunoglobulin domain; Immunoglobulin V region; Signal.  
FT SIGNAL 1 19  
FT CHAIN 20 117 Ig heavy chain V-III region VH26.  
FT DOMAIN 20 >117 Ig-like.  
FT NON\_TER 117 117  
FT SEQUENCE 117 AA; 12582 MW; E826733FIA3CB0F1 CRC64;  
Query Match 65.2%; Score 58; DB 1; Length 117;  
Best Local Similarity 68.8%; Pred. No. 0.38; Mismatches 0; Gaps 0;  
Matches 11; Conservative 0; Indels 5; Indels 0; Gaps 0;  
OY 2 ISSGGSGTYSDSVK 17  
DB 70 ISGGSGTYGDSVK 85  
RESULT 24  
Q9UL71 HUMAN  
ID Q9UL71 HUMAN PRELIMINARY; PRT; 121 AA.  
AC Q9UL71  
DT 01-MAY-2000 (TRENBLrel. 13, Created)  
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)  
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)  
DE Myosin-reactive immunoglobulin heavy chain variable region  
DE (Fragment).  
OS Homo sapiens (Human)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;  
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,  
RA Young D.C.;  
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
RT fetus";  
RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
DR EMBL; AF035043; AAD56279.1; -; mRNA.  
DR HSSP; P01852; INF0.  
DR SMR; Q9UL71; 1-121.  
DR Ensembl; ENSG00000130076; Homo sapiens.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.

DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
FT NON\_TER 1 121  
SQ SEQUENCE 121 AA; 13154 MW; 2F045CCFA5D50736 CRC64;  
Query Match 65.2%; Score 58; DB 2; Length 121;  
Best Local Similarity 68.8%; Pred. No. 0.39; Mismatches 1; Indels 0; Gaps 0;  
Matches 11; Conservative 1; Indels 0; Gaps 0;  
OY 2 ISSGGSGTYSDSVK 17  
DB 51 ISGGSGTYADSVK 66  
RESULT 25  
HV3A HUMAN  
ID HV3A HUMAN STANDARD; PRT; 122 AA.  
AC P01762;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 10-MAY-2005 (Rel. 47, Last annotation update)  
DE Ig heavy chain V-III region TRO.  
OS Homo sapiens (Human)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP PROTEIN SEQUENCE (MYELOMA PROTEIN TRO).  
RX MEDLINE=76023781; PubMed=809331;  
RA Kratzin H., Altevogt P., Ruban E., Kortt A., Starosck K.,  
RA Hilschmann N.;  
RT "The primary structure of a monoclonal IgA-immunoglobulin (IgA Tro.),  
RT II. The amino acid sequence of the H-chain, alpha-type, subgroup III;  
RL Hoppe-Seyler's Z. Physiol. Chem. 356:1337-1342(1975).  
CC -!- MUSCELLANEOUS: The sequence of the C region is also given.  
CC -!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.  
CC -----  
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.  
CC -----  
CC PIR; A02045; ALHUTR.  
DR HSSP; P01783; IIGC.  
DR GO; GO:0005576; C:extracellular region; NAS.  
DR GO; GO:0003823; F:antigen binding; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW Direct protein sequencing; Immunoglobulin domain;  
KW Immunoglobulin V region; Pyrrolidone carboxylic acid.  
FT DOMAIN 1 108  
FT MOD\_RES 1 1 Pyrrolidone carboxylic acid.  
FT NON\_TER 122 122  
SQ SEQUENCE 122 AA; 13473 MW; 2E21A11DA04D80F9 CRC64;  
Query Match 65.2%; Score 58; DB 1; Length 122;  
Best Local Similarity 64.7%; Pred. No. 0.4; Mismatches 5; Indels 0; Gaps 0;  
Matches 11; Conservative 1; Mismatches 5; Indels 0; Gaps 0;  
OY 1 YISSGGSGTYSDSVK 17  
DB 50 YIGGGSTLYADSVK 66  
RESULT 26  
HV16 MOUSE



ID HV16\_MOUSE STANDARD; PRT; 136 AA.  
AC P01783;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 10-MAY-2005 (Rel. 47, Last annotation update)  
DE IG heavy chain V region MOPC 21 precursor (Fragment).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridea; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=81234548; PubMed=6788376; DOI=10.1016/0092-8674(81)90089-1;  
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,  
RA Baltimore D.;  
RT "Heavy chain variable region contribution to the NPb family of  
antibodies: somatic mutation evident in a gamma 2a variable region.";  
RL Cell 24:625-637(1981).  
RN [2]  
RP PROTEIN SEQUENCE OF 17-136.  
RX MEDLINE=77100368; PubMed=401950;  
RA Adecugbo K., Milstein C., Secher D.S.;  
RT "Molecular analysis of spontaneous somatic mutants.";  
RL Nature 265:299-304(1977).  
CC -----  
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.  
CC -----  
CC EMBL: J00522; AAD1250.1; -; mRNA.  
DR PIR; E30809; GIMS21.  
DR PDB; 1IGC; X-ray; H=17-136.  
DR Ensembl; ENSMUSG00000021155; Mus musculus.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003596; IG\_V.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
DR 3D-structure; Direct protein sequencing; Immunoglobulin domain;  
KW Immunoglobulin V region; Signal.  
FT SIGNAL <1 16  
FT CHAIN 17 136 Ig heavy chain V region MOPC 21.  
FT REGION 115 119 D segment.  
FT REGION 120 136 JH4 segment.  
FT DISULFID 38 112  
FT CONFLICT 75 78 HYAD -> DYAH (in Ref. 2).  
FT CONFLICT 89 90 DN -> ND (in Ref. 2).  
FT CONFLICT 115 115 W -> H (in Ref. 2).  
FT CONFLICT 120 120 Y -> W (in Ref. 2).  
FT NON\_TER 1 1  
FT NON\_TER 136 136  
FT STRAND 19 23  
FT STRAND 26 28  
FT STRAND 30 31  
FT TURN 30 30  
FT STRAND 34 41  
FT STRAND 45 47  
FT HELIX 50 55  
FT STRAND 50 55  
FT STRAND 61 67  
FT TURN 69 70  
FT STRAND 74 76  
FT STRAND 78 80  
FT STRAND 81 81  
FT TURN 82 83  
FT STRAND 84 89  
FT TURN 90 93  
FT STRAND 94 99  
FT STRAND 104 106  
FT STRAND 108 114  
FT TURN 118 119  
FT STRAND 125 126  
FT STRAND 130 134

SQ SEQUENCE 136 AA; 15071 MW; 2276A98DBDF7016 CRC64;  
Query Match 65.2%; Score 58; DB 1; Length 136;  
Best Local Similarity 64.7%; Pred. No. 0.45;  
Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;  
Qy 1 YISSGGSGTYYSVSVKG 17  
Db 66 YISSGSSSLHYADTVKG 82  
RESULT 27  
Q91Z05\_MOUSE  
ID Q91Z05\_MOUSE PRELIMINARY; PRT; 473 AA.  
AC Q91Z05;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Immunoglobulin heavy chain (Gamma polypeptide).  
GN Name=Ighg; Synonym=AU044919;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridea; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C28CH II;  
RC TISSUE=Mammary tumor metastasized to lung. MMTV-LTR/Wnt1 model.  
RC Expression driven by an MMTV-LTR enhancer.;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,  
RA Diatchenko L., Marusina K., Farmer A.F., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
RA Rosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Sanchez A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Bouffard G.G.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C28CH II;  
RC TISSUE=Mammary tumor metastasized to lung. MMTV-LTR/Wnt1 model.  
RC Expression driven by an MMTV-LTR enhancer.;  
RA Director MGC Project;  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBSJ databases.  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RX PubMed=7498516; DOI=10.1016/0014-5793(95)01224-3;  
RA Takagi M., Kohda K., Hamuro T., Harada A., Yamaguchi H., Kamachi M.,  
RA Imanaka T.;  
RT "Thermostable peroxidase activity with a recombinant antibody L chain-  
RT porphyrin Fe(III) complex.";  
RL FEBS Lett. 375:273-276(1995).  
DR EMBL; BC010327; AAH10327.1; -; mRNA.  
DR PIR; S68213; S68213.  
DR HSP; P01783; IIGC.  
DR SMR; Q91Z05; 20-469.  
DR MGI; MGI:2144967; AU044919.  
DR MGI; MGI:2144967; Ighg.  
DR GO; GO:0003823; F:antigen binding; IEA.



DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig cl.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF07654; C1-set; 3.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS00835; IG LIKE; 4.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
 KW Immunoglobulin domain.  
 SQ SEQUENCE 473 AA; 51946 MW; CF625F008932AF12 CRC64;

Query Match 64.0%; Score 57; DB 2; Length 473;  
 Best Local Similarity 58.8%; Pred. No. 2.5;  
 Matches 10; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 YISGGSGTYSDSVK 17  
 :||: ||: ||: ||:  
 Db 69 YINSGSTTIYADTVKG 85

## RESULT 28

Q91WP5 MOUSE  
 ID Q91WP5 MOUSE PRELIMINARY; PRT; 479 AA.  
 AC Q91WP5;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE IgH-VJ558 protein.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=FVB/N; TISSUE=Colon;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Uesdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahay J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skaleka U., Smailus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=FVB/N; TISSUE=Colon;  
 RA Strausberg R.;  
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC013656; AAH13656.1; -; mRNA.  
 DR HSSP; P01789; 1MCP.  
 DR SMR; Q91WP5; 20-236.  
 DR Ensembl; ENSMUSG0000021155; Mus musculus.  
 DR GO; GO:0003623; F-antigen binding; IEA.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig cl.  
 DR InterPro; IPR003597; Ig cl.  
 DR InterPro; IPR003597; Ig cl.  
 DR Pfam; PF07654; C1-set; 2.  
 DR SMART; SM00406; IGV; 1.

DR PROSITE; PS00835; IG LIKE; 4.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
 KW Immunoglobulin domain.  
 SQ SEQUENCE 479 AA; 51604 MW; ECB2D0877748584F CRC64;

Query Match 64.0%; Score 57; DB 2; Length 479;  
 Best Local Similarity 62.5%; Pred. No. 2.5;  
 Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 ISSGGSGTYSDSVK 17  
 :||: ||: ||: ||:  
 Db 70 INSNGSTIYSDTMKG 85

## RESULT 29

Q6INK3 XENLA  
 ID Q6INK3 XENLA PRELIMINARY; PRT; 584 AA.  
 AC Q6INK3;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Hypothetical protein.  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;  
 OC Xenopodinae; Xenopus; Xenopus.  
 OX NCBI\_TaxID=8335;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Lung;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Uesdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahay J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skaleka U., Smailus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Lung;  
 RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;  
 RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,  
 RA Richardson P.;  
 RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus  
 initiative.";  
 RL Dev. Dyn. 225:384-391 (2002).  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Lung;  
 RA Klein S., Strausberg R.;  
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC072277; AAH72277.1; -; mRNA.  
 DR HSSP; P01842; 1AQK.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR InterPro; IPR003599; Ig.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig cl.  
 DR InterPro; IPR003597; Ig cl.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_v.

```

DR Pfam; PF07654; C1-set; 3.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00409; IG; 4.
DR SMART; SM00407; IG1; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 5.
DR PROSITE; PS00290; IG MHC; UNKNOWN_3.
KW Hypothetical protein_1.
SQ SEQUENCE 584 AA; 64449 MW; F134A9DD169F1D64 CRC64;

Query Match 64.0%; Score 57; DB 2; Length 584;
Best Local Similarity 68.8%; Pred. No. 3.1;
Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 ISSGSGTYYSDSVKVG 17
DB 70 ISDGGSTVYADSVKVG 85

RESULT 30
Q4QW0 RAT PRELIMINARY; PRT; 591 AA.
AC Q4QW0;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DE LOC299357 protein (Fragment).
GN Name=LOC299357;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1];
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg E., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong F.,
RA Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,
RA Stapleton M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Green E.D., Dickson M.C.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2];
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RG NIH MGC Project;
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC097958; AAH97958.1; -, mRNA.
FT NON_TER 1
SQ SEQUENCE 591 AA; 64928 MW; CBA9194EC1386E10 CRC64;

Query Match 64.0%; Score 57; DB 2; Length 591;
Best Local Similarity 52.9%; Pred. No. 3.1;
Matches 9; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 YISSGSGTYYSDSVKVG 17
DB 68 YINTGSGTYYNEKPKG 84

RESULT 31
HV05 CARAU STANDARD; PRT; 116 AA.
ID HV05 CARAU
AC AC
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig heavy chain V region 5A precursor.
OS Carassius auratus (Goldfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Carassius.
OX NCBI_TaxID=7957;
RN [1];
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=88144476; PubMed=3125551;
RA Wilson M.R., Middleton D., Warr G.W.;
RT "Immunoglobulin heavy chain variable region gene evolution: structure
and family relationships of two genes and a pseudogene in a teleost
fish."
RL Proc. Natl. Acad. Sci. U.S.A. 85:1566-1570(1988).
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC HSSP; P01783; IIGC.
DR SMR; P19181; 20-116.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Immunoglobulin domain; Immunoglobulin V region; Signal.
FT SIGNAL 1
FT CHAIN 20 116 Ig heavy chain V region 5A.
FT REGION 20 49 Framework-1.
FT REGION 50 54 Complementarity-determining-1.
FT REGION 55 68 Framework-2.
FT REGION 69 84 Complementarity-determining-2.
FT REGION 85 116 Framework-3.
FT DISULFID 41 114 By similarity.
FT NON_TER 116
SQ SEQUENCE 116 AA; 12808 MW; 9C2279E2DF199B12 CRC64;

Query Match 63.5%; Score 56.5; DB 1; Length 116;
Best Local Similarity 81.2%; Pred. No. 0.65;
Matches 13; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 2 ISSGSGTYYSDSVKVG 17
DB 70 IYSGGS-TYADSVKVG 84

RESULT 32
Q6DFE5 XENLA PRELIMINARY; PRT; 367 AA.
ID Q6DFE5 XENLA
AC Q6DFE5;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE MGC83717 protein.
GN Name=MGC83717;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
OX NCBI_TaxID=8355;
RN [1];
RP NUCLEOTIDE SEQUENCE.

```

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McSwain P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Vallalon D.K., Muzy D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakeley R.W., Touchman J.W., Green E.D., Dickson W.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
ET and mouse cDNA sequences";  
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
[2]  
NN NUCLEOTIDE SEQUENCE.  
RP STRAIN=FVB/N; TISSUE=Mammary tumor. C3;  
RC Director MGC Project;  
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.  
RR EMBL; BC031419; AH31419.1; -, mRNA.  
DR Ensembl; ENSMUSG0000047434; Mus musculus.  
DR MGI; MGI:2146443; AI480653.  
DR Hypothetical protein.  
KW SEQUENCE 379 AA; 42636 MW; 654AF6F18E435EBA CRC64;  
SQ

Query Match 62.9%; Score 56; DB 2; Length 379;  
Best Local Similarity 83.3%; Pred. No. 2.8;  
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 SGSGTGYSDSV 15  
| | | | | | | | | | :  
Db 179 SAGSGTGYSDSI 190

RESULT 34  
Q6MZU6\_HUMAN  
ID Q6MZU6\_HUMAN PRELIMINARY; PRT; 464 AA.  
AC Q6MZU6;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DI 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DS 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Hypothetical protein DKFP686C15213.  
GN Names=DKFP686C15213;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa;  
OC Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea;  
OC Homo  
OX NCBI\_TaxId=9606;  
[1]  
RP NUCLEOTIDE SEQUENCE.  
RR TISSUE=Rectum tumor;  
RC The German cDNA Consortium;  
RG Bloembergen H., Boecker M., Brandt P., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;  
RA Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.  
RL EMBL; BX640874; CAE45931.1; -, mRNA.  
DR HSP; P01861; IADQ.  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig-cl.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF07654; Cl-set; 3.  
DR SMART; SM00409; IG\_2;  
DR SMART; SM00407; IGL1; 3.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS0835; IGLIKE; 4.  
DR PROSITE; PS00290; IGMHC; UNKNOWN\_2.  
KW Hypothetical protein\_  
SQ SEQUENCE 464 AA; 51099 MW; 2FCA72C66EB8A0ABC CRC64;  
Query Match 62.9%; Score 56; DB 2; Length 464;  
Best Local Similarity 64.7%; Pred. No. 3.5;  
Matches 11; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

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QY 1 YISSGGSGTYYSDSVKG 17
DB 70 FSRGGSYYADSVKG 86

RESULT 35
Q6GMV2 HUMAN
ID Q6GMV2 HUMAN PRELIMINARY; PRT; 606 AA.
AC Q6GMV2
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE IGHM protein.
GN Name=IGHM;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Munz D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalios D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RG NIH MGC Project;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073758; AAH73758.1; -; mRNA.
DR SMR; Q6GMV2; 20-256.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG.c1.
DR InterPro; IPR003006; IG.MHC.
DR InterPro; IPR003596; IG.v.
DR Pfam; PF07654; C1-set; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 4.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS0835; IG LIKE; 5.
DR PROSITE; PS00290; IG.MHC; UNKNOWN 3.
SQ SEQUENCE 606 AA; 56185 MW; B6B38B51114E4C55 CRC64;

Query Match 62.9%; Score 56; DB 2; Length 606;
Best Local Similarity 70.6%; Pred. No. 4.7;
Matches 12; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 YISSGGSGTYYSDSVKG 17
DB 69 YISSSSSYTNADSVKG 85

RESULT 36
HV53 MOUSE
ID HV53 MOUSE STANDARD; PRT; 117 AA.
AC P18524;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE IG heavy chain V region RF precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BAJB/cJ;
RX MEDLINE=89279149; PubMed=2499654; DOI=10.1084/jem.169.6.2007;
RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during the
RL primary immune response.";
RL J. Exp. Med. 169:2007-2019 (1989).
CC -!- MISCELLANEOUS: This sequence belongs to the VH7183 subfamily.
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC PIR; JT0503; HVMSRF.
DR HSSP; P18529; 118K.
DR SMR; P18524; 20-117.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG.v.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS0835; IG LIKE; 1.
KW Hybridoma; Immunoglobulin domain; Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG heavy chain V region RF.
FT REGION 20 49 Framework-1.
FT REGION 50 54 Complementarity-determining-1.
FT REGION 55 68 Framework-2.
FT REGION 69 85 Complementarity-determining-2.
FT REGION 86 117 Framework-3.
FT DISULFID 41 115 By similarity.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12866 MW; 2CE3295F390F725B CRC64;

Query Match 61.8%; Score 55; DB 1; Length 117;
Best Local Similarity 62.5%; Pred. No. 1.1;
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 ISSGGSGTYYSDSVKG 17
DB 70 INSGSGSYTPDVKG 85

RESULT 37
HV59 MOUSE
ID HV59 MOUSE STANDARD; PRT; 117 AA.
AC P18530;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE IG heavy chain V region 7-39 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BAJB/cJ;
```

RA MEDLINE=89279149; PubMed=2499654; DOI=10.1084/jem.169.6.2007;  
RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;  
RT "Early onset of somatic mutation in immunoglobulin VH genes during the  
RT primary immune response.";  
RL J. Exp. Med. 169:2007-2019(1989).  
CC -!- MISCELLANEOUS: This sequence belongs to the VH7183 subfamily.  
CC -----  
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CC use as long as its content is in no way modified and this statement is not  
CC removed.  
CC -----  
CC PIR: J70507; HVM639.  
DR HSSP: P18529; I18K.  
DR SMR: P18530; 20-117.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW Immunoglobulin domain; immunoglobulin V region; Signal.  
FT SIGNAL 1 19  
FT CHAIN 20 117 Ig heavy chain V region 7-39.  
FT REGION 20 49 Framework-1.  
FT REGION 20 47 Complementarity-determining-1.  
FT REGION 50 54 Complementarity-determining-1.  
FT REGION 55 68 Framework-2.  
FT REGION 69 85 Complementarity-determining-2.  
FT REGION 86 117 Framework-3.  
FT DISULFID 41 115 By similarity.  
FT NON\_TER 117 117  
SQ SEQUENCE 117 AA; 12972 MW; D5CA4167D0F1774F CRC64;  
  
Query Match 61.8%; Score 55; DB 1; Length 117;  
Best Local Similarity 75.0%; Pred. No. 1.1;  
Matches 12; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
  
QY 2 ISSGGSGTYSDSVK 17  
DB 70 ISGGVSYTYPSVK 85  
  
RESULT 38  
Q569F4 HUMAN PRELIMINARY; PRT; 469 AA.  
AC Q569F4;  
DT 10-MAY-2005 (TrEMBLrel. 30, Created)  
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)  
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)  
DE IGHG1 protein.  
GN Name=IGHG1;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP TISSUE=Lymph;  
RC MEDLINE=23388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mollany S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S.J., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywicki M.I., Skalska U., Smallos D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Lymph;  
RG NIH MGC Project;  
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC092518; AAH92518.1; -, mRNA.  
SQ SEQUENCE 469 AA; 51254 MW; AC13448E3047784F CRC64;  
  
Query Match 61.8%; Score 55; DB 2; Length 469;  
Best Local Similarity 68.8%; Pred. No. 5.1;  
Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
  
QY 2 ISSGGSGTYSDSVK 17  
DB 70 ISWDGGSTYADSVK 85  
  
RESULT 39  
HV3B HUMAN  
ID HV3B HUMAN STANDARD; PRT; 114 AA.  
AC P01763;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 10-MAY-2005 (Rel. 47, Last annotation update)  
DE Ig heavy chain V-III region WEA.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP PROTEIN SEQUENCE.  
RX MEDLINE=83273707; PubMed=6410398;  
RA Goni F., Frangione B.;  
RT "Amino acid sequence of the Fv region of a human monoclonal IgM  
RT (protein WEA) with antibody activity against 3,4-pyruvylated galactose  
RT in Klebsiella polysaccharides K30 and K33.";  
RL Proc. Natl. Acad. Sci. U.S.A. 80:4837-4841(1983).  
CC -!- MISCELLANEOUS: This chain was obtained from a monoclonal antibody  
CC against 3,4-pyruvylated galactose and isolated from a patient with  
CC Waldenstrom's macroglobulinemia.  
CC -!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.  
CC -----  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.  
CC -----  
CC PIR: A02046; M3HUWE.  
DR HSSP: P01772; 2FB4.  
DR SMR: P01763; 1-114.  
DR GO; GO:0005576; C:extracellular region; NAS.  
DR GO; GO:0003823; F:antigen binding; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; IGV.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW Direct protein sequencing; Immunoglobulin domain;  
KW Immunoglobulin V region; Pyridoxine carboxylic acid.  
FT DOMAIN 1 112 Ig-like.  
FT MOD\_RES 1 114 Pyridoxine carboxylic acid.  
FT NON\_TER 114 114  
SQ SEQUENCE 114 AA; 12256 MW; D88294FB418A07B7 CRC64;  
  
Query Match 60.7%; Score 54; DB 1; Length 114;

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Best Local Similarity  58.8%;  Pred. No. 1.6;
Matches 10;  Conservative  2;  Mismatches  5;  Indels  0;  Gaps  0;

Qy  1 YISGSGSTYYSDSVKG 17
      : || || || || || ||
Db  50 FIGGSGSTIYYADSVKG 66

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RESULT 40	
Q9UL93_HUMAN	
ID	Q9UL93_HUMAN PRELIMINARY; PRT; 116 AA.
AC	Q9UL93;
DC	01-MAY-2000 (TrEMBLrel. 13, Created)
DT	01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE	Myosin-reactive immunoglobulin heavy chain variable region (Fragment).
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC	Homo.
NCBI_TaxID=9606;	
{1}	
RN	NCLETTIDE SEQUENCE.
RP	MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA	Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA	Young D.C.;
RT	"Myosin-reactive autoantibodies in rheumatic carditis and normal
RT	fetus.";
RL	Clin. Immunol. Immunopathol. 87:184-192(1998).

DOI=10.1084/jem.178.1.331;  
MEDLINE=93301610; PubMed=9315388;  
Hillson J.L., Karr N.S., Oppiger I.R., Mannik M., Sasso E.H.;  
"The structural basis of germ-line-encoded VH3 immunoglobulin binding  
to staphylococcal protein A,";  
J. Exp. Med. 178:331-336(1993).

RP	NUCLEOTIDE SEQUENCE.
RA	PubMed-2840480.
RX	Bird J., Galli N., Link M., Stites D., Sklar J.;
RY	"Continuing rearrangement but absence of somatic hypermutation in
RT	immunoglobulin genes of human B cell precursor leukemia.";
RL	J. Exp. Med. 168:229-245 (1988).
RR	EMBL; AF035021; AAD56257.1; -; mRNA.
DR	PIR; PH1644; PH1644.
DR	PIR; PLO120; PLO120.
DR	HSSP; P01772; 2FB4.
DR	SMR; Q9UL93; 1-116.
DR	InterPro; IPR007110; Ig-like.
DR	InterPro; IPR003596; Ig_V.
DR	SMART; SM00406; IGV; 1.
DR	PROSITE; PS50835; IG_LIKE; 1.
FT	NON TER 1
FT	NON TER 116
FT	NON TER 116 AA; 12434 MW;
SQ	0DA0348154DD6061 CRC64;

Query Match	60.7%	Score 54;	DB 2;	Length 116;
Best Local Similarity	68.8%	Pred. No. 1.6;		
Matches 11;	Conservative	1;	Mismatches	4;
			Indels	0;
			Gaps	0;

Qy 2 ISSGGSGTYYSDSVKG 17  
||| ||| ||| : |||  
Db 50 ISYDGSNKYYADSVKG 65

RESULT 41  
Q65ZC9 HUMAN  
ID Q65ZC9 HUMAN PRELIMINARY;  
PRT: 240 AA.

DT	25-OCT-2004	(TREM)rel. 28, Created)
DT	25-OCT-2004	(TREM)rel. 28, Last sequence update)
DT	25-OCT-2004	(TREM)rel. 28, Last annotation update)

DE	Single-chain Fv (Fragment).
GN	Name=sctfv;
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea;
OC	Homo.
OX	NCBI_TaxID=9606;
EN	[1]
RP	NUCLEOTIDE SEQUENCE.
RC	STRAIN=C1q/7;
RX	MEDLINE=97362799; PubMed=9219263; DOI=10.1038/nbt0797-629;
RA	Kontermann R.E., Wing M.G., Winter G.;
RT	"Complement recruitment using bispecific diabodies.";
RL	Nat. Biotechnol. 15:629-631(1997).
DR	EMBL; Y13056; CAA73499.1; -, mRNA.
DR	InterPro; IPR003599; Ig.
DR	InterPro; IPR007110; Ig-like.
DR	InterPro; IPR003596; Ig_v.
DR	SMART; SM00409; Ig; 2.
DR	SMART; SM00406; IgV; 2.
DR	PROSITE; PS50835; IG_LIKE; 2.
FT	NON_TER 1 1
FT	NON_TER 240 240
SQ	SEQUENCE 240 AA; 25569 MW; FDCFD3645F64B373 CRC64;

Query Match	60.7%;	Score 54;	DB 2;	Length 240;
Best Local Similarity	68.8%;	Pred. No. 3.6;		
Matches 11:	Conservative	1;	Mismatches	4;
	Indels	0;	Gaps	0;

Qy 2 ISSGSGTYYSDSVKG 17  
||| ||| : |||  
Db 51 ISYDGSNKYYADSVKG 66

RESULT 42

Q4VBH1_RAT	Q4VBH1_RAT	PRELIMINARY;	PRT;	467 AA.
AC	Q4VBH1;			
DT	13-SEP-2005	(T-EMBLrel. 31,	Created)	
DT	13-SEP-2005	(T-EMBLrel. 31,	Last sequence update)	
DT	13-SEP-2005	(T-EMBLrel. 31,	Last annotation update)	
DE	LOC299354	protein.		
GN	Name=LOC299354;			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;			
OC	Muroidea; Muridae; Murinae; Rattus.			
OX	NCBI TaxID=10116;			

RP NUCLEOTIDE SEQUENCE.

TTSJUE=Thymus;  
 MEDLINE=22388257; PubMed=12477332; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.F., Bhat N.K.,  
 RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,  
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Vallon J.D., Munz D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinaki M.I., Skaleka U., Smailus D.E.,  
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A., "generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002) .  
 RN

```
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Thymus;
RG NIH MGC Project;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Beta-2-microglobulin is the beta-chain of major
CC histocompatibility complex class I molecules (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).
DR EMBL; BC095846; AAH95846.1; -; mRNA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 2.
DR PROSITE; PS0835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
KW Immunoglobulin domain; Repeat.
SQ SEQUENCE 467 AA; 51651 MW; 1FF0328F50160ED3 CRC64;

Query Match 60.7%; Score 54; DB 2; Length 467;
Best Local Similarity 62.5%; Pred. No. 7.3;
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 ISSGGSGTYSPSVKVG 17
Db 70 INTDGGSTYPSVKVG 85
|::| |||||
|::| |||||

RESULT 43
Q6GMX2 HUMAN
ID Q6GMX2_HUMAN PRELIMINARY; PRT; 493 AA.
AC Q6GMX2;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE IGHAI protein.
GN Name=IGHAI;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gumaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RA and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RG NIH MGC Project;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073771; AAH73771.1; -; mRNA.
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DR SMR; Q6GMX2; 263-471.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF07654; C1-set; 2.
DR SMART; SM00409; IG; 4.
DR SMART; SM00407; IGC1; 2.
DR PROSITE; PS0835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
SQ SEQUENCE 493 AA; 52865 MW; 55B999303B286203 CRC64;

Query Match 60.7%; Score 54; DB 2; Length 493;
Best Local Similarity 68.8%; Pred. No. 7.7;
Matches 11; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 ISSGGSGTYSPSVKVG 17
Db 70 INSDGSSYADSVKVG 85
|::| |||||
|::| |||||

RESULT 44
Q6INM5 XENLA
ID Q6INM5_XENLA PRELIMINARY; PRT; 593 AA.
AC Q6INM5;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE MGC69066 protein.
GN Name=MGC69066;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
OX NCBI_TaxID=8355;
RN [1]_TaxID=8355;
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gumaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RA and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RL Dev. Dyn. 225:384-391(2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
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RA Klein S., Strausberg R.;  
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC072253; AAH72253.1; -; mRNA.  
DR HSSP; P01842; IAOK.  
DR GO; GO:0030106; F:MHC class I receptor activity; IEA.  
DR GO; GO:0019883; P:antigen presentation, endogenous antigen; IEA.  
DR GO; GO:0019885; P:antigen processing, endogenous antigen via . . . IEA.  
DR InterPro; IPR003599; IG.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003597; IG-cl.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_v.  
DR InterPro; IPR001680; WD40.  
DR Pfam; PF07654; CI-set; 4.  
DR SMART; SM00409; IG; 4.  
DR SMART; SM00407; IGcl; 4.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG LIKE; 5.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN 4.  
DR PROSITE; PS00678; WD REPEATS 1; UNKNOWN 1.  
SQ SEQUENCE 593 AA; 65875 MW; BE314FF9211E12FC CRC64;

Query Match 60.7%; Score 54; DB 2; Length 593;  
Best Local Similarity 62.5%; Pred. No. 9.4;  
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 2 ISSGGSGTYSPSVK 17  
I: |||||  
Db 68 INPDGGSTYADSVK 83

RESULT 45  
Q8WUK1 HUMAN  
ID Q8WUK1\_HUMAN PRELIMINARY; PRT; 613 AA.  
AC Q8WUK1;  
DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE IGHM protein.  
GN Name=IGHM;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]\_TaxID=9606;  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Primary B-Cells;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,  
RA Diatchenko K.L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullighy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.K., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalios D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Primary B-Cells;  
RG NIH MGC Project;

RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RX PubMed=2117273;  
RA Schroeder H.W. Jr, Wang J.Y.;  
RT "Preferential utilization of conserved immunoglobulin heavy chain  
RT variable gene segments during human fetal life.";  
RL Proc. Natl. Acad. Sci. U.S.A. 87:6146-6150(1990).  
RN [4]  
RP NUCLEOTIDE SEQUENCE.  
RX PubMed=1383695; DOI=10.1016/0161-5890(92)90173-U;  
RA Cuisinier A.M., Fumoux F., Fougereau M., Tonnel C.;  
RT "IGM kappa/lambda EBV human B cell clone: an early step of  
RT differentiation of fetal B cells or a distinct B lineage?";  
RL Mol. Immunol. 29:1363-1373(1992).  
RN [5]  
RP NUCLEOTIDE SEQUENCE.  
RX PubMed=1730252;  
RA Raaphorst F.M., Timmers E., Kenter M.J., Van Tol M.J., Vossen J.M.,  
RA Schuurman R.K.;  
RT "Restricted utilization of germ-line VH3 genes and short diverse third  
RT complementarity-determining regions (CDR3) in human fetal B lymphocyte  
RT immunoglobulin heavy chain rearrangements.";  
RL Eur. J. Immunol. 22:247-251(1992).  
RN [6]  
RP NUCLEOTIDE SEQUENCE.  
RX PubMed=1904154;  
RA Neale G.A., Kitchingman G.R.;  
RT "mRNA transcripts initiating within the human immunoglobulin mu heavy  
RT chain enhancer region contain a non-translatable exon and are  
RT extremely heterogeneous at the 5' end.";  
RL Nucleic Acids Res. 19:2427-2433(1991).  
RN [7]  
RP NUCLEOTIDE SEQUENCE.  
RX PubMed=2840480; DOI=10.1084/jem.168.1.229;  
RA Bird J., Gallili N., Link M., Stices D., Sklar J.;  
RT "Continuing rearrangement but absence of somatic hypermutation in  
RT immunoglobulin genes of human B cell precursor leukemia.";  
RL J. Exp. Med. 168:229-245(1988).  
RN [8]  
RP NUCLEOTIDE SEQUENCE.  
RX PubMed=2538551; DOI=10.1084/jem.169.4.1391;  
RA Nickerson K.G., Berman J., Glickman E., Chess L., Alt F.W.;  
RT "Early human IGH gene assembly in Epstein-Barr virus-transformed fetal  
RT B cell lines. Preferential utilization of the most JH-proximal D  
RT segment (DQ52) and two unusual VH-related rearrangements.";  
RL J. Exp. Med. 169:1391-1403(1989).  
RN [9]  
RP NUCLEOTIDE SEQUENCE.  
RX PubMed=93301610; PubMed=8315388; DOI=10.1084/jem.178.1.331;  
RA Hillson J.L., Karr N.S., Opplinger I.R., Mannik M., Sasso E.H.;  
RT "The structural basis of germline-encoded VH3 immunoglobulin binding  
RT to staphylococcal protein A.";  
RL J. Exp. Med. 178:331-336(1993).  
DR EMBL; BC020240; AAH20240.1; -; mRNA.  
DR PIR; F36005; F36005.  
DR PIR; G36005; G36005.  
DR PIR; PH1642; PH1642.  
DR PIR; PH1643; PH1643.  
DR PIR; PH1645; PH1645.  
DR PIR; PH1646; PH1646.  
DR PIR; PL0098; PL0098.  
DR PIR; PL0120; PL0120.  
DR PIR; S15590; S15590.  
DR PIR; S31116; S31116.  
DR PIR; S31119; S31119.  
DR PIR; S70442; S70442.  
DR HSSP; P01861; IADQ.  
DR SMR; Q8WUK1; 20-242.  
DR Ensembl; ENSG00000130076; Homo sapiens.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003597; IG-cl.  
DR InterPro; IPR003006; IG\_MHC.



DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF07654; CI-set; 4.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00835; IG LIKE; 5.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_3.  
KW Immunoglobulin domain.  
SQ SEQUENCE 613 AA; 67296 MW; 60C7F5950671E315 CRC64;

Query Match 60.7%; Score 54; DB 2; Length 613;  
Best Local Similarity 68.8%; Pred. No. 9.8;  
Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 2 ISSGSGTYYSDSVKG 17  
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Db 70 ISYDGSNKYADSVKG 85

RESULT 46  
Q9UL84\_HUMAN  
ID Q9UL84 HUMAN PRELIMINARY; PRT; 122 AA.  
AC Q9UL84;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Myosin-reactive immunoglobulin heavy chain variable region  
DE (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;  
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,  
RA Young D.C.;  
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
RT fetus.";  
RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
DR EMBL; AF035030; AAD56266.1; -, mRNA.  
DR HSP; P01772; 2FB4.  
DR SMR; Q9UL84; 1-122.  
DR Ensembl; ENSG00000130076; Homo sapiens.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003596; IG\_v.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PSS0835; IG\_LIKE; 1.  
FT NON TER 1  
FT NON TER 122 122  
SQ SEQUENCE 122 AA; 13579 MW; 36054D4136654588 CRC64;

Query Match 59.6%; Score 53; DB 2; Length 122;  
Best Local Similarity 62.5%; Pred. No. 2.5;  
Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 2 ISSGSGTYYSDSVKG 17  
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Db 51 ISNDGSNKFYADSVKG 66

RESULT 47  
Q510J0\_RAT  
ID Q510J0\_RAT PRELIMINARY; PRT; 465 AA.  
AC Q510J0;  
DT 10-MAY-2005 (TrEMBLrel. 30, Created)  
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)  
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)  
DE Hypothetical LOC299354.  
GN Name=LOC299354;  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Myriophora; Muridae; Murinae; Rattus.

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.C.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skaleka U., Smailus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE-Spleen;  
RA Strausberg R.;  
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC073782; AAH73782.1; -; mRNA.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR InterPro; IPR003599; IG.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003597; IG.cl.  
DR InterPro; IPR003006; IG.MHC.  
DR InterPro; IPR003596; IG.v.  
DR Pfam; PF07654; CI-set; 3.  
DR SMART; SM00409; IG1; 2.  
DR SMART; SM00407; IG1; 3.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG LIKE; 4.  
DR PROSITE; PS00290; IG MHC; UNKNOWN\_2.  
KW Hypothetical protein.  
SQ SEQUENCE 475 AA; 51987 MW; 2A1PE55D736860F8 CRC64;  
  
Query Match 59.6%; Score 53; DB 2; Length 475;  
Best Local Similarity 62.5%; Pred. No. 11;  
Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;  
  
Qy 2 ISSGGSGTYSDSVKVG 17  
||: : |||||  
Db 70 ISNSENYYADSVKVG 85  
  
RESULT 49  
ID Q8NCL6\_HUMAN PRELIMINARY; PRT; 493 AA.  
AC Q8NCL6;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE CDNA FLJ90170 fis, clone MAMWA1000370, highly similar to Ig alpha-1  
DE Chain C region.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Mammary gland;  
RA Otsuki T., Ota T., Nishikawa T., Hayaashi K., Suzuki Y., Yamamoto J.,  
RA Wakamatsu A., Kimura K., Sakamoto K., Hatanoto K., Kawai Y., Ishii S.,  
RA Saito K., Kojima S., Sugiyama T., Ono T., Okano K., Yoshikawa Y.,  
RA Aotsuka S., Sasaki N., Hattori A., Okumura K., Nagai K., Sugano S.,  
RA Isozaki T.;  
RT "Signal Sequence and Keyword Trap in silico for Selection of Full-  
RT Length Human cDNAs Encoding Secretion or Membrane Proteins from Oligo-

RT Capped cDNA Libraries.";  
RL DNA Res. 12:117-126 (2005).  
DR EMBL; AK074651; BAC11114.1; -; mRNA.  
DR HSSP; P01876; 10W0.  
DR SMR; Q8NCL6; 263-471.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003597; IG.cl.  
DR InterPro; IPR003006; IG.MHC.  
DR InterPro; IPR003596; IG.v.  
DR Pfam; PF07654; CI-set; 2.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG LIKE; 4.  
DR PROSITE; PS00290; IG MHC; UNKNOWN\_1.  
KW Immunoglobulin domain.  
SQ SEQUENCE 493 AA; 53224 MW; 12ECD7E094777101 CRC64;  
  
Query Match 59.6%; Score 53; DB 2; Length 493;  
Best Local Similarity 83.3%; Pred. No. 11;  
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 6 GSGTYSDSVKVG 17  
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Db 74 GTKTYSDSVKVG 85  
  
RESULT 50  
ID Q9UL90\_HUMAN PRELIMINARY; PRT; 113 AA.  
AC Q9UL90;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Myosin-reactive immunoglobulin heavy chain variable region  
DE (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;  
RX Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,  
RA Young D.C.;  
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
RT fetus.";  
RL Clin. Immunol. Immunopathol. 87:184-192 (1998).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC PubMed=1730252;  
RA Raaphorst P.M., Timmers E., Kenter M.J., Van Tol M.J., Vossen J.M.,  
RA Schuurman R.K.;  
RT "Restricted utilization of germ-line VH3 genes and short diverse third  
RT complementarity-determining regions (CDR3) in human fetal B lymphocyte  
RT immunoglobulin heavy chain rearrangements.";  
RL Eur. J. Immunol. 22:247-251 (1992).  
DR EMBL; AF035024; AAD56260.1; -; mRNA.  
DR PIR; S78486; S78486.  
DR HSSP; P01772; 2FB4.  
DR SMR; Q9UL90; 1-113.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003596; IG.v.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG LIKE; 1.  
DR NON\_TER 1  
FT NON\_TER 113  
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Best Local Similarity 58.8%; Pred. No. 3.3;  
Matches 10; Conservative 2; Mismatches 5; Indels 0; Gaps 0;  
  
Qy 1 YISGGSGTYSDSVKVG 17

Db :| || ||:||||  
50 FTRYDGSNKYADSVKG 66

Search completed: April 6, 2006, 09:12:36  
Job time : 153.116 secs

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GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: April 6, 2006, 08:58:56 ; Search time 22.7627 Seconds  
(without alignments)  
61.745 Million cell updates/sec

Title: US-10-089-500-4

Perfect score: 89

Sequence: 1 YISSGGSGTYRSDSVKG 17

Scoring table: BLOSUM62

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Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

Issued Patents AA:\*  
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2: /cgn2\_6/prodata/1/iaa/6 COMB.pep.\*  
3: /cgn2\_6/prodata/1/iaa/H COMB.pep.\*  
4: /cgn2\_6/prodata/1/iaa/PCITUS COMB.pep.\*  
5: /cgn2\_6/prodata/1/iaa/RE COMB.pep.\*  
6: /cgn2\_6/prodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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3	82	92.1	130	2	US-09-225-322B-8
4	82	92.1	130	2	US-09-764-304-8
5	77	86.5	119	4	PCT-US94-07659-6
6	77	86.5	247	4	PCT-US94-07659-2
7	75	84.3	118	1	US-08-326-362-2
8	70	78.7	119	1	US-08-207-996-18
9	70	78.7	119	1	US-08-207-996-19
10	70	78.7	119	1	US-08-207-996-20
11	70	78.7	119	1	US-08-207-996-21
12	70	78.7	119	1	US-08-207-996-22
13	70	78.7	119	1	US-08-207-996-27
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15	70	78.7	119	1	US-08-760-840A-19
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19	70	78.7	119	1	US-08-760-840A-28
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35	69	77.5	22	2	US-09-497-997C-20
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38	69	77.5	30	2	US-09-497-997C-7
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51	68	76.4	98	2	US-09-840-459-41
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79	67	75.3	136	1	US-08-452-164A-57
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88	67	75.3	241	1	US-08-926-789-18
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90	67	75.3	245	2	US-09-956-086-5
91	67	75.3	245	2	US-09-956-087-5
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93	67	75.3	265	2	US-09-985-442-5
94	67	75.3	265	2	US-09-985-442-5
95	66	74.2	22	2	US-08-918-148-16
96	66	74.2	22	2	US-09-138-091A-16
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99	66	74.2	98	2	US-10-194-975-17
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Sequence 20, Appl  
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Sequence 22, Appl  
Sequence 28, Appl  
Sequence 31, Appl  
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Sequence 4, Appl  
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Sequence 5, Appl  
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Sequence 49, Appl  
Sequence 38, Appl  
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101	66	74.2	98	2	US-09-534-717-639	Sequence 639, App	174	62	69.7	120	2	US-09-705-392A-4	Sequence 4, Appl
102	66	74.2	117	2	US-08-545-809A-99	Sequence 99, Appl	175	62	69.7	120	2	US-09-705-398-4	Sequence 4, Appl
103	66	74.2	117	2	US-09-515-697-99	Sequence 99, Appl	176	62	69.7	120	2	US-09-232-290-38	Sequence 38, Appl
104	66	74.2	123	1	US-08-665-202-30	Sequence 30, Appl	177	62	69.7	120	2	US-10-014-012-230	Sequence 230, App
105	66	74.2	123	1	US-08-665-202-30	Sequence 30, Appl	178	61	68.5	17	1	US-08-053-171-31	Sequence 31, Appl
106	66	74.2	245	2	US-08-918-148-75	Sequence 75, Appl	179	61	68.5	32	2	US-08-525-539A-35	Sequence 35, Appl
107	66	74.2	245	2	US-08-918-148-75	Sequence 75, Appl	180	61	68.5	116	2	US-08-537-871A-18	Sequence 18, Appl
108	65	73.0	122	1	US-08-276-852-80	Sequence 80, Appl	181	61	68.5	119	1	US-08-053-171-12	Sequence 12, Appl
109	65	73.0	122	1	US-08-899-575-80	Sequence 80, Appl	182	61	68.5	119	1	US-08-053-171-13	Sequence 13, Appl
110	65	73.0	122	1	US-08-899-575-80	Sequence 80, Appl	183	61	68.5	119	1	US-08-053-171-14	Sequence 14, Appl
111	65	73.0	122	4	PCT-US95-08743-80	Sequence 80, Appl	184	61	68.5	119	1	US-08-053-171-17	Sequence 17, Appl
112	64	71.9	98	2	US-09-840-459-45	Sequence 45, Appl	185	61	68.5	119	2	US-08-815-190A-13	Sequence 13, Appl
113	64	71.9	98	2	US-09-497-625A-45	Sequence 45, Appl	186	61	68.5	119	2	US-09-232-290-55	Sequence 55, Appl
114	64	71.9	120	2	US-08-435-516-1	Sequence 1, Appl	187	61	68.5	126	2	US-09-232-290-42	Sequence 42, Appl
115	64	71.9	120	2	US-08-435-516-2	Sequence 2, Appl	188	61	68.5	126	2	US-09-554-765-7	Sequence 7, Appl
116	64	71.9	120	2	US-08-435-516-3	Sequence 3, Appl	189	61	68.5	138	1	US-08-053-171-7	Sequence 7, Appl
117	64	71.9	123	1	US-08-356-272-3	Sequence 3, Appl	190	61	68.5	138	1	US-08-053-171-11	Sequence 11, Appl
118	64	71.9	123	1	US-09-344-587-13	Sequence 13, Appl	191	61	68.5	147	2	US-09-554-765-10	Sequence 10, Appl
119	64	71.9	300	1	US-08-661-052-4	Sequence 4, Appl	192	61	68.5	409	2	US-09-554-765-14	Sequence 14, Appl
120	64	71.9	300	2	US-09-188-082-4	Sequence 4, Appl	193	61	68.5	456	2	US-09-495-880A-11	Sequence 11, Appl
121	64	71.9	300	2	US-09-364-088-4	Sequence 4, Appl	194	60.5	68.0	88	2	US-09-840-459-51	Sequence 51, Appl
122	64	71.9	300	2	US-09-102-716-4	Sequence 4, Appl	195	60.5	68.0	88	2	US-09-497-625A-51	Sequence 51, Appl
123	64	71.9	301	1	US-08-661-052-14	Sequence 14, Appl	196	60	67.4	98	1	US-08-211-202-116	Sequence 116, App
124	64	71.9	301	2	US-09-188-082-14	Sequence 14, Appl	197	60	67.4	98	2	US-10-194-975-28	Sequence 28, App
125	64	71.9	301	2	US-09-364-088-14	Sequence 14, Appl	198	60	67.4	98	2	US-09-534-717-656	Sequence 656, App
126	64	71.9	301	2	US-09-102-716-14	Sequence 14, Appl	199	60	67.4	98	2	US-09-534-717-660	Sequence 660, App
127	64	71.9	352	2	US-09-203-958A-2	Sequence 2, Appl	200	60	67.4	110	1	US-08-211-202-117	Sequence 117, App
128	64	71.9	553	1	US-08-661-052-16	Sequence 16, Appl	201	60	67.4	111	1	US-08-211-202-134	Sequence 134, App
129	64	71.9	553	2	US-09-188-082-16	Sequence 16, Appl	202	60	67.4	117	1	US-08-652-558-3	Sequence 3, Appl
130	64	71.9	553	2	US-09-364-088-16	Sequence 16, Appl	203	60	67.4	117	1	US-08-652-558-44	Sequence 44, Appl
131	64	71.9	553	2	US-09-102-716-16	Sequence 16, Appl	204	60	67.4	117	1	US-08-652-558-45	Sequence 45, Appl
132	63	70.8	17	1	US-08-264-093-22	Sequence 22, Appl	205	60	67.4	117	1	US-08-652-558-46	Sequence 46, Appl
133	63	70.8	17	2	US-09-424-840B-72	Sequence 72, Appl	206	60	67.4	117	1	US-08-652-558-51	Sequence 51, Appl
134	63	70.8	17	2	US-09-424-840B-88	Sequence 88, Appl	207	60	67.4	117	1	US-08-652-558-51	Sequence 51, Appl
135	63	70.8	17	2	US-10-226-795-34	Sequence 34, Appl	208	60	67.4	117	2	US-08-545-809A-130	Sequence 130, App
136	63	70.8	89	2	US-09-840-459-50	Sequence 50, Appl	209	60	67.4	120	1	US-08-428-197-20	Sequence 20, App
137	63	70.8	89	2	US-09-497-625A-50	Sequence 50, Appl	210	60	67.4	120	1	US-08-428-197-22	Sequence 22, App
138	63	70.8	98	2	US-09-534-717-620	Sequence 620, App	211	60	67.4	120	1	US-08-428-197-24	Sequence 24, App
139	63	70.8	98	2	US-09-534-717-621	Sequence 621, App	212	60	67.4	120	1	US-08-428-197-26	Sequence 26, App
140	63	70.8	98	2	US-09-534-717-633	Sequence 633, App	213	60	67.4	120	1	US-08-428-197-28	Sequence 28, App
141	63	70.8	98	2	US-09-534-717-634	Sequence 634, App	214	60	67.4	120	1	US-08-428-197-30	Sequence 30, App
142	63	70.8	111	2	US-09-899-896-7	Sequence 7, Appl	215	60	67.4	120	1	US-08-428-197-32	Sequence 32, App
143	63	70.8	113	1	US-08-956-047-30	Sequence 30, Appl	216	60	67.4	120	1	US-08-428-197-34	Sequence 34, App
144	63	70.8	118	1	US-08-652-816A-11	Sequence 11, Appl	217	60	67.4	120	1	US-08-428-197-40	Sequence 40, App
145	63	70.8	120	1	US-08-264-093-14	Sequence 14, Appl	218	60	67.4	120	1	PCT-US93-10555-20	Sequence 20, App
146	63	70.8	121	2	US-09-424-840B-26	Sequence 26, Appl	219	60	67.4	120	4	PCT-US93-10555-22	Sequence 22, App
147	63	70.8	125	2	US-09-266-805-7	Sequence 7, Appl	220	60	67.4	120	4	PCT-US93-10555-24	Sequence 24, App
148	63	70.8	131	2	US-10-148-737A-3	Sequence 34, Appl	221	60	67.4	120	4	PCT-US93-10555-26	Sequence 26, App
149	63	70.8	135	1	US-08-956-047-34	Sequence 34, Appl	222	60	67.4	120	4	PCT-US93-10555-28	Sequence 28, App
150	63	70.8	141	2	US-09-069-628-8	Sequence 8, Appl	223	60	67.4	120	4	PCT-US93-10555-30	Sequence 30, App
151	63	70.8	141	2	US-09-069-628-15	Sequence 15, Appl	224	60	67.4	120	4	PCT-US93-10555-32	Sequence 32, App
152	63	70.8	141	2	US-09-069-628-25	Sequence 25, Appl	225	60	67.4	120	4	PCT-US93-10555-34	Sequence 34, App
153	63	70.8	142	2	US-09-069-628-14	Sequence 14, Appl	226	60	67.4	120	4	PCT-US93-10555-40	Sequence 40, App
154	63	70.8	143	2	US-09-069-628-7	Sequence 7, Appl	227	60	67.4	126	2	US-08-983-607-48	Sequence 48, App
155	63	70.8	143	2	US-09-069-628-11	Sequence 11, Appl	228	60	67.4	144	2	US-09-069-628-13	Sequence 13, App
156	63	70.8	145	2	US-09-069-628-12	Sequence 12, Appl	229	60	67.4	144	2	US-08-652-558-40	Sequence 40, App
157	63	70.8	147	2	US-09-069-628-9	Sequence 9, Appl	230	59.5	66.9	98	2	US-08-652-558-40	Sequence 40, App
158	63	70.8	147	2	US-09-069-628-10	Sequence 10, Appl	231	59.5	66.9	98	2	US-09-627-956B-32	Sequence 32, App
159	63	70.8	147	2	US-09-069-628-16	Sequence 16, Appl	232	59	66.3	17	2	US-09-339-922A-104	Sequence 104, App
160	63	70.8	147	2	US-09-069-628-17	Sequence 17, Appl	233	59	66.3	17	2	US-09-192-854-10	Sequence 107, App
161	63	70.8	158	2	US-10-226-795-32	Sequence 32, Appl	234	59	66.3	17	2	US-09-424-840B-107	Sequence 14, App
162	63	70.8	223	1	US-08-190-199A-63	Sequence 63, Appl	235	59	66.3	17	2	US-09-511-939-14	Sequence 14, App
163	63	70.8	236	1	US-08-190-199A-65	Sequence 65, Appl	236	59	66.3	17	2	US-09-511-939-38	Sequence 38, App
164	63	70.8	240	1	US-08-956-047-25	Sequence 25, Appl	237	59	66.3	17	2	US-09-511-939-68	Sequence 68, App
165	63	70.8	255	2	US-09-553-498-8	Sequence 8, Appl	238	59	66.3	17	2	US-09-511-939-74	Sequence 74, App
166	63	70.8	255	2	US-09-618-869-8	Sequence 8, Appl	239	59	66.3	17	2	US-09-511-939-80	Sequence 80, App
167	63	70.8	268	2	US-08-976-118-1	Sequence 1, Appl	240	59	66.3	17	2	US-09-511-939-86	Sequence 86, App
168	62	69.7	119	2	US-08-875-674A-1	Sequence 1, Appl	241	59	66.3	17	2	US-09-511-939-92	Sequence 92, App
169	62	69.7	119	2	US-08-875-674A-3	Sequence 3, Appl	242	59	66.3	17	2	US-09-511-939-122	Sequence 122, App
170	62	69.7	120	1	US-07-934-373C-4	Sequence 4, Appl	243	59	66.3	17	2	US-09-511-939-128	Sequence 128, App
171	62	69.7	120	1	US-08-437-642B-4	Sequence 4, Appl	244	59	66.3	17	2	US-09-511-939-134	Sequence 134, App
172	62	69.7	120	2	US-08-146-206C-4	Sequence 4, Appl	245	59	66.3	17	2	US-09-511-939-140	Sequence 140, App
173	62	69.7	120	2	US-09-705-686-4	Sequence 4, Appl	246	59	66.3	17	2	US-09-511-939-146	Sequence 146, App

247	59	66.3	17	2	US-09-511-9339-188	Sequence 188, App	320	59	66.3	240	2	US-09-193-854-2	Sequence 2, Appl1
248	59	66.3	17	2	US-09-511-9339-194	Sequence 194, App	321	59	66.3	240	2	US-09-511-9339-2	Sequence 2, Appl1
249	59	66.3	17	2	US-09-511-9339-212	Sequence 212, App	322	59	66.3	247	6	5455030-9	Patent No. 5455030
250	59	66.3	17	2	US-09-511-9339-218	Sequence 218, App	323	59	66.3	248	6	5455030-11	Patent No. 5455030
251	59	66.3	17	2	US-09-511-9339-236	Sequence 236, App	324	59	66.3	281	2	US-09-025-769B-178	Sequence 178, App
252	59	66.3	17	2	US-09-511-9339-260	Sequence 260, App	325	59	66.3	281	2	US-09-490-070A-178	Sequence 178, App
253	59	66.3	17	2	US-09-511-9339-266	Sequence 266, App	326	59	66.3	281	2	US-09-490-153-178	Sequence 178, App
254	59	66.3	17	2	US-09-511-9339-272	Sequence 272, App	327	59	66.3	281	2	US-09-490-324-178	Sequence 178, App
255	59	66.3	17	2	US-09-511-9339-284	Sequence 284, App	328	59	66.3	288	2	US-09-818-247-22	Sequence 22, Appl
256	59	66.3	17	2	US-09-511-9339-296	Sequence 296, App	329	59	66.3	447	6	5455030-1	Patent No. 5455030
257	59	66.3	17	2	US-09-511-9339-308	Sequence 308, App	330	58	65.2	17	1	US-08-650-262-14	Sequence 14, Appl
258	59	66.3	17	2	US-09-511-9339-314	Sequence 314, App	331	58	65.2	17	2	US-09-339-922A-102	Sequence 102, App
259	59	66.3	98	2	US-10-194-975-22	Sequence 22, Appl	332	58	65.2	17	2	US-09-497-997C-30	Sequence 30, Appl
260	59	66.3	98	2	US-10-194-975-30	Sequence 30, Appl	333	58	65.2	17	2	US-09-534-717-359	Sequence 359, App
261	59	66.3	98	2	US-09-534-717-619	Sequence 619, App	334	58	65.2	21	2	US-09-497-997C-5	Sequence 5, Appl1
262	59	66.3	98	2	US-08-896-535-74	Sequence 74, Appl	335	58	65.2	52	2	US-09-497-997C-36	Sequence 36, App
263	59	66.3	116	2	US-08-983-607-36	Sequence 36, Appl	336	58	65.2	89	2	US-09-840-459-48	Sequence 48, Appl
264	59	66.3	116	2	US-09-840-459-80	Sequence 80, Appl	337	58	65.2	89	2	US-09-497-625A-48	Sequence 48, Appl
265	59	66.3	116	2	US-09-497-625A-80	Sequence 80, Appl	338	58	65.2	98	1	US-08-428-197-48	Sequence 48, Appl
266	59	66.3	117	1	US-08-428-197-36	Sequence 36, Appl	339	58	65.2	98	2	US-09-534-717-622	Sequence 622, App
267	59	66.3	117	2	US-08-545-809A-109	Sequence 109, App	340	58	65.2	98	4	PCT-US93-10555-48	Sequence 48, Appl
268	59	66.3	117	2	US-08-983-607-46	Sequence 46, Appl	341	58	65.2	102	2	US-08-477-347-9	Sequence 9, Appl1
269	59	66.3	117	2	US-09-840-459-83	Sequence 83, Appl	342	58	65.2	102	2	US-09-800-908-9	Sequence 9, Appl1
270	59	66.3	117	2	US-09-497-625A-83	Sequence 83, Appl	343	58	65.2	105	2	US-09-497-997C-25	Sequence 25, Appl
271	59	66.3	117	4	PCT-US93-10555-35	Sequence 109, App	344	58	65.2	113	2	US-08-974-899-6	Sequence 6, Appl1
272	59	66.3	118	1	US-08-652-818A-12	Sequence 12, Appl	345	58	65.2	113	2	US-09-795-798-6	Sequence 6, Appl1
273	59	66.3	119	2	US-08-983-607-22	Sequence 22, Appl	346	58	65.2	113	2	US-08-908-469-11	Sequence 11, Appl
274	59	66.3	120	2	US-09-025-769B-38	Sequence 38, Appl	347	58	65.2	117	1	US-08-478-039-97	Sequence 97, Appl
275	59	66.3	120	2	US-09-025-769B-63	Sequence 63, Appl	348	58	65.2	117	1	US-08-476-349A-97	Sequence 97, Appl
276	59	66.3	120	2	US-09-490-070A-38	Sequence 38, Appl	349	58	65.2	117	1	US-08-650-262-4	Sequence 4, Appl1
277	59	66.3	120	2	US-09-490-070A-63	Sequence 63, Appl	350	58	65.2	117	2	US-09-339-922A-2	Sequence 2, Appl1
278	59	66.3	120	2	US-09-840-459-85	Sequence 85, Appl	351	58	65.2	117	2	US-09-339-922A-6	Sequence 6, Appl1
279	59	66.3	120	2	US-09-490-153-38	Sequence 38, Appl	352	58	65.2	117	2	US-08-791-391A-6	Sequence 6, Appl1
280	59	66.3	120	2	US-09-490-324-38	Sequence 38, Appl	353	58	65.2	117	2	US-09-016-061-2	Sequence 2, Appl1
281	59	66.3	121	1	US-08-887-352B-4	Sequence 4, Appl1	354	58	65.2	117	2	US-09-016-061-6	Sequence 6, Appl1
282	59	66.3	121	2	US-09-109-207C-4	Sequence 4, Appl1	355	58	65.2	118	2	US-08-545-809A-145	Sequence 145, App
283	59	66.3	121	2	US-09-296-005-4	Sequence 4, Appl1	356	58	65.2	118	2	US-09-515-697-145	Sequence 145, App
284	59	66.3	121	2	US-09-887-352B-4	Sequence 4, Appl1	357	58	65.2	119	2	US-09-648-067A-15	Sequence 15, Appl
285	59	66.3	121	2	US-09-920-171-4	Sequence 4, Appl1	358	58	65.2	119	2	US-09-602-812A-6	Sequence 6, Appl1
286	59	66.3	121	2	US-09-840-459-92	Sequence 92, Appl	359	58	65.2	122	1	US-07-934-373C-21	Sequence 21, Appl
287	59	66.3	121	2	US-09-716-028-4	Sequence 4, Appl1	360	58	65.2	122	2	US-08-437-642B-21	Sequence 21, Appl
288	59	66.3	121	2	US-09-840-459-92	Sequence 92, Appl	361	58	65.2	122	2	US-08-146-266C-21	Sequence 21, Appl
289	59	66.3	121	2	US-09-497-625A-92	Sequence 4, Appl1	362	58	65.2	122	2	US-09-705-686-21	Sequence 21, Appl
290	59	66.3	121	2	US-10-113-996-4	Sequence 4, Appl1	363	58	65.2	122	2	US-09-705-392A-21	Sequence 21, Appl
291	59	66.3	121	2	US-08-958-201-6	Sequence 6, Appl1	364	58	65.2	122	2	PCT-US93-07832-21	Sequence 21, Appl
292	59	66.3	122	1	US-08-428-197-38	Sequence 38, Appl	365	58	65.2	122	4	US-09-534-717-346	Sequence 346, App
293	59	66.3	122	1	US-08-958-201-6	Sequence 84, Appl	366	58	65.2	124	2	US-09-530-119-58	Sequence 58, Appl
294	59	66.3	123	4	PCT-US93-10555-38	Sequence 1, Appl1	367	58	65.2	255	1	US-07-690-132-4	Sequence 4, Appl1
295	59	66.3	123	4	US-08-983-607-51	Sequence 26, Appl	368	58	65.2	284	2	US-08-564-164A-2	Sequence 2, Appl1
296	59	66.3	124	2	US-09-840-459-89	Sequence 89, Appl	369	58	65.2	97	2	US-10-194-975-48	Sequence 48, Appl
297	59	66.3	124	2	US-09-840-459-77	Sequence 77, Appl	370	58	65.2	97	2	US-09-534-717-617	Sequence 617, App
298	59	66.3	124	2	US-09-840-459-77	Sequence 77, Appl	371	57.5	64.6	97	2	US-09-534-717-618	Sequence 618, App
299	59	66.3	125	1	US-08-478-039-99	Sequence 99, App	372	57.5	64.6	97	2	US-08-579-378A-16	Sequence 16, App
300	59	66.3	125	1	US-08-476-349A-99	Sequence 99, App	373	57.5	64.6	135	2	US-08-579-378A-20	Sequence 20, Appl
301	59	66.3	125	1	US-08-428-197-1	Sequence 1, App	374	57.5	64.6	443	4	PCT-US96-13152-4	Sequence 4, Appl1
302	59	66.3	125	2	US-09-840-459-76	Sequence 76, Appl	375	57.5	64.6	17	2	US-09-534-717-346	Sequence 346, App
303	59	66.3	125	2	US-09-840-459-84	Sequence 84, Appl	376	57	64.0	116	1	US-08-428-197-2	Sequence 2, Appl1
304	59	66.3	125	2	US-09-497-625A-76	Sequence 76, Appl	377	57	64.0	116	1	PCT-US93-10555-2	Sequence 2, Appl1
305	59	66.3	125	4	PCT-US93-10555-1	Sequence 1, Appl1	378	57	64.0	116	1	US-08-537-871A-24	Sequence 24, Appl1
306	59	66.3	126	2	US-08-983-607-26	Sequence 26, Appl	379	57	64.0	123	2	US-08-284-516C-56	Sequence 56, Appl
307	59	66.3	128	2	US-09-840-459-77	Sequence 77, Appl	380	57	64.0	136	2	US-09-537-911A-56	Sequence 56, Appl
308	59	66.3	128	2	US-09-840-459-78	Sequence 78, App	381	57	64.0	136	2	US-09-393-627B-28	Sequence 28, Appl
309	59	66.3	128	2	US-09-840-459-79	Sequence 79, App	382	57	64.0	354	2	US-09-479-614-17	Sequence 17, Appl
310	59	66.3	128	2	US-09-497-625A-77	Sequence 77, App	383	57	64.0	64	2	US-09-479-614-17	Sequence 17, Appl
311	59	66.3	128	2	US-09-497-625A-78	Sequence 78, App	384	56.5	63.5	95	2	US-09-043-514-2	Sequence 2, Appl1
312	59	66.3	128	2	US-09-497-625A-78	Sequence 78, App	385	56.5	63.5	95	2	US-10-194-975-29	Sequence 29, Appl
313	59	66.3	131	2	US-08-983-607-28	Sequence 28, App	386	56.5	63.5	97	2	US-10-194-975-31	Sequence 31, Appl
314	59	66.3	131	2	US-08-983-607-28	Sequence 28, App	387	56.5	63.5	97	2	US-09-534-717-616	Sequence 16, App
315	59	66.3	140	2	US-08-983-607-32	Sequence 32, App	388	56.5	63.5	116	2	US-08-545-809A-135	Sequence 135, App
316	59	66.3	144	1	US-08-026-320A-2	Sequence 2, Appl1	389	56.5	63.5	496	2	US-09-515-697-135	Sequence 135, App
317	59	66.3	225	6	5455030-5	Patent No. 5455030	390	56.5	63.5	496	2	US-09-479-614-2	Sequence 2, Appl1
318	59	66.3	236	6	5455030-7	Patent No. 5455030	391	56.5	63.5	496	2	US-09-479-614-29	Sequence 29, Appl
319	59	66.3	239	1	US-08-553-497A-18	Sequence 18, Appl	392	56.5	63.5	496	2		

393	56	62.9	17	1	US-07-988-925-2	Sequence 2, Appli	466	55	61.8	158	1	US-08-653-402B-10	Sequence 10, Appl
394	56	62.9	17	1	US-08-362-780-2	Sequence 2, Appli	467	55	61.8	251	1	US-08-398-612A-30	Sequence 30, Appl
395	56	62.9	17	1	US-08-478-684G-2	Sequence 2, Appli	468	55	61.8	251	1	US-08-398-611A-30	Sequence 30, Appl
396	56	62.9	17	2	US-09-534-717-337	Sequence 337, App	469	55	61.8	251	1	US-08-491-334A-30	Sequence 30, Appl
397	56	62.9	98	2	US-09-534-717-602	Sequence 602, App	470	55	61.8	251	2	US-08-027-449-27	Sequence 27, Appl
398	56	62.9	102	1	US-08-273-146-65	Sequence 65, Appl	471	55	61.8	251	2	US-08-804-444A-27	Sequence 27, Appl
399	56	62.9	112	1	US-08-211-202-133	Sequence 133, App	472	55	61.8	251	2	US-09-026-985-27	Sequence 27, Appl
400	56	62.9	117	2	US-09-025-769B-24	Sequence 24, Appl	473	55	61.8	251	2	US-09-121-952A-27	Sequence 27, Appl
401	56	62.9	117	2	US-09-490-070A-24	Sequence 24, Appl	474	55	61.8	251	2	US-09-234-340A-27	Sequence 27, Appl
402	56	62.9	117	2	US-09-490-153-24	Sequence 24, Appl	475	55	61.8	251	2	US-09-355-014-27	Sequence 27, Appl
403	56	62.9	117	2	US-09-490-324-24	Sequence 24, Appl	476	55	61.8	252	1	US-08-398-613A-30	Sequence 30, Appl
404	56	62.9	119	1	US-07-988-925-11	Sequence 11, Appl	477	55	61.8	259	2	US-09-742-693-33	Sequence 33, Appl
405	56	62.9	119	1	US-08-362-780-11	Sequence 11, Appl	478	55	61.8	260	2	US-09-742-693-31	Sequence 31, Appl
406	56	62.9	119	1	US-08-362-780-25	Sequence 25, Appl	479	55	61.8	260	2	US-09-742-693-32	Sequence 32, Appl
407	56	62.9	119	2	US-08-478-684G-11	Sequence 11, Appl	480	55	61.8	334	2	US-09-646-028-53	Sequence 53, Appl
408	56	62.9	124	2	US-08-983-607-47	Sequence 47, Appl	481	55	61.8	339	2	US-09-646-028-55	Sequence 55, Appl
409	56	62.9	126	1	US-08-478-039-95	Sequence 95, Appl	482	55	61.8	348	2	US-09-646-028-51	Sequence 51, Appl
410	56	62.9	126	1	US-08-476-349A-95	Sequence 95, Appl	483	55	61.8	408	2	US-09-554-765-15	Sequence 15, Appl
411	56	62.9	135	2	US-08-619-491-4	Sequence 4, Appli	484	54.5	61.2	16	2	US-09-170-769A-11	Sequence 11, Appl
412	56	62.9	135	2	US-08-619-491-8	Sequence 8, Appli	485	54.5	61.2	110	2	US-10-014-012-210	Sequence 210, App
413	56	62.9	135	4	PCT-US95-07302-4	Sequence 4, Appli	486	54.5	61.2	110	2	US-10-014-012-211	Sequence 211, App
414	56	62.9	135	4	PCT-US95-07302-8	Sequence 8, Appli	487	54.5	61.2	112	2	US-10-014-012-212	Sequence 212, App
415	56	62.9	137	2	US-09-019-441A-8	Sequence 8, Appli	488	54	60.7	17	2	US-09-383-667-16	Sequence 16, Appl
416	56	62.9	217	4	PCT-US94-14106-59	Sequence 59, Appl	489	54	60.7	17	2	US-09-497-997C-32	Sequence 32, Appl
417	56	61.8	17	2	US-09-192-854-93	Sequence 93, Appl	490	54	60.7	17	2	US-08-030-175-17	Sequence 17, Appl
418	55	61.8	17	2	US-09-192-854-139	Sequence 139, App	491	54	60.7	17	2	US-09-424-840B-36	Sequence 36, Appl
419	55	61.8	17	2	US-09-511-939-164	Sequence 164, App	492	54	60.7	17	2	US-09-424-840B-63	Sequence 63, Appl
420	55	61.8	17	2	US-09-511-939-248	Sequence 248, App	493	54	60.7	17	2	US-09-424-840B-74	Sequence 74, Appl
421	55	61.8	17	4	PCT-US93-08435-18	Sequence 18, Appl	494	54	60.7	17	2	US-09-424-840B-76	Sequence 76, Appl
422	55	61.8	83	2	US-10-014-012-223	Sequence 223, App	495	54	60.7	17	2	US-09-424-840B-77	Sequence 77, Appl
423	55	61.8	98	2	US-09-534-717-600	Sequence 600, App	496	54	60.7	17	2	US-09-424-840B-84	Sequence 84, Appl
424	55	61.8	98	2	US-08-896-535-75	Sequence 75, Appl	497	54	60.7	17	2	US-09-424-840B-95	Sequence 95, Appl
425	55	61.8	99	2	US-10-194-975-27	Sequence 27, Appl	498	54	60.7	17	2	US-09-424-840B-97	Sequence 97, Appl
426	55	61.8	115	1	US-08-379-057-31	Sequence 31, Appl	499	54	60.7	17	2	US-09-424-840B-108	Sequence 108, App
427	55	61.8	115	1	US-08-428-197-42	Sequence 42, Appl	500	54	60.7	17	2	US-09-424-840B-111	Sequence 111, App
428	55	61.8	115	4	PCT-US93-10555-42	Sequence 42, Appl	501	54	60.7	17	2	US-09-424-840B-113	Sequence 113, App
429	55	61.8	117	1	US-07-942-245-38	Sequence 38, Appl	502	54	60.7	17	2	US-09-534-717-352	Sequence 352, App
430	55	61.8	118	2	US-08-545-809A-125	Sequence 125, App	503	54	60.7	17	2	US-09-534-717-354	Sequence 354, App
431	55	61.8	118	2	US-09-515-697-125	Sequence 125, App	504	54	60.7	23	2	US-09-497-997C-6	Sequence 6, Appli
432	55	61.8	118	4	PCT-US93-08435-10	Sequence 10, Appl	505	54	60.7	23	2	US-09-497-997C-22	Sequence 22, Appl
433	55	61.8	122	2	US-09-155-106-18	Sequence 18, Appl	506	54	60.7	23	2	US-09-534-717-653	Sequence 653, App
434	55	61.8	122	2	US-09-155-106-19	Sequence 19, Appl	507	54	60.7	95	2	US-08-211-202-118	Sequence 118, App
435	55	61.8	122	2	US-09-155-106-20	Sequence 20, Appl	508	54	60.7	98	1	US-10-194-975-23	Sequence 23, Appl
436	55	61.8	122	2	US-09-155-106-26	Sequence 26, Appl	509	54	60.7	98	2	US-10-194-975-24	Sequence 24, Appl
437	55	61.8	122	2	US-09-155-106-32	Sequence 32, Appl	510	54	60.7	98	2	US-10-194-975-25	Sequence 25, Appl
438	55	61.8	122	4	PCT-US93-08435-12	Sequence 12, Appl	511	54	60.7	98	2	US-10-194-975-33	Sequence 33, Appl
439	55	61.8	122	4	PCT-US93-08435-14	Sequence 14, Appl	512	54	60.7	98	2	US-09-534-717-624	Sequence 624, App
440	55	61.8	122	4	PCT-US93-08435-43	Sequence 43, Appl	513	54	60.7	98	2	US-09-534-717-625	Sequence 625, App
441	55	61.8	123	2	US-09-840-459-82	Sequence 82, Appl	514	54	60.7	98	2	US-09-534-717-626	Sequence 626, App
442	55	61.8	123	2	US-09-497-625A-82	Sequence 82, Appl	515	54	60.7	98	2	US-09-534-717-627	Sequence 627, App
443	55	61.8	124	2	US-09-840-459-81	Sequence 81, Appl	516	54	60.7	98	2	US-09-534-717-628	Sequence 628, App
444	55	61.8	124	2	US-09-497-625A-81	Sequence 81, Appl	517	54	60.7	98	2	US-09-534-717-629	Sequence 629, App
445	55	61.8	125	2	US-09-554-765-9	Sequence 9, Appli	518	54	60.7	98	2	US-09-534-717-630	Sequence 630, App
446	55	61.8	128	1	US-08-478-039-73	Sequence 73, Appl	519	54	60.7	98	2	US-09-534-717-631	Sequence 631, App
447	55	61.8	128	1	US-08-478-039-102	Sequence 102, App	520	54	60.7	98	2	US-09-534-717-632	Sequence 632, App
448	55	61.8	128	1	US-08-476-349A-73	Sequence 73, App	521	54	60.7	98	2	US-09-534-717-633	Sequence 633, App
449	55	61.8	128	1	US-08-476-349A-102	Sequence 102, App	522	54	60.7	98	2	US-09-534-717-635	Sequence 635, App
450	55	61.8	130	1	US-08-398-613A-22	Sequence 22, Appl	523	54	60.7	98	2	US-09-534-717-636	Sequence 636, App
451	55	61.8	130	1	US-08-478-039-70	Sequence 70, Appl	524	54	60.7	98	2	US-09-534-717-637	Sequence 637, App
452	55	61.8	130	1	US-08-478-039-93	Sequence 93, Appl	525	54	60.7	98	2	US-09-534-717-640	Sequence 640, App
453	55	61.8	130	1	US-08-398-612A-22	Sequence 22, Appl	526	54	60.7	98	2	US-09-534-717-641	Sequence 641, App
454	55	61.8	130	1	US-08-398-611A-22	Sequence 22, Appl	527	54	60.7	98	2	US-09-534-717-642	Sequence 642, App
455	55	61.8	130	1	US-08-476-349A-70	Sequence 70, Appl	528	54	60.7	98	2	US-09-534-717-643	Sequence 643, App
456	55	61.8	130	1	US-08-476-349A-93	Sequence 93, Appl	529	54	60.7	98	2	US-09-534-717-644	Sequence 644, App
457	55	61.8	130	1	US-08-491-334A-22	Sequence 22, Appl	530	54	60.7	98	2	US-09-534-717-645	Sequence 645, App
458	55	61.8	130	2	US-09-027-449-19	Sequence 19, Appl	531	54	60.7	98	2	US-09-534-717-646	Sequence 646, App
459	55	61.8	130	2	US-08-804-444A-19	Sequence 19, Appl	532	54	60.7	98	2	US-09-534-717-648	Sequence 648, App
460	55	61.8	130	2	US-09-026-985-19	Sequence 19, Appl	533	54	60.7	98	2	US-09-534-717-650	Sequence 650, App
461	55	61.8	130	2	US-09-121-952A-19	Sequence 19, Appl	534	54	60.7	98	2	US-09-534-717-654	Sequence 654, App
462	55	61.8	130	2	US-09-234-340A-19	Sequence 19, Appl	535	54	60.7	98	2	US-09-534-717-652	Sequence 652, App
463	55	61.8	130	2	US-09-355-014-19	Sequence 19, Appl	536	54	60.7	98	2	US-09-534-717-663	Sequence 663, App
464	55	61.8	146	2	US-09-554-765-11	Sequence 11, Appl	537	54	60.7	98	2	US-10-330-613A-61	Sequence 61, Appl
465	55	61.8	158	1	US-08-653-402B-6	Sequence 6, Appli	538	54	60.7	98	2	US-10-330-613A-62	Sequence 62, Appl



539	54	60.7	110	2	US-09-497-997C-27	Sequence 27, Appl	612	52	58.4	17	2	US-09-534-717-3	Sequence 3, Appl1
540	54	60.7	113	1	US-07-789-344A-10	Sequence 10, Appl	613	52	58.4	17	2	US-09-534-717-19	Sequence 19, Appl
541	54	60.7	114	1	US-08-652-558-52	Sequence 52, Appl	614	52	58.4	17	2	US-09-534-717-27	Sequence 27, Appl
542	54	60.7	115	2	US-09-726-219A-167	Sequence 167, Appl	615	52	58.4	17	2	US-09-534-717-344	Sequence 344, App
543	54	60.7	115	2	US-09-269-332-89	Sequence 89, Appl	616	52	58.4	17	2	US-09-534-717-348	Sequence 348, App
544	54	60.7	115	2	US-09-196-522-167	Sequence 167, Appl	617	52	58.4	17	2	US-09-534-717-350	Sequence 350, App
545	54	60.7	116	1	US-08-211-202-141	Sequence 141, Appl	618	52	58.4	17	2	US-09-534-717-358	Sequence 358, App
546	54	60.7	117	1	US-07-942-245-34	Sequence 34, Appl	619	52	58.4	17	2	US-09-534-717-381	Sequence 381, App
547	54	60.7	117	2	US-08-545-809A-115	Sequence 115, Appl	620	52	58.4	17	2	US-09-534-717-384	Sequence 384, App
548	54	60.7	117	2	US-09-515-697-115	Sequence 115, Appl	621	52	58.4	17	2	US-09-534-717-387	Sequence 387, App
549	54	60.7	119	1	US-08-331-398A-46	Sequence 46, Appl	622	52	58.4	17	2	US-09-534-717-397	Sequence 397, App
550	54	60.7	119	1	US-08-331-397B-46	Sequence 46, Appl	623	52	58.4	17	2	US-09-534-717-398	Sequence 398, App
551	54	60.7	119	1	US-08-759-804A-46	Sequence 46, Appl	624	52	58.4	22	2	US-08-918-148-39	Sequence 39, Appl
552	54	60.7	119	2	US-09-227-693-46	Sequence 46, Appl	625	52	58.4	22	2	US-09-138-091A-39	Sequence 39, Appl
553	54	60.7	120	1	US-08-211-202-135	Sequence 135, Appl	626	52	58.4	96	2	US-09-905-243-14	Sequence 14, Appl
554	54	60.7	120	1	US-07-942-245-35	Sequence 35, Appl	627	52	58.4	98	2	US-10-194-975-21	Sequence 21, Appl
555	54	60.7	120	2	US-10-330-613A-29	Sequence 29, Appl	628	52	58.4	98	2	US-09-534-717-612	Sequence 612, App
556	54	60.7	123	1	US-08-199-911-4	Sequence 4, Appl1	629	52	58.4	98	2	US-09-534-717-614	Sequence 614, App
557	54	60.7	123	1	US-08-983-607-38	Sequence 38, Appl	630	52	58.4	98	2	US-09-534-717-649	Sequence 649, App
558	54	60.7	123	2	US-09-424-840B-6	Sequence 6, Appl1	631	52	58.4	98	2	US-09-534-717-657	Sequence 657, App
559	54	60.7	123	2	US-09-424-840B-10	Sequence 10, Appl	632	52	58.4	98	2	US-09-534-717-659	Sequence 659, App
560	54	60.7	123	2	US-09-424-840B-22	Sequence 22, Appl	633	52	58.4	98	2	US-09-534-717-667	Sequence 667, App
561	54	60.7	124	2	US-09-424-840B-16	Sequence 16, Appl	634	52	58.4	111	2	US-10-014-012-226	Sequence 226, App
562	54	60.7	125	2	US-08-635-109-4	Sequence 4, Appl1	635	52	58.4	114	2	US-09-534-717-15	Sequence 15, Appl
563	54	60.7	125	2	US-08-844-215-4	Sequence 4, Appl1	636	52	58.4	115	2	US-09-534-717-23	Sequence 23, Appl
564	54	60.7	128	1	US-08-478-039-96	Sequence 96, Appl	637	52	58.4	115	2	US-09-534-717-31	Sequence 31, Appl
565	54	60.7	128	1	US-08-476-349A-96	Sequence 96, Appl	638	52	58.4	115	2	US-09-534-717-33	Sequence 33, Appl
566	54	60.7	137	2	US-08-030-175-39	Sequence 39, Appl	639	52	58.4	115	2	US-09-534-717-35	Sequence 35, Appl
567	54	60.7	137	2	US-08-030-175-40	Sequence 40, Appl	640	52	58.4	115	2	US-09-534-717-37	Sequence 37, Appl
568	54	60.7	225	2	US-09-456-090A-102	Sequence 102, App	641	52	58.4	115	2	US-09-534-717-39	Sequence 39, Appl
569	54	60.7	225	2	US-09-456-090A-108	Sequence 108, App	642	52	58.4	115	2	US-09-534-717-41	Sequence 41, Appl
570	54	60.7	225	2	US-09-456-090A-110	Sequence 110, App	643	52	58.4	115	2	US-09-534-717-43	Sequence 43, Appl
571	54	60.7	225	2	US-09-453-234-102	Sequence 102, App	644	52	58.4	115	2	US-09-534-717-45	Sequence 45, Appl
572	54	60.7	225	2	US-09-453-234-108	Sequence 108, App	645	52	58.4	115	2	US-09-534-717-47	Sequence 47, Appl
573	54	60.7	225	2	US-09-453-234-110	Sequence 110, App	646	52	58.4	115	2	US-09-534-717-49	Sequence 49, Appl
574	54	60.7	248	2	US-09-315-926A-80	Sequence 80, Appl	647	52	58.4	115	2	US-09-534-717-51	Sequence 51, Appl
575	54	60.7	467	2	US-08-030-175-41	Sequence 41, Appl	648	52	58.4	115	2	US-09-534-717-53	Sequence 53, Appl
576	54	60.7	467	2	US-08-030-175-42	Sequence 42, Appl	649	52	58.4	115	2	US-09-534-717-55	Sequence 55, Appl
577	53.5	60.1	121	1	US-08-339-582-2	Sequence 2, Appl1	650	52	58.4	115	2	US-09-534-717-57	Sequence 57, Appl
578	53	59.6	17	2	US-09-192-854-29	Sequence 29, Appl	651	52	58.4	115	2	US-09-534-717-59	Sequence 59, Appl
579	53	59.6	17	2	US-09-192-854-164	Sequence 164, Appl	652	52	58.4	115	2	US-09-534-717-61	Sequence 61, Appl
580	53	59.6	17	2	US-09-511-939-44	Sequence 44, Appl	653	52	58.4	115	2	US-09-534-717-63	Sequence 63, Appl
581	53	59.6	17	2	US-09-511-939-290	Sequence 290, App	654	52	58.4	115	2	US-09-534-717-65	Sequence 65, Appl
582	53	59.6	17	2	US-09-534-717-345	Sequence 345, App	655	52	58.4	115	2	US-09-534-717-67	Sequence 67, Appl
583	53	59.6	17	2	US-09-534-717-349	Sequence 349, App	656	52	58.4	115	2	US-09-534-717-69	Sequence 69, Appl
584	53	59.6	17	2	US-09-534-717-351	Sequence 351, App	657	52	58.4	115	2	US-09-534-717-71	Sequence 71, Appl
585	53	59.6	17	2	US-09-534-717-353	Sequence 353, App	658	52	58.4	115	2	US-09-534-717-73	Sequence 73, Appl
586	53	59.6	17	2	US-09-534-717-360	Sequence 360, App	659	52	58.4	115	2	US-09-534-717-75	Sequence 75, Appl
587	53	59.6	17	2	US-09-534-717-364	Sequence 364, App	660	52	58.4	116	2	US-09-184-658-48	Sequence 48, Appl
588	53	59.6	17	2	US-09-534-717-367	Sequence 367, App	661	52	58.4	116	2	US-09-504-282D-48	Sequence 48, Appl
589	53	59.6	100	2	US-09-513-999C-4106	Sequence 4106, App	662	52	58.4	117	1	US-07-942-245-32	Sequence 32, Appl
590	53	59.6	118	1	US-08-958-201-2	Sequence 2, Appl1	663	52	58.4	117	2	US-08-545-809A-119	Sequence 119, App
591	53	59.6	118	1	US-08-958-201-4	Sequence 4, Appl1	664	52	58.4	117	2	US-08-545-809A-119	Sequence 119, App
592	53	59.6	119	1	US-08-285-936-2	Sequence 2, Appl1	665	52	58.4	117	2	US-09-515-697-107	Sequence 107, App
593	53	59.6	119	1	US-08-285-936-6	Sequence 6, Appl1	666	52	58.4	117	2	US-09-515-697-119	Sequence 119, App
594	53	59.6	119	1	US-08-285-936-10	Sequence 10, Appl	667	52	58.4	120	1	US-08-652-558-39	Sequence 39, Appl
595	53	59.6	119	1	US-08-487-860-6	Sequence 6, Appl1	668	52	58.4	121	2	US-09-233-290-60	Sequence 60, Appl
596	53	59.6	119	1	US-08-487-860-6	Sequence 6, Appl1	669	52	58.4	121	2	US-09-433-404-3	Sequence 3, Appl1
597	53	59.6	119	1	US-08-487-860-10	Sequence 10, Appl	670	52	58.4	124	2	US-08-844-215-5	Sequence 5, Appl1
598	53	59.6	236	2	US-09-456-090A-64	Sequence 64, Appl	671	52	58.4	126	1	US-08-276-852-81	Sequence 81, Appl
599	53	59.6	236	2	US-09-456-090A-104	Sequence 104, App	672	52	58.4	126	1	US-08-276-852-145	Sequence 145, App
600	53	59.6	236	2	US-09-453-234-64	Sequence 64, Appl	673	52	58.4	126	1	US-08-899-575-81	Sequence 81, Appl
601	53	59.6	236	2	US-09-453-234-104	Sequence 104, App	674	52	58.4	126	1	US-08-899-575-145	Sequence 145, App
602	53	59.6	533	2	US-10-104-047-3224	Sequence 3224, App	675	52	58.4	126	1	US-08-899-575-81	Sequence 81, Appl
603	52	58.4	17	1	US-07-977-696C-40	Sequence 40, Appl	676	52	58.4	126	1	US-08-899-575-145	Sequence 145, App
604	52	58.4	17	1	US-08-129-930B-40	Sequence 40, Appl	677	52	58.4	126	4	PCT-US95-08743-81	Sequence 81, Appl
605	52	58.4	17	2	US-08-134-348A-27	Sequence 27, Appl	678	52	58.4	127	2	PCT-US95-08743-145	Sequence 145, App
606	52	58.4	17	2	US-08-976-288A-40	Sequence 40, Appl	679	52	58.4	127	2	US-09-840-459-87	Sequence 87, Appl
607	52	58.4	17	2	US-09-383-667-11	Sequence 11, Appl	680	52	58.4	127	2	US-09-497-625A-87	Sequence 87, Appl
608	52	58.4	17	2	US-09-192-854-37	Sequence 37, Appl	681	52	58.4	129	2	US-09-240-274-143	Sequence 143, App
609	52	58.4	17	2	US-09-192-854-124	Sequence 124, App	682	52	58.4	129	1	US-09-848-798-143	Sequence 143, App
610	52	58.4	17	2	US-09-511-939-56	Sequence 56, Appl	683	52	58.4	139	1	US-08-129-930B-96	Sequence 96, Appl
611	52	58.4	17	2	US-09-511-939-224	Sequence 224, App	684	52	58.4	139	2	US-08-134-346A-51	Sequence 51, Appl

685	52	58.4	139	2	US-08-976-288A-96	Sequence 96, Appl	758	50	56.2	132	1	US-08-899-575-144	Sequence 144, Appl
686	52	58.4	142	1	US-08-860-174A-7	Sequence 7, Appl1	759	50	56.2	132	4	PCT-US95-08743-144	Sequence 144, Appl
687	52	58.4	149	1	US-08-653-402B-2	Sequence 2, Appl1	760	50	56.2	137	1	US-08-331-398A-61	Sequence 61, Appl
688	52	58.4	179	2	US-08-862-124-2	Sequence 2, Appl1	761	50	56.2	137	1	US-08-331-397B-61	Sequence 61, Appl
689	52	58.4	245	2	US-08-918-148-78	Sequence 78, Appl	762	50	56.2	137	1	US-08-759-804A-60	Sequence 60, Appl
690	52	58.4	245	2	US-09-138-091A-76	Sequence 76, Appl	763	50	56.2	140	2	US-08-836-561-23	Sequence 23, Appl
691	52	58.4	274	1	US-08-860-174A-12	Sequence 12, Appl	764	50	56.2	140	2	US-09-434-122-23	Sequence 23, Appl
692	52	58.4	282	1	US-08-860-174A-10	Sequence 10, Appl	765	50	56.2	225	2	US-09-456-090A-94	Sequence 94, Appl
693	52	58.4	287	2	US-08-862-124-17	Sequence 17, Appl	766	50	56.2	225	2	US-09-453-234-94	Sequence 94, Appl
694	52	58.4	289	2	US-09-184-658-63	Sequence 63, Appl	767	50	56.2	236	2	US-09-530-139-46	Sequence 46, Appl
695	52	58.4	289	2	US-09-504-262D-63	Sequence 63, Appl	768	50	56.2	238	2	US-09-530-139-36	Sequence 36, Appl
696	52	58.4	304	2	US-08-862-124-14	Sequence 14, Appl	769	50	56.2	239	2	US-09-530-139-40	Sequence 40, Appl
697	52	58.4	467	1	US-08-704-744-81	Sequence 81, Appl	770	50	56.2	250	2	US-09-530-139-44	Sequence 44, Appl
698	51.5	57.9	19	2	US-09-563-222C-51	Sequence 51, Appl	771	50	56.2	508	2	US-10-104-047-3233	Sequence 2233, Appl
699	51.5	57.9	117	2	US-09-157-370-1	Sequence 1, Appl1	772	49.5	55.6	20	2	US-09-497-997C-21	Sequence 21, Appl
700	51.5	57.9	263	2	US-09-069-821-3	Sequence 3, Appl1	773	49.5	55.6	98	1	US-09-534-717-611	Sequence 611, Appl
701	51.5	57.9	263	2	US-09-956-086-3	Sequence 3, Appl1	774	49.5	55.6	118	1	US-08-379-057-30	Sequence 30, Appl
702	51.5	57.9	263	2	US-09-956-087-3	Sequence 3, Appl1	775	49	55.1	17	2	US-09-424-840B-64	Sequence 64, Appl
703	51.5	57.9	283	2	US-09-420-592A-6	Sequence 6, Appl1	776	49	55.1	17	2	US-09-534-717-335	Sequence 335, Appl
704	51.5	57.9	283	2	US-09-985-443-6	Sequence 6, Appl1	777	49	55.1	17	2	US-09-534-717-336	Sequence 336, Appl
705	51.5	57.9	283	2	US-09-983-580-6	Sequence 6, Appl1	778	49	55.1	17	2	US-09-534-717-339	Sequence 339, Appl
706	51	57.3	17	2	US-09-406-535-6	Sequence 6, Appl1	779	49	55.1	17	2	US-09-534-717-340	Sequence 340, Appl
707	51	57.3	17	2	US-09-192-854-64	Sequence 64, Appl	780	49	55.1	17	2	US-08-534-717-341	Sequence 341, Appl
708	51	57.3	17	2	US-09-511-939-104	Sequence 104, Appl	781	49	55.1	17	2	US-09-534-717-342	Sequence 342, Appl
709	51	57.3	17	2	US-09-534-717-338	Sequence 338, Appl	782	49	55.1	17	2	US-09-534-717-343	Sequence 343, Appl
710	51	57.3	17	2	US-09-534-717-347	Sequence 347, Appl	783	49	55.1	17	2	US-09-534-717-369	Sequence 369, Appl
711	51	57.3	17	2	US-09-534-717-355	Sequence 355, Appl	784	49	55.1	17	2	US-09-534-717-370	Sequence 370, Appl
712	51	57.3	17	2	US-09-534-717-356	Sequence 356, Appl	785	49	55.1	17	2	US-09-534-717-385	Sequence 385, Appl
713	51	57.3	17	2	US-09-534-717-359	Sequence 359, Appl	786	49	55.1	17	2	US-09-534-717-390	Sequence 390, Appl
714	51	57.3	17	2	US-09-534-717-362	Sequence 362, Appl	787	49	55.1	17	2	US-09-534-717-394	Sequence 394, Appl
715	51	57.3	17	2	US-09-534-717-363	Sequence 363, Appl	788	49	55.1	22	2	US-08-918-148-28	Sequence 28, Appl
716	51	57.3	17	2	US-09-534-717-365	Sequence 365, Appl	789	49	55.1	22	2	US-09-138-091A-28	Sequence 28, Appl
717	51	57.3	17	2	US-09-534-717-366	Sequence 366, Appl	790	49	55.1	67	1	US-08-162-102C-36	Sequence 36, Appl
718	51	57.3	98	2	US-09-534-717-665	Sequence 665, Appl	791	49	55.1	89	2	US-09-472-102C-72	Sequence 72, Appl
719	51	57.3	115	2	US-10-014-012-222	Sequence 222, Appl	792	49	55.1	98	2	US-10-194-975-26	Sequence 26, Appl
720	51	57.3	129	2	US-09-406-535-2	Sequence 2, Appl1	793	49	55.1	98	2	US-09-534-717-647	Sequence 647, Appl
721	51	57.3	124	1	US-08-276-852-146	Sequence 146, Appl	794	49	55.1	98	2	US-09-534-717-651	Sequence 651, Appl
722	51	57.3	124	1	US-08-899-575-146	Sequence 146, Appl	795	49	55.1	98	2	US-09-534-717-652	Sequence 652, Appl
723	51	57.3	124	1	US-08-899-575-146	Sequence 146, Appl	796	49	55.1	109	1	US-08-428-197-3	Sequence 3, Appl1
724	51	57.3	124	4	PCT-US95-08743-146	Sequence 146, Appl	797	49	55.1	109	4	PCT-US93-10555-3	Sequence 3, Appl1
725	51	57.3	146	2	US-09-472-087-11	Sequence 11, Appl	798	49	55.1	110	2	US-09-471-276-868	Sequence 868, Appl
726	51	57.3	146	2	US-09-472-087-82	Sequence 82, Appl	799	49	55.1	114	2	US-09-232-290-44	Sequence 44, Appl
727	51	57.3	474	2	US-09-848-832-3	Sequence 3, Appl1	800	49	55.1	118	1	US-08-077-252B-1	Sequence 1, Appl1
728	50.5	56.7	115	2	US-10-014-013-227	Sequence 227, Appl	801	49	55.1	118	2	US-09-002-753A-1	Sequence 1, Appl1
729	50.5	56.7	138	1	US-08-379-057-14	Sequence 14, Appl	802	49	55.1	118	4	US-09-657-274-1	Sequence 1, Appl1
730	50	56.2	17	2	US-08-836-561-35	Sequence 35, Appl	803	49	55.1	118	4	PCT-US94-06687-1	Sequence 1, Appl1
731	50	56.2	17	2	US-09-560-198A-12	Sequence 12, Appl	804	49	55.1	119	1	US-08-331-398A-45	Sequence 45, Appl
732	50	56.2	17	2	US-09-434-123-35	Sequence 35, Appl	805	49	55.1	119	1	US-08-331-398A-47	Sequence 47, Appl
733	50	56.2	17	2	US-09-534-717-357	Sequence 357, Appl	806	49	55.1	119	1	US-08-331-397B-45	Sequence 45, Appl
734	50	56.2	17	2	US-09-534-717-361	Sequence 361, Appl	807	49	55.1	119	1	US-08-331-397B-47	Sequence 47, Appl
735	50	56.2	17	2	US-09-534-717-368	Sequence 368, Appl	808	49	55.1	119	1	US-08-759-804A-45	Sequence 45, Appl
736	50	56.2	17	2	US-09-534-717-371	Sequence 371, Appl	809	49	55.1	119	1	US-08-759-804A-47	Sequence 47, Appl
737	50	56.2	17	2	US-09-534-717-386	Sequence 386, Appl	810	49	55.1	119	1	US-08-759-804A-68	Sequence 68, Appl
738	50	56.2	17	2	US-09-534-717-388	Sequence 388, Appl	811	49	55.1	119	2	US-09-227-693-45	Sequence 45, Appl
739	50	56.2	17	2	US-09-534-717-393	Sequence 393, Appl	812	49	55.1	119	2	US-09-227-693-47	Sequence 47, Appl
740	50	56.2	51	1	US-08-765-179B-3	Sequence 3, Appl1	813	49	55.1	124	1	US-08-428-197-44	Sequence 44, Appl
741	50	56.2	114	2	US-08-545-809A-124	Sequence 124, Appl	814	49	55.1	124	4	PCT-US93-10555-44	Sequence 44, Appl1
742	50	56.2	114	2	US-09-515-697-124	Sequence 124, Appl	815	49	55.1	125	2	US-09-240-274-8	Sequence 20, Appl
743	50	56.2	123	1	US-08-478-039-94	Sequence 94, Appl	816	49	55.1	125	2	US-09-240-274-20	Sequence 21, Appl
744	50	56.2	123	1	US-08-476-349A-94	Sequence 94, Appl	817	49	55.1	125	2	US-09-240-274-21	Sequence 22, Appl
745	50	56.2	123	1	US-09-560-198A-2	Sequence 2, Appl1	818	49	55.1	125	2	US-09-240-274-22	Sequence 22, Appl
746	50	56.2	123	2	US-09-560-198A-4	Sequence 4, Appl1	819	49	55.1	125	2	US-09-240-274-23	Sequence 23, Appl
747	50	56.2	123	2	US-09-560-198A-10	Sequence 10, Appl	820	49	55.1	125	2	US-09-848-798-8	Sequence 8, Appl1
748	50	56.2	126	2	US-09-240-274-16	Sequence 16, Appl	821	49	55.1	125	2	US-09-848-798-20	Sequence 20, Appl
749	50	56.2	126	2	US-09-240-274-152	Sequence 152, Appl	822	49	55.1	125	2	US-09-848-798-21	Sequence 21, Appl
750	50	56.2	126	2	US-09-848-798-16	Sequence 16, Appl	823	49	55.1	125	2	US-09-848-798-22	Sequence 22, Appl
751	50	56.2	126	2	US-09-848-798-152	Sequence 152, Appl	824	49	55.1	125	2	US-09-848-798-23	Sequence 23, Appl
752	50	56.2	127	2	US-09-240-274-139	Sequence 139, Appl	825	49	55.1	126	2	US-09-240-274-14	Sequence 14, Appl
753	50	56.2	127	2	US-09-848-798-139	Sequence 139, Appl	826	49	55.1	126	2	US-09-240-274-15	Sequence 15, Appl
754	50	56.2	131	2	US-09-530-139-16	Sequence 16, Appl	827	49	55.1	126	2	US-09-240-274-147	Sequence 147, Appl
755	50	56.2	132	1	US-08-537-871A-14	Sequence 14, Appl	828	49	55.1	126	2	US-09-240-274-148	Sequence 148, Appl
756	50	56.2	132	1	US-08-276-852-144	Sequence 144, Appl	829	49	55.1	126	2	US-09-848-798-14	Sequence 14, Appl
757	50	56.2	132	1	US-08-899-575-144	Sequence 144, Appl	830	49	55.1	126	2	US-09-848-798-15	Sequence 15, Appl

831	49	55.1	126	2	US-09-848-798-147	Sequence 147, App	904	48	53.9	253	2	US-09-443-213-17	Sequence 17, Appl
832	49	55.1	126	2	US-09-848-798-148	Sequence 148, App	905	47.5	53.4	115	2	US-08-545-809A-122	Sequence 122, App
833	49	55.1	126	2	US-10-148-737A-1	Sequence 1, Appl	906	47.5	53.4	115	2	US-09-515-697-122	Sequence 122, App
834	49	55.1	129	1	US-08-162-102C-21	Sequence 21, Appl	907	47	52.8	17	2	US-09-192-854-135	Sequence 135, App
835	49	55.1	129	2	US-09-000-088-4	Sequence 4, Appl	908	47	52.8	17	2	US-09-511-939-242	Sequence 242, App
836	49	55.1	129	2	US-08-920-100B-21	Sequence 21, Appl	909	47	52.8	97	2	US-09-534-717-661	Sequence 661, App
837	49	55.1	129	4	PCT-US93-08786-21	Sequence 21, Appl	910	47	52.8	98	1	US-07-942-245-37	Sequence 37, Appl
838	49	55.1	141	1	US-08-259-372A-2	Sequence 2, Appl	911	47	52.8	98	2	US-10-194-975-15	Sequence 15, Appl
839	49	55.1	141	1	US-08-468-671-2	Sequence 2, Appl	912	47	52.8	98	2	US-09-534-717-660	Sequence 610, App
840	49	55.1	167	2	US-09-472-087-9	Sequence 9, Appl	913	47	52.8	98	2	US-09-534-717-664	Sequence 664, App
841	49	55.1	167	2	US-09-472-087-80	Sequence 80, Appl	914	47	52.8	98	2	US-09-534-717-666	Sequence 666, App
842	49	55.1	169	2	US-09-472-087-5	Sequence 5, Appl	915	47	52.8	110	2	US-08-545-809A-129	Sequence 129, App
843	49	55.1	169	2	US-09-472-087-73	Sequence 73, Appl	916	47	52.8	110	2	US-09-515-697-129	Sequence 129, App
844	49	55.1	171	2	US-09-472-087-83	Sequence 83, Appl	917	47	52.8	117	2	US-08-545-809A-95	Sequence 95, Appl
845	49	55.1	174	2	US-09-472-087-12	Sequence 12, Appl	918	47	52.8	117	2	US-09-515-697-95	Sequence 95, Appl
846	49	55.1	228	4	PCT-US92-08257-9	Sequence 9, Appl	919	47	52.8	118	2	US-09-530-139-22	Sequence 22, Appl
847	49	55.1	239	1	US-07-956-399-4	Sequence 4, Appl	920	47	52.8	118	2	US-09-823-746-4	Sequence 4, Appl
848	49	55.1	245	2	US-08-918-148-76	Sequence 76, Appl	921	47	52.8	120	4	PCT-US93-07832-4	Sequence 4, Appl
849	49	55.1	245	2	US-09-138-091A-74	Sequence 74, Appl	922	47	52.8	124	2	US-09-240-274-5	Sequence 5, Appl
850	49	55.1	247	2	US-09-227-693-34	Sequence 34, Appl	923	47	52.8	124	2	US-09-240-274-6	Sequence 6, Appl
851	49	55.1	248	1	US-08-331-398A-34	Sequence 34, Appl	924	47	52.8	124	2	US-09-848-798-5	Sequence 5, Appl
852	49	55.1	248	1	US-08-331-397B-34	Sequence 34, Appl	925	47	52.8	124	2	US-09-848-798-6	Sequence 6, Appl
853	49	55.1	248	1	US-08-759-804A-34	Sequence 34, Appl	926	47	52.8	126	2	US-09-240-274-25	Sequence 25, Appl
854	49	55.1	323	2	US-09-237-543-6	Sequence 6, Appl	927	47	52.8	126	2	US-09-240-274-26	Sequence 26, Appl
855	49	55.1	323	2	US-09-644-450-6	Sequence 6, Appl	928	47	52.8	126	2	US-09-240-274-153	Sequence 153, App
856	49	55.1	451	2	US-09-472-087-70	Sequence 70, Appl	929	47	52.8	126	2	US-09-848-798-25	Sequence 25, Appl
857	49	55.1	470	2	US-09-291-299A-1	Sequence 1, Appl	930	47	52.8	126	2	US-09-848-798-26	Sequence 26, Appl
858	49	55.1	476	2	US-09-291-299A-3	Sequence 3, Appl	931	47	52.8	126	2	US-09-848-798-153	Sequence 153, App
859	48	53.9	17	2	US-09-383-667-28	Sequence 28, Appl	932	47	52.8	150	2	US-09-472-087-81	Sequence 81, Appl
860	48	53.9	17	2	US-09-192-854-115	Sequence 115, App	933	47	52.8	151	2	US-09-472-087-10	Sequence 10, Appl
861	48	53.9	17	2	US-09-511-939-200	Sequence 200, App	934	47	52.8	225	2	US-09-530-139-42	Sequence 42, Appl
862	48	53.9	17	2	US-09-511-939-206	Sequence 206, App	935	47	52.8	225	2	US-09-456-090A-56	Sequence 56, Appl
863	48	53.9	17	2	US-09-534-717-391	Sequence 391, App	936	47	52.8	225	2	US-09-456-090A-92	Sequence 92, Appl
864	48	53.9	17	2	US-09-534-717-392	Sequence 392, App	937	47	52.8	225	2	US-09-456-090A-106	Sequence 106, App
865	48	53.9	35	2	US-08-525-539A-33	Sequence 33, Appl	938	47	52.8	225	2	US-09-453-234-56	Sequence 56, Appl
866	48	53.9	109	1	US-07-942-245-21	Sequence 21, Appl	940	47	52.8	225	2	US-09-453-234-60	Sequence 60, Appl
867	48	53.9	118	2	US-09-232-290-58	Sequence 58, Appl	941	47	52.8	225	2	US-09-453-234-92	Sequence 92, Appl
868	48	53.9	121	2	US-09-553-943-7	Sequence 7, Appl	942	47	52.8	225	2	US-09-453-234-106	Sequence 106, App
869	48	53.9	121	2	US-09-530-139-60	Sequence 60, Appl	943	47	52.8	312	2	US-09-079-029-10	Sequence 10, Appl
870	48	53.9	123	2	US-08-537-871A-17	Sequence 17, Appl	944	47	52.8	473	2	US-09-828-995B-20	Sequence 20, Appl
871	48	53.9	124	1	US-08-300-386A-63	Sequence 63, Appl	945	46	51.7	16	1	US-08-208-886C-84	Sequence 84, Appl
872	48	53.9	124	2	US-08-931-645-63	Sequence 63, Appl	946	46	51.7	16	1	US-08-704-744-86	Sequence 86, Appl
873	48	53.9	124	4	PCT-US95-11235-63	Sequence 63, Appl	947	46	51.7	16	1	US-08-469-557-65	Sequence 65, Appl
874	48	53.9	144	2	US-08-537-871A-35	Sequence 35, Appl	948	46	51.7	16	1	US-08-290-793B-65	Sequence 65, Appl
875	48	53.9	242	1	US-08-224-591-14	Sequence 14, Appl	949	46	51.7	17	1	US-08-285-936-52	Sequence 52, Appl
876	48	53.9	242	1	US-08-392-338A-23	Sequence 23, Appl	950	46	51.7	17	1	US-08-285-936-54	Sequence 54, Appl
877	48	53.9	242	1	US-08-926-789-14	Sequence 14, Appl	951	46	51.7	17	1	US-08-487-860-52	Sequence 52, Appl
878	48	53.9	242	2	US-09-166-750-23	Sequence 23, Appl	952	46	51.7	17	1	US-08-487-860-54	Sequence 54, Appl
879	48	53.9	242	2	US-09-166-093-23	Sequence 23, Appl	953	46	51.7	17	2	US-09-383-667-20	Sequence 20, Appl
880	48	53.9	242	2	US-09-166-093-23	Sequence 23, Appl	954	46	51.7	17	2	US-09-192-854-96	Sequence 96, Appl
881	48	53.9	242	2	US-09-172-019-23	Sequence 23, Appl	955	46	51.7	17	2	US-09-192-854-96	Sequence 96, Appl
882	48	53.9	242	2	US-09-166-094-23	Sequence 23, Appl	956	46	51.7	17	2	US-09-511-939-62	Sequence 62, Appl
883	48	53.9	242	2	US-09-443-213-23	Sequence 23, Appl	957	46	51.7	17	2	US-09-511-939-98	Sequence 98, Appl
884	48	53.9	242	6	5455030-17	Patent No. 5455030	958	46	51.7	17	2	US-09-511-939-170	Sequence 170, App
885	48	53.9	244	1	US-08-392-338A-13	Sequence 13, Appl	959	46	51.7	17	2	US-09-534-717-374	Sequence 374, App
886	48	53.9	244	2	US-09-166-750-13	Sequence 13, Appl	960	46	51.7	17	2	US-09-534-717-378	Sequence 378, App
887	48	53.9	244	2	US-09-166-093-13	Sequence 13, Appl	961	46	51.7	116	2	US-08-545-809A-134	Sequence 134, App
888	48	53.9	244	2	US-09-172-019-13	Sequence 13, Appl	962	46	51.7	115	2	US-09-515-697-134	Sequence 134, App
889	48	53.9	244	2	US-09-166-094-13	Sequence 13, Appl	963	46	51.7	119	1	US-08-285-936-8	Sequence 8, Appl
890	48	53.9	244	4	PCT-US93-11138-14	Sequence 14, Appl	964	46	51.7	119	1	US-08-285-936-12	Sequence 12, Appl
891	48	53.9	247	2	US-08-823-746-6	Sequence 6, Appl	965	46	51.7	119	1	US-08-487-860-8	Sequence 8, Appl
892	48	53.9	250	1	US-08-392-338A-15	Sequence 15, Appl	966	46	51.7	119	1	US-08-487-860-12	Sequence 12, Appl
893	48	53.9	250	2	US-09-166-750-15	Sequence 15, Appl	967	46	51.7	119	1	US-08-487-860-57	Sequence 57, Appl
894	48	53.9	250	2	US-09-166-093-15	Sequence 15, Appl	968	46	51.7	123	2	US-10-083-424-18	Sequence 18, Appl
895	48	53.9	250	2	US-09-166-093-15	Sequence 15, Appl	969	46	51.7	123	2	US-10-083-424-24	Sequence 24, Appl
896	48	53.9	250	2	US-09-172-019-15	Sequence 15, Appl	970	46	51.7	126	2	US-09-240-274-17	Sequence 17, Appl
897	48	53.9	250	2	US-09-166-094-15	Sequence 15, Appl	971	46	51.7	126	2	US-09-848-798-17	Sequence 17, App
898	48	53.9	253	1	US-08-392-338A-17	Sequence 17, Appl	972	46	51.7	127	2	US-09-240-274-145	Sequence 145, App
899	48	53.9	253	2	US-09-166-750-17	Sequence 17, Appl	973	46	51.7	127	2	US-09-848-798-145	Sequence 145, App
900	48	53.9	253	2	US-09-166-093-17	Sequence 17, Appl	974	46	51.7	129	2	US-09-530-139-24	Sequence 24, Appl
901	48	53.9	253	2	US-09-166-093-17	Sequence 17, Appl	975	46	51.7	225	2	US-09-456-090A-100	Sequence 100, App
902	48	53.9	253	2	US-09-172-019-17	Sequence 17, Appl	976	46	51.7	225	2	US-09-453-234-100	Sequence 100, App
903	48	53.9	253	2	US-09-166-094-17	Sequence 17, Appl							

977 46 51.7 265 2 US-09-742-693-30 Sequence 30, Appl  
978 45.5 51.1 118 1 US-08-487-761-15 Sequence 15, Appl  
979 45.5 51.1 131 1 US-08-259-372A-4 Sequence 4, Appl  
980 45.5 51.1 131 1 US-08-468-671-4 Sequence 4, Appl  
981 45 50.6 17 2 US-09-534-711-372 Sequence 372, Appl  
982 45 50.6 17 2 US-09-798-058-6 Sequence 6, Appl  
983 45 50.6 19 1 US-08-737-085A-4 Sequence 4, Appl  
984 45 50.6 19 2 US-09-246-258-4 Sequence 4, Appl  
985 45 50.6 19 2 US-09-532-106-4 Sequence 4, Appl  
986 45 50.6 19 2 US-09-839-666-4 Sequence 4, Appl  
987 45 50.6 19 2 US-10-372-735-46 Sequence 46, Appl  
988 45 50.6 22 2 US-08-918-148-32 Sequence 32, Appl  
989 45 50.6 22 2 US-09-138-091A-32 Sequence 32, Appl  
990 45 50.6 27 1 US-08-737-085A-21 Sequence 21, Appl  
991 45 50.6 27 2 US-09-246-258-21 Sequence 21, Appl  
992 45 50.6 27 2 US-09-532-106-21 Sequence 21, Appl  
993 45 50.6 27 2 US-09-839-666-21 Sequence 21, Appl  
994 45 50.6 27 2 US-10-372-735-126 Sequence 126, Appl  
995 45 50.6 47 2 US-09-497-997C-24 Sequence 24, Appl  
996 45 50.6 98 2 US-09-534-717-655 Sequence 655, Appl  
997 45 50.6 98 2 US-09-905-243-45 Sequence 45, Appl  
998 45 50.6 115 2 US-09-534-717-7 Sequence 7, Appl  
999 45 50.6 116 2 US-08-545-809A-143 Sequence 143, Appl  
1000 45 50.6 116 2 US-09-515-697-143 Sequence 143, Appl

## ALIGNMENTS

RESULT 1  
US-09-225-322B-18  
; Sequence 18, Application US/09225322B  
; Patent No. 6437098  
; GENERAL INFORMATION:  
; APPLICANT: SHITARA, KENYA  
; APPLICANT: HANAI, NOBUO  
; APPLICANT: HASEGAWA, MAMORU  
; APPLICANT: MIYAJI, HIROMASA  
; APPLICANT: KUWANA, YOSHIIISA  
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY  
; FILE REFERENCE: 249-101  
; CURRENT APPLICATION NUMBER: US/09/225,322B  
; PRIOR FILING DATE: 1999-01-05  
; PRIOR APPLICATION NUMBER: US 08/454,680  
; PRIOR FILING DATE: 1995-05-31  
; PRIOR APPLICATION NUMBER: US 08/408,133  
; PRIOR FILING DATE: 1995-03-21  
; PRIOR APPLICATION NUMBER: US 08/292,178  
; PRIOR FILING DATE: 1994-08-17  
; PRIOR APPLICATION NUMBER: US07/947,674  
; PRIOR FILING DATE: 1992-09-17  
; PRIOR APPLICATION NUMBER: JP 3-238375  
; PRIOR FILING DATE: 1991-09-18  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 18  
; LENGTH: 130  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:cdna KM-641

Query Match 100.0%; Score 89; DB 2; Length 130;  
Best Local Similarity 100.0%; Pred. No. 2.6e-05;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YISGGSGTYSDSVKG 17  
|||  
Db 60 YISGGSGTYSDSVKG 76

RESULT 2

US-09-764-304-18  
; Sequence 18, Application US/09764304  
; Patent No. 6495666  
; GENERAL INFORMATION:  
; APPLICANT: SHITARA, KENYA  
; APPLICANT: HANAI, NOBUO  
; APPLICANT: HASEGAWA, MAMORU  
; APPLICANT: MIYAJI, HIROMASA  
; APPLICANT: KUWANA, YOSHIIISA  
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY  
; FILE REFERENCE: 249-101  
; CURRENT APPLICATION NUMBER: US/09/764,304  
; CURRENT FILING DATE: 2001-01-19  
; EARLIER APPLICATION NUMBER: 09/225,322  
; EARLIER FILING DATE: 1999-01-05  
; EARLIER APPLICATION NUMBER: US 08/454,680  
; EARLIER FILING DATE: 1995-05-31  
; EARLIER APPLICATION NUMBER: US 08/408,133  
; EARLIER FILING DATE: 1995-03-21  
; EARLIER APPLICATION NUMBER: US 08/292,178  
; EARLIER FILING DATE: 1994-08-17  
; EARLIER APPLICATION NUMBER: US07/947,674  
; EARLIER FILING DATE: 1992-09-17  
; EARLIER APPLICATION NUMBER: JP 3-238375  
; EARLIER FILING DATE: 1991-09-18  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 18  
; LENGTH: 130  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: cdna KM-641

Query Match 100.0%; Score 89; DB 2; Length 130;  
Best Local Similarity 100.0%; Pred. No. 2.6e-05;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YISGGSGTYSDSVKG 17  
|||  
Db 60 YISGGSGTYSDSVKG 76

RESULT 3  
US-09-225-322B-8  
; Sequence 8, Application US/09225322B  
; Patent No. 6437098  
; GENERAL INFORMATION:  
; APPLICANT: SHITARA, KENYA  
; APPLICANT: HANAI, NOBUO  
; APPLICANT: HASEGAWA, MAMORU  
; APPLICANT: MIYAJI, HIROMASA  
; APPLICANT: KUWANA, YOSHIIISA  
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY  
; FILE REFERENCE: 249-101  
; CURRENT APPLICATION NUMBER: US/09/225,322B  
; CURRENT FILING DATE: 1999-01-05  
; PRIOR APPLICATION NUMBER: US 08/454,680  
; PRIOR FILING DATE: 1995-05-31  
; PRIOR APPLICATION NUMBER: US 08/408,133  
; PRIOR FILING DATE: 1995-03-21  
; PRIOR APPLICATION NUMBER: US 08/292,178  
; PRIOR FILING DATE: 1994-08-17  
; PRIOR APPLICATION NUMBER: US07/947,674  
; PRIOR FILING DATE: 1992-09-17  
; PRIOR APPLICATION NUMBER: JP 3-238375  
; PRIOR FILING DATE: 1991-09-18  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 8  
; LENGTH: 130  
; TYPE: PRT

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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: cDNA KM-641
US-09-225-322B-8

Query Match          92.1%; Score 82; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.00025;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 ISSGGSGTYSDSVKVG 17
Db      61 ISSGGSGTYSDSVKVG 76

RESULT 4
US-09-764-304-8
; Sequence 8, Application US/09764304
; Patent No. 6495666
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUWANA, YOSHIHISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/09/764,304
; CURRENT FILING DATE: 2001-01-19
; EARLIER APPLICATION NUMBER: 09/225,322
; EARLIER FILING DATE: 1999-01-05
; EARLIER APPLICATION NUMBER: US 08/454,680
; EARLIER FILING DATE: 1995-05-31
; EARLIER APPLICATION NUMBER: US 08/408,133
; EARLIER FILING DATE: 1995-03-21
; EARLIER APPLICATION NUMBER: US 08/292,178
; EARLIER FILING DATE: 1994-08-17
; EARLIER APPLICATION NUMBER: US07/947,674
; EARLIER FILING DATE: 1992-09-17
; EARLIER APPLICATION NUMBER: JP 3-238375
; EARLIER FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: cDNA KM-641
US-09-764-304-8

Query Match          92.1%; Score 82; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.00025;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 ISSGGSGTYSDSVKVG 17
Db      61 ISSGGSGTYSDSVKVG 76

RESULT 5
PCT-US94-07659-6
; Sequence 6, Application PC/TUS9407659
; GENERAL INFORMATION:
; APPLICANT: Young, Peter
; APPLICANT: Gross, Mitchell
; APPLICANT: Jonak, Zdenka L.
; APPLICANT: Theisen, Timothy
; APPLICANT: Hurlie, Mark
; APPLICANT: Jackson, Jeffrey R.
; TITLE OF INVENTION: Recombinant and Humanized Il-1 beta
; TITLE OF INVENTION: Antibodies for Treatment of Il-1 Mediated Inflammatory
; TITLE OF INVENTION: Disorders in Man
; NUMBER OF SEQUENCES: 21

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: cDNA KM-641
US-09-225-322B-8

Query Match          92.1%; Score 82; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.00025;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 ISSGGSGTYSDSVKVG 17
Db      61 ISSGGSGTYSDSVKVG 76

RESULT 6
PCT-US94-07659-2
; Sequence 2, Application PC/TUS9407659
; GENERAL INFORMATION:
; APPLICANT: Young, Peter
; APPLICANT: Gross, Mitchell
; APPLICANT: Jonak, Zdenka L.
; APPLICANT: Theisen, Timothy
; APPLICANT: Hurlie, Mark
; APPLICANT: Jackson, Jeffrey R.
; TITLE OF INVENTION: Recombinant and Humanized Il-1 beta
; TITLE OF INVENTION: Antibodies for Treatment of Il-1 Mediated Inflammatory
; TITLE OF INVENTION: Disorders in Man
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation - Corp.
; ADDRESSEE: Intellectual Property
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-2799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/07659
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/090,534
; FILING DATE: 09-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Sutton, Jeffrey A.
; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: P50171-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 270-5024
; TELEFAX: (610) 270-5090
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US94-07659-6

Query Match          86.5%; Score 77; DB 4; Length 119;
Best Local Similarity 82.4%; Pred. No. 0.0011;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 YISSGGSGTYSDSVKVG 17
Db      50 YISSGGSGTYSDSVKVG 66

RESULT 6
PCT-US94-07659-2
; Sequence 2, Application PC/TUS9407659
; GENERAL INFORMATION:
; APPLICANT: Young, Peter
; APPLICANT: Gross, Mitchell
; APPLICANT: Jonak, Zdenka L.
; APPLICANT: Theisen, Timothy
; APPLICANT: Hurlie, Mark
; APPLICANT: Jackson, Jeffrey R.
; TITLE OF INVENTION: Recombinant and Humanized Il-1 beta
; TITLE OF INVENTION: Antibodies for Treatment of Il-1 Mediated Inflammatory
; TITLE OF INVENTION: Disorders in Man
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation - Corp.
; ADDRESSEE: Intellectual Property
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-2799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/07659

```



;; GENERAL INFORMATION:  
;; APPLICANT: Scotgen Biopharmaceuticals, Inc.  
;; APPLICANT: 1014 Hamilton Court  
;; APPLICANT: Menlo Park, California 94025  
;; APPLICANT: United States of America  
;; APPLICANT: 1345 Avenue of the Americas  
;; APPLICANT: New York, New York 10105  
;; APPLICANT: United States of America  
;; TITLE OF INVENTION: RECOMBINANT HUMAN ANTI-LK26  
;; TITLE OF INVENTION: ANTIBODIES  
;; NUMBER OF SEQUENCES: 29  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Felfe & Lynch  
;; STREET: 805 Third Avenue  
;; CITY: New York  
;; STATE: New York  
;; COUNTRY: U.S.A.  
;; ZIP: 10022  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: 3.5 inch  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: WordPerfect 6.0/ASCII standard  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/207,996  
;; FILING DATE: 08-MAR-1994  
;; CLASSIFICATION: 530  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Pasqualini, Patricia A.  
;; REGISTRATION NUMBER: 34,894  
;; REFERENCE/DOCKET NUMBER: LUD-5363  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 212-688-9200  
;; TELEFAX: 212-838-3884  
;; INFORMATION FOR SEQ ID NO: 19:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 119 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: DNA (genomic)  
US-08-207-996-19  
  
Query Match 78.7%; Score 70; DB 1; Length 119;  
Best Local Similarity 87.5%; Pred. No. 0.011;  
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 2 ISSGSGTYYSDSVKG 17  
Db 51 ISSGSGTYTADSVKG 66  
  
RESULT 10  
US-08-207-996-20  
; Sequence 20, Application US/08207996  
; Patent No. 5646253  
; GENERAL INFORMATION:  
; APPLICANT: Scotgen Biopharmaceuticals, Inc.  
; APPLICANT: 1014 Hamilton Court  
; APPLICANT: Menlo Park, California 94025  
; APPLICANT: United States of America  
; APPLICANT: 1345 Avenue of the Americas  
; APPLICANT: New York, New York 10105  
; APPLICANT: United States of America  
; TITLE OF INVENTION: RECOMBINANT HUMAN ANTI-LK26  
; TITLE OF INVENTION: ANTIBODIES  
; NUMBER OF SEQUENCES: 29  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Felfe & Lynch  
; STREET: 805 Third Avenue  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.

;; ZIP: 10022  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: 3.5 inch  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: WordPerfect 6.0/ASCII standard  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/207,996  
;; FILING DATE: 08-MAR-1994  
;; CLASSIFICATION: 530  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Pasqualini, Patricia A.  
;; REGISTRATION NUMBER: 34,894  
;; REFERENCE/DOCKET NUMBER: LUD-5363  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 212-688-9200  
;; TELEFAX: 212-838-3884  
;; INFORMATION FOR SEQ ID NO: 20:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 119 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: DNA (genomic)  
US-08-207-996-20  
  
Query Match 78.7%; Score 70; DB 1; Length 119;  
Best Local Similarity 87.5%; Pred. No. 0.011;  
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 2 ISSGSGTYYSDSVKG 17  
Db 51 ISSGSGTYTADSVKG 66  
  
RESULT 11  
US-08-207-996-21  
; Sequence 21, Application US/08207996  
; Patent No. 5646253  
; GENERAL INFORMATION:  
; APPLICANT: Scotgen Biopharmaceuticals, Inc.  
; APPLICANT: 1014 Hamilton Court  
; APPLICANT: Menlo Park, California 94025  
; APPLICANT: United States of America  
; APPLICANT: 1345 Avenue of the Americas  
; APPLICANT: New York, New York 10105  
; APPLICANT: United States of America  
; TITLE OF INVENTION: RECOMBINANT HUMAN ANTI-LK26  
; TITLE OF INVENTION: ANTIBODIES  
; NUMBER OF SEQUENCES: 29  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Felfe & Lynch  
; STREET: 805 Third Avenue  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10022  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WordPerfect 6.0/ASCII standard  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/207,996  
; FILING DATE: 08-MAR-1994  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Pasqualini, Patricia A.  
; REGISTRATION NUMBER: 34,894  
; REFERENCE/DOCKET NUMBER: LUD-5363  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-688-9200  
; TELEFAX: 212-838-3884

; INFORMATION FOR SEQ ID NO: 21:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 119 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-207-996-21

Query Match 78.7%; Score 70; DB 1; Length 119;  
Best Local Similarity 87.5%; Pred. No. 0.011;  
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 ISSGGSGTYSDSVK 17  
DB 51 ISSGGSYTYADSVKG 66

RESULT 12  
US-08-207-996-22  
; Sequence 22, Application US/08207996  
; Patent No. 5646253  
; GENERAL INFORMATION:  
; APPLICANT: Scotgen Biopharmaceuticals, Inc.  
; APPLICANT: 1014 Hamilton Court  
; APPLICANT: Menlo Park, California 94025  
; APPLICANT: United States of America  
; APPLICANT: 1345 Avenue of the Americas  
; APPLICANT: New York, New York 10105  
; APPLICANT: United States of America  
; TITLE OF INVENTION: RECOMBINANT HUMAN ANTI-LK26  
; NUMBER OF SEQUENCES: 29  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Felfe & Lynch  
; STREET: 805 Third Avenue  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10022

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WordPerfect 6.0/ASCII standard  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/207,996  
FILING DATE: 08-MAR-1994  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Pasqualini, Patricia A.  
REGISTRATION NUMBER: 34,894  
REFERENCE/DOCKET NUMBER: LUD-5363  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-688-9200  
TELEFAX: 212-838-3884

INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 119 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-207-996-22

Query Match 78.7%; Score 70; DB 1; Length 119;  
Best Local Similarity 87.5%; Pred. No. 0.011;  
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 ISSGGSGTYSDSVK 17  
DB 51 ISSGGSYTYADSVKG 66

RESULT 13  
US-08-207-996-27  
; Sequence 27, Application US/08207996  
; Patent No. 5646253  
; GENERAL INFORMATION:  
; APPLICANT: Scotgen Biopharmaceuticals, Inc.  
; APPLICANT: 1014 Hamilton Court  
; APPLICANT: Menlo Park, California 94025  
; APPLICANT: United States of America  
; APPLICANT: 1345 Avenue of the Americas  
; APPLICANT: New York, New York 10105  
; APPLICANT: United States of America  
; TITLE OF INVENTION: RECOMBINANT HUMAN ANTI-LK26  
; NUMBER OF SEQUENCES: 29  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Felfe & Lynch  
; STREET: 805 Third Avenue  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10022

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WordPerfect 6.0/ASCII standard  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/207,996  
FILING DATE: 08-MAR-1994  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Pasqualini, Patricia A.  
REGISTRATION NUMBER: 34,894  
REFERENCE/DOCKET NUMBER: LUD-5363  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-688-9200  
TELEFAX: 212-838-3884  
INFORMATION FOR SEQ ID NO: 27:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 119 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-207-996-27

Query Match 78.7%; Score 70; DB 1; Length 119;  
Best Local Similarity 87.5%; Pred. No. 0.011;  
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 ISSGGSGTYSDSVK 17  
DB 51 ISSGGSYTYADSVKG 66

RESULT 14  
US-08-760-840A-18  
; Sequence 18, Application US/08760840A  
; Patent No. 5952484  
; GENERAL INFORMATION:  
; APPLICANT: Paul WALLACE;  
; APPLICANT: William J. HARRIS;  
; APPLICANT: Wolfgang J. RETTIG;  
; APPLICANT: Pilar GARIN-CHESA;  
; APPLICANT: Lloyd J. OLD  
; TITLE OF INVENTION: RECOMBINANT HUMAN ANTI-LK26 ANTIBODIES  
; NUMBER OF SEQUENCES: 31  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Felfe & Lynch  
; STREET: 805 Third Avenue  
; CITY: New York  
; STATE: New York



```

; COUNTRY: U.S.A.
; ZIP: 10022
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/760,840A
; FILING DATE: 05-DEC-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US 95/03094
; FILING DATE: 08-MAR-1995
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 5952484man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5363.1 DIV. - JEL/NDH/SLH
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-688-9200
; TELEFAX: 212-838-3884
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: protein
; MOLECULE TYPE: protein
; US-08-760-840A-18

Query Match 78.7%; Score 70; DB 1; Length 119;
Best Local Similarity 87.5%; Pred. No. 0.011;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ISSGGSGTYSDSVKVG 17
Db 51 ISSGGSYTYADSVKVG 66

RESULT 15
US-08-760-840A-19
; Sequence 19, Application US/08760840A
; Patent No. 5952484
; GENERAL INFORMATION:
; APPLICANT: Paul WALLACE;
; APPLICANT: William J. HARRIS;
; APPLICANT: Wolfgang J. RETTIG;
; APPLICANT: Pilar GARIN-CHESA;
; APPLICANT: Lloyd J. OLD
; TITLE OF INVENTION: RECOMBINANT HUMAN ANTI-LK26 ANTIBODIES
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/760,840A
; FILING DATE: 05-DEC-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US 95/03094
; FILING DATE: 08-MAR-1995
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 5952484man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5363.1 DIV. - JEL/NDH/SLH
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-688-9200
; TELEFAX: 212-838-3884
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: protein
; MOLECULE TYPE: protein
; US-08-760-840A-19

Query Match 78.7%; Score 70; DB 1; Length 119;
Best Local Similarity 87.5%; Pred. No. 0.011;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ISSGGSGTYSDSVKVG 17
Db 51 ISSGGSYTYADSVKVG 66

RESULT 16
US-08-760-840A-20
; Sequence 20, Application US/08760840A
; Patent No. 5952484
; GENERAL INFORMATION:
; APPLICANT: Paul WALLACE;
; APPLICANT: William J. HARRIS;
; APPLICANT: Wolfgang J. RETTIG;
; APPLICANT: Pilar GARIN-CHESA;
; APPLICANT: Lloyd J. OLD
; TITLE OF INVENTION: RECOMBINANT HUMAN ANTI-LK26 ANTIBODIES
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/760,840A
; FILING DATE: 05-DEC-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US 95/03094
; FILING DATE: 08-MAR-1995
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 5952484man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5363.1 DIV. - JEL/NDH/SLH
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-688-9200
; TELEFAX: 212-838-3884
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: protein
; MOLECULE TYPE: protein
; US-08-760-840A-20

Query Match 78.7%; Score 70; DB 1; Length 119;
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; NAME: Hanson, No. 5952484man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5363.1 DIV. - JEL/NDH/SLH
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-688-9200
; TELEFAX: 212-838-3884
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: protein
; MOLECULE TYPE: protein
; US-08-760-840A-19

Query Match 78.7%; Score 70; DB 1; Length 119;
Best Local Similarity 87.5%; Pred. No. 0.011;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ISSGGSGTYSDSVKVG 17
Db 51 ISSGGSYTYADSVKVG 66

RESULT 16
US-08-760-840A-20
; Sequence 20, Application US/08760840A
; Patent No. 5952484
; GENERAL INFORMATION:
; APPLICANT: Paul WALLACE;
; APPLICANT: William J. HARRIS;
; APPLICANT: Wolfgang J. RETTIG;
; APPLICANT: Pilar GARIN-CHESA;
; APPLICANT: Lloyd J. OLD
; TITLE OF INVENTION: RECOMBINANT HUMAN ANTI-LK26 ANTIBODIES
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/760,840A
; FILING DATE: 05-DEC-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US 95/03094
; FILING DATE: 08-MAR-1995
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 5952484man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5363.1 DIV. - JEL/NDH/SLH
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-688-9200
; TELEFAX: 212-838-3884
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: protein
; MOLECULE TYPE: protein
; US-08-760-840A-20

Query Match 78.7%; Score 70; DB 1; Length 119;
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/760,840A
; FILING DATE: 05-DEC-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US 95/03094
; FILING DATE: 08-MAR-1995
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 595248man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5363.1 DIV. - JEL/NDH/SLH
; TELEPHONE: 212-688-9200
; TELEFAX: 212-838-3884
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-760-840A-28

Query Match 78.7%; Score 70; DB 1; Length 119;
Best Local Similarity 87.5%; Pred. No. 0.011;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 ISSGGSGTYSDSVK 17
Db 51 ISSGGSYTYADSVKG 66

RESULT 20
US-09-266-119-18
; Sequence 18, Application US/09266119
; Patent No. 6124106
; GENERAL INFORMATION:
; APPLICANT: Paul WALLACE;
; APPLICANT: William J. HARRIS;
; APPLICANT: Wolfgang J. RETTIG;
; APPLICANT: Pilar GARIN-CHESA;
; APPLICANT: Lloyd J. OLD
; TITLE OF INVENTION: RECOMBINANT HUMAN ANTI-LK26 ANTIBODIES
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/266,119
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/760,840
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6124106man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5363.1 DIV. - JEL/NDH/SLH
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-688-9200
; TELEFAX: 212-838-3884
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-09-266-119-19

Query Match 78.7%; Score 70; DB 2; Length 119;
Best Local Similarity 87.5%; Pred. No. 0.011;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 ISSGGSGTYSDSVK 17
Db 51 ISSGGSYTYADSVKG 66

US-09-266-119-19
; Sequence 19, Application US/09266119
; Patent No. 6124106
; GENERAL INFORMATION:
; APPLICANT: Paul WALLACE;
; APPLICANT: William J. HARRIS;
; APPLICANT: Wolfgang J. RETTIG;
; APPLICANT: Pilar GARIN-CHESA;
; APPLICANT: Lloyd J. OLD
; TITLE OF INVENTION: RECOMBINANT HUMAN ANTI-LK26 ANTIBODIES
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/266,119
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/760,840
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6124106man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5363.1 DIV. - JEL/NDH/SLH
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-688-9200
; TELEFAX: 212-838-3884
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-09-266-119-19

Query Match 78.7%; Score 70; DB 2; Length 119;
Best Local Similarity 87.5%; Pred. No. 0.011;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 ISSGGSGTYSDSVK 17
Db 51 ISSGGSYTYADSVKG 66

US-09-266-119-19
; Sequence 19, Application US/09266119
; Patent No. 6124106
; GENERAL INFORMATION:
; APPLICANT: Paul WALLACE;
; APPLICANT: William J. HARRIS;
; APPLICANT: Wolfgang J. RETTIG;
; APPLICANT: Pilar GARIN-CHESA;
; APPLICANT: Lloyd J. OLD
; TITLE OF INVENTION: RECOMBINANT HUMAN ANTI-LK26 ANTIBODIES
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/266,119
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/760,840
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6124106man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5363.1 DIV. - JEL/NDH/SLH
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-688-9200
; TELEFAX: 212-838-3884
; INFORMATION FOR SEQ ID NO: 19:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-09-266-119-18

Query Match 78.7%; Score 70; DB 2; Length 119;
Best Local Similarity 87.5%; Pred. No. 0.011;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 ISSGGSGTYSDSVK 17
Db 51 ISSGGSYTYADSVKG 66

RESULT 21
US-09-266-119-19
; Sequence 19, Application US/09266119
; Patent No. 6124106
; GENERAL INFORMATION:
; APPLICANT: Paul WALLACE;
; APPLICANT: William J. HARRIS;
; APPLICANT: Wolfgang J. RETTIG;
; APPLICANT: Pilar GARIN-CHESA;
; APPLICANT: Lloyd J. OLD
; TITLE OF INVENTION: RECOMBINANT HUMAN ANTI-LK26 ANTIBODIES
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/266,119
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/760,840
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6124106man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5363.1 DIV. - JEL/NDH/SLH
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-688-9200
; TELEFAX: 212-838-3884
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-09-266-119-19

Query Match 78.7%; Score 70; DB 2; Length 119;
Best Local Similarity 87.5%; Pred. No. 0.011;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 ISSGGSGTYSDSVK 17
Db 51 ISSGGSYTYADSVKG 66

US-09-266-119-19
; Sequence 19, Application US/09266119
; Patent No. 6124106
; GENERAL INFORMATION:
; APPLICANT: Paul WALLACE;
; APPLICANT: William J. HARRIS;
; APPLICANT: Wolfgang J. RETTIG;
; APPLICANT: Pilar GARIN-CHESA;
; APPLICANT: Lloyd J. OLD
; TITLE OF INVENTION: RECOMBINANT HUMAN ANTI-LK26 ANTIBODIES
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/266,119
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/760,840
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6124106man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5363.1 DIV. - JEL/NDH/SLH
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-688-9200
; TELEFAX: 212-838-3884
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-09-266-119-19

Query Match 78.7%; Score 70; DB 2; Length 119;
Best Local Similarity 87.5%; Pred. No. 0.011;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 ISSGGSGTYSDSVK 17
Db 51 ISSGGSYTYADSVKG 66

US-09-266-119-19
; Sequence 19, Application US/09266119
; Patent No. 6124106
; GENERAL INFORMATION:
; APPLICANT: Paul WALLACE;
; APPLICANT: William J. HARRIS;
; APPLICANT: Wolfgang J. RETTIG;
; APPLICANT: Pilar GARIN-CHESA;
; APPLICANT: Lloyd J. OLD
; TITLE OF INVENTION: RECOMBINANT HUMAN ANTI-LK26 ANTIBODIES
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/266,119
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/760,840
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6124106man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5363.1 DIV. - JEL/NDH/SLH
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-688-9200
; TELEFAX: 212-838-3884
; INFORMATION FOR SEQ ID NO: 19:

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RESULT 22
US-09-266-119-20
; Sequence 20, Application US/09266119
; Patent No. 6124106
; GENERAL INFORMATION:
; APPLICANT: Paul WALLACE;
; APPLICANT: William J. HARRIS;
; APPLICANT: Wolfgang J. RETTIG;
; APPLICANT: Pilar GARIN-CHESA;
; APPLICANT: Lloyd J. OLD
; TITLE OF INVENTION: RECOMBINANT HUMAN ANTI-LK26 ANTIBODIES
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; CITY: 805 Third Avenue
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/266,119
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/760,840
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6124106man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5363.1 DIV. - JEL/NDH/SLH
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-688-9200
; TELEFAX: 212-838-3884
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-09-266-119-20

Query Match 78.7%; Score 70; DB 2; Length 119;
Best Local Similarity 87.5%; Pred. No. 0.011;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 ISSGGSGTYYSVSKG 17
||| ||| ||| ||| |||
Db 51 ISSGGSYTYADSVKG 66

RESULT 23
US-09-266-119-21
; Sequence 21, Application US/09266119
; Patent No. 6124106
; GENERAL INFORMATION:
; APPLICANT: Paul WALLACE;
; APPLICANT: William J. HARRIS;
; APPLICANT: Wolfgang J. RETTIG;
; APPLICANT: Pilar GARIN-CHESA;
; APPLICANT: Lloyd J. OLD
; TITLE OF INVENTION: RECOMBINANT HUMAN ANTI-LK26 ANTIBODIES
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; CITY: 805 Third Avenue
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/266,119
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/760,840
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6124106man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5363.1 DIV. - JEL/NDH/SLH
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-688-9200
; TELEFAX: 212-838-3884
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-09-266-119-20

Query Match 78.7%; Score 70; DB 2; Length 119;
Best Local Similarity 87.5%; Pred. No. 0.011;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 ISSGGSGTYYSVSKG 17
||| ||| ||| ||| |||
Db 51 ISSGGSYTYADSVKG 66

RESULT 24
US-09-266-119-22
; Sequence 22, Application US/09266119
; Patent No. 6124106
; GENERAL INFORMATION:
; APPLICANT: Paul WALLACE;
; APPLICANT: William J. HARRIS;
; APPLICANT: Wolfgang J. RETTIG;
; APPLICANT: Pilar GARIN-CHESA;
; APPLICANT: Lloyd J. OLD
; TITLE OF INVENTION: RECOMBINANT HUMAN ANTI-LK26 ANTIBODIES
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; CITY: 805 Third Avenue
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/266,119
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/760,840
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6124106man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5363.1 DIV. - JEL/NDH/SLH
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-688-9200
; TELEFAX: 212-838-3884
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-09-266-119-21

Query Match 78.7%; Score 70; DB 2; Length 119;
Best Local Similarity 87.5%; Pred. No. 0.011;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 ISSGGSGTYYSVSKG 17
||| ||| ||| ||| |||
Db 51 ISSGGSYTYADSVKG 66

```

CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Hanson, No. 6124106man D.  
REGISTRATION NUMBER: 30,946  
REFERENCE/DOCKET NUMBER: LUD 5363.1 DIV. - JEL/NDH/SLH  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-688-9200  
TELEFAX: 212-838-3884  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 119 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
US-09-266-119-22

Query Match 78.7%; Score 70; DB 2; Length 119;  
Best Local Similarity 87.5%; Pred. No. 0.011;  
Matches 14; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

QY 2 ISSGGSGTYSDSVK 17  
Db 51 ISSGGSYTYADSVKG 66

RESULT 25  
US-09-266-119-28  
Sequence 28, Application US/09266119  
Patent No. 6124106  
GENERAL INFORMATION:  
APPLICANT: Paul WALLACE;  
APPLICANT: William J. HARRIS;  
APPLICANT: Wolfgang J. RETTIG;  
APPLICANT: Pilar GARIN-CHESA;  
APPLICANT: Lloyd J. OLD  
TITLE OF INVENTION: RECOMBINANT HUMAN ANTI-LK26 ANTIBODIES  
NUMBER OF SEQUENCES: 31  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Felfe & Lynch  
STREET: 805 Third Avenue  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10022  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Wordperfect  
CURRENT APPLICATION NUMBER: US/09/266,119  
FILING DATE: 26-Jun-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/266,119  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Hanson, No. 6124106man D.  
REGISTRATION NUMBER: 30,946  
REFERENCE/DOCKET NUMBER: LUD 5363.1 DIV. - JEL/NDH/SLH  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-688-9200  
TELEFAX: 212-838-3884  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 119 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/760,840  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Hanson, No. 6124106man D.  
REGISTRATION NUMBER: 30,946  
REFERENCE/DOCKET NUMBER: LUD 5363.1 DIV. - JEL/NDH/SLH  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-688-9200  
TELEFAX: 212-838-3884  
INFORMATION FOR SEQ ID NO: 28:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 119 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
US-09-266-119-28

Query Match 78.7%; Score 70; DB 2; Length 119;  
Best Local Similarity 87.5%; Pred. No. 0.011;  
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 ISSGGSGTYSDSVK 17  
Db 51 ISSGGSYTYADSVKG 66

RESULT 26  
US-09-602-709-18  
Sequence 18, Application US/09602709  
Patent No. 6348195  
GENERAL INFORMATION:  
APPLICANT: Paul WALLACE;  
APPLICANT: William J. HARRIS;  
APPLICANT: Wolfgang J. RETTIG;  
APPLICANT: Pilar GARIN-CHESA;  
APPLICANT: Lloyd J. OLD  
TITLE OF INVENTION: RECOMBINANT HUMAN ANTI-LK26 ANTIBODIES  
NUMBER OF SEQUENCES: 31  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Felfe & Lynch  
STREET: 805 Third Avenue  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10022  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Wordperfect  
CURRENT APPLICATION NUMBER: US/09/602,709  
FILING DATE: 26-Jun-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/266,119  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Hanson, No. 6348195man D.  
REGISTRATION NUMBER: 30,946  
REFERENCE/DOCKET NUMBER: LUD 5363.1 DIV. - JEL/NDH/SLH  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-688-9200  
TELEFAX: 212-838-3884  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 119 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 18:  
US-09-602-709-18

Query Match 78.7%; Score 70; DB 2; Length 119;  
Best Local Similarity 87.5%; Pred. No. 0.011;  
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 ISSGGSGTYSDSVK 17  
Db 51 ISSGGSYTYADSVKG 66

RESULT 27  
US-09-602-709-19  
Sequence 19, Application US/09602709  
Patent No. 6348195  
GENERAL INFORMATION:  
APPLICANT: Paul WALLACE;  
APPLICANT: William J. HARRIS;  
APPLICANT: Wolfgang J. RETTIG;  
APPLICANT: Pilar GARIN-CHESA;  
APPLICANT: Lloyd J. OLD  
TITLE OF INVENTION: RECOMBINANT HUMAN ANTI-LK26 ANTIBODIES  
NUMBER OF SEQUENCES: 31  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Felfe & Lynch  
STREET: 805 Third Avenue  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10022  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Wordperfect  
CURRENT APPLICATION NUMBER: US/09/266,119  
FILING DATE: 26-Jun-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/266,119  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Hanson, No. 6348195man D.  
REGISTRATION NUMBER: 30,946  
REFERENCE/DOCKET NUMBER: LUD 5363.1 DIV. - JEL/NDH/SLH  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-688-9200  
TELEFAX: 212-838-3884  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 119 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 18:  
US-09-602-709-18

William J. HARRIS;  
Wolfgang J. RETTIG;  
Pilar GARIN-CHESA;  
Lloyd J. OLD  
TITLE OF INVENTION: RECOMBINANT HUMAN ANTI-LK26 ANTIBODIES  
NUMBER OF SEQUENCES: 31  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Felfe & Lynch  
STREET: 805 Third Avenue  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10022  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Wordperfect  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/602,709  
FILING DATE: 26-Jun-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/266,119  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Hanson, No. 6348195man D.  
REGISTRATION NUMBER: 30,946  
REFERENCE/DOCKET NUMBER: LUD 5363.1 DIV. - JEL/NDH/SLH  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-688-9200  
TELEFAX: 212-838-3884  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 119 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 19:  
US-09-602-709-19  
Query Match 78.7%; Score 70; DB 2; Length 119;  
Best Local Similarity 87.5%; Pred. No. 0.011;  
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
Qy 2 ISSGGSGTYSDSVKVG 17  
Db 51 ISSGGSGTYADSVKVG 66  
RESULT 28  
US-09-602-709-20  
; Sequence 20, Application US/09602709  
; Patent No. 6348195  
; GENERAL INFORMATION:  
; APPLICANT: Paul WALLACE;  
; William J. HARRIS;  
; Wolfgang J. RETTIG;  
; Pilar GARIN-CHESA;  
; Lloyd J. OLD  
TITLE OF INVENTION: RECOMBINANT HUMAN ANTI-LK26 ANTIBODIES  
NUMBER OF SEQUENCES: 31  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Felfe & Lynch  
STREET: 805 Third Avenue  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10022  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Wordperfect  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/602,709  
FILING DATE: 26-Jun-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/266,119  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Hanson, No. 6348195man D.  
REGISTRATION NUMBER: 30,946  
REFERENCE/DOCKET NUMBER: LUD 5363.1 DIV. - JEL/NDH/SLH  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-688-9200  
TELEFAX: 212-838-3884  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 119 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 20:  
US-09-602-709-20  
Query Match 78.7%; Score 70; DB 2; Length 119;  
Best Local Similarity 87.5%; Pred. No. 0.011;  
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
Qy 2 ISSGGSGTYSDSVKVG 17  
Db 51 ISSGGSGTYADSVKVG 66  
RESULT 29  
US-09-602-709-21  
; Sequence 21, Application US/09602709  
; Patent No. 6348195  
; GENERAL INFORMATION:  
; APPLICANT: Paul WALLACE;  
; William J. HARRIS;  
; Wolfgang J. RETTIG;  
; Pilar GARIN-CHESA;  
; Lloyd J. OLD  
TITLE OF INVENTION: RECOMBINANT HUMAN ANTI-LK26 ANTIBODIES  
NUMBER OF SEQUENCES: 31  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Felfe & Lynch  
STREET: 805 Third Avenue  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10022  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Wordperfect  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/602,709  
FILING DATE: 26-Jun-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/266,119  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Hanson, No. 6348195man D.  
REGISTRATION NUMBER: 30,946  
REFERENCE/DOCKET NUMBER: LUD 5363.1 DIV. - JEL/NDH/SLH  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-688-9200  
TELEFAX: 212-838-3884

;  
; INFORMATION FOR SEQ ID NO: 21:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 119 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 21:  
US-09-602-709-21

Query Match 78.7%; Score 70; DB 2; Length 119;  
Best Local Similarity 87.5%; Pred. No. 0.011;  
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 ISSGGSGTYSDSVK 17  
|||||:|||||  
DB 51 ISSGGSYTYADSVKG 66

RESULT 30  
US-09-602-709-22  
; Sequence 22, Application US/09602709  
; Patent No. 6348195  
; GENERAL INFORMATION:  
; APPLICANT: PAUL WALLACE;  
; WILLIAM J. HARRIS;  
; WOLFGANG J. RETTIG;  
; PILAR GARIN-CHESA;  
; LLOYD J. OLD  
; TITLE OF INVENTION: RECOMBINANT HUMAN ANTI-LK26 ANTIBODIES  
; NUMBER OF SEQUENCES: 31  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Felfe & Lynch  
; STREET: 805 Third Avenue  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10022

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Wordperfect  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/602,709  
FILING DATE: 26-Jun-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/266,119  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Hanson, No. 6348195man D.  
REGISTRATION NUMBER: 30,946  
REFERENCE/DOCKET NUMBER: LUD 5363.1 DIV. - JEL/NDH/SLH

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-688-9200  
TELEFAX: 212-838-3884  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 119 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 22:

Query Match 78.7%; Score 70; DB 2; Length 119;  
Best Local Similarity 87.5%; Pred. No. 0.011;  
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 ISSGGSGTYSDSVK 17  
|||||:|||||

Db 51 ISSGGSYTYADSVKG 66  
RESULT 31  
US-09-602-709-28  
; Sequence 28, Application US/09602709  
; Patent No. 6348195  
; GENERAL INFORMATION:  
; APPLICANT: PAUL WALLACE;  
; WILLIAM J. HARRIS;  
; WOLFGANG J. RETTIG;  
; PILAR GARIN-CHESA;  
; LLOYD J. OLD  
; TITLE OF INVENTION: RECOMBINANT HUMAN ANTI-LK26 ANTIBODIES  
; NUMBER OF SEQUENCES: 31  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Felfe & Lynch  
; STREET: 805 Third Avenue  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10022

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Wordperfect  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/602,709  
FILING DATE: 26-Jun-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/266,119  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Hanson, No. 6348195man D.  
REGISTRATION NUMBER: 30,946  
REFERENCE/DOCKET NUMBER: LUD 5363.1 DIV. - JEL/NDH/SLH

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-688-9200  
TELEFAX: 212-838-3884  
INFORMATION FOR SEQ ID NO: 28:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 119 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 28:

US-09-602-709-28  
Query Match 78.7%; Score 70; DB 2; Length 119;  
Best Local Similarity 87.5%; Pred. No. 0.011;  
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 ISSGGSGTYSDSVK 17  
|||||:|||||

Db 51 ISSGGSYTYADSVKG 66  
RESULT 32  
US-09-497-997C-31  
; Sequence 31, Application US/09497997C  
; Patent No. 6635248  
; GENERAL INFORMATION:  
; APPLICANT: TERNYNCK, THERESA  
; APPLICANT: AVAMEAS, ALEXANDRE  
; APPLICANT: BUTTIN, GERARD  
; APPLICANT: AVAMEAS, STRAITIS  
; APPLICANT: SARON, MARIE-FRANCOISE  
; APPLICANT: BLONDEL, BRUNO  
; APPLICANT: COUDERC, THERESA  
; APPLICANT: MICHELSON, SUSAN





```
; Patent No. 6348185
; GENERAL INFORMATION:
; APPLICANT: Washington University School of Medicine
; TITLE OF INVENTION: MEMBRANE-PERMEANT PEPTIDE COMPLEXES FOR MEDICAL
; FILE OF INVENTION: IMAGING, DIAGNOSTICS, AND PHARMACEUTICAL THERAPY
; FILE REFERENCE: WSHU 2001
; CURRENT APPLICATION NUMBER: US/09/336,093A
; CURRENT FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: peptide
; OTHER INFORMATION: derivable from the heavy chain variable region of
; OTHER INFORMATION: an anti-DNA monoclonal antibody
US-09-336-093-4

Query Match 77.5%; Score 69; DB 2; Length 30;
Best Local Similarity 76.5%; Pred. No. 0.0038;
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 YISGGSGTYYSDSVKG 17
Db 3 YISRGGVSTYYSDTVKG 19

RESULT 37
US-09-557-465D-4
; Sequence 4, Application US/09557465D
; Patent No. 6589503
; GENERAL INFORMATION:
; APPLICANT: Washington University
; APPLICANT: Pwinnica-Womms, David
; TITLE OF INVENTION: MEMBRANE-PERMEANT PEPTIDE COMPLEXES FOR MEDICAL IMAGING, DIAGNOSTICS, AND PHARMACEUTICAL THERAPY
; FILE OF INVENTION: PHARMACEUTICAL THERAPY
; FILE REFERENCE: WSHU 2020
; CURRENT APPLICATION NUMBER: US/09/557,465D
; CURRENT FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US 09/557,465
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US 09/336,093
; PRIOR FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: US 60/090,087
; PRIOR FILING DATE: 1998-06-20
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: peptide derivable from the heavy chain variable region of an anti-DNA monoclonal antibody
US-09-557-465D-4

Query Match 77.5%; Score 69; DB 2; Length 30;
Best Local Similarity 76.5%; Pred. No. 0.0038;
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 YISGGSGTYYSDSVKG 17
Db 3 YISRGGVSTYYSDTVKG 19

RESULT 38
US-09-497-997C-7
; Sequence 7, Application US/09497997C
; Patent No. 6635248
; GENERAL INFORMATION:
; APPLICANT: TERNYNCK, THERESA
```

```
; APPLICANT: AVAMEAS, ALEXANDRE
; APPLICANT: BUTTIN GERARD
; APPLICANT: AVAMEAS, STRAITIS
; APPLICANT: SARON, MARIE-FRANCOISE
; APPLICANT: BLONDEL, BRUNO
; APPLICANT: COUDERC, THERESA
; APPLICANT: MICHELSON, SUSAN
; APPLICANT: ZIPETO, DONATO
; TITLE OF INVENTION: VECTOR DERIVED FROM ANTIBODIES FOR TRANSFERRING SUBSTANCES INTO CELLS
; FILE REFERENCE: 0660-0166-0XCONT
; CURRENT APPLICATION NUMBER: US/09/497,997C
; CURRENT FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: PCT/FR98/01740
; PRIOR FILING DATE: 1998-08-04
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SYNTHETIC PEPTIDE
US-09-497-997C-7

Query Match 77.5%; Score 69; DB 2; Length 30;
Best Local Similarity 76.5%; Pred. No. 0.0038;
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 YISGGSGTYYSDSVKG 17
Db 3 YISRGGVSTYYSDTVKG 19

RESULT 39
US-09-720-003C-5
; Sequence 5, Application US/09720003C
; Patent No. 6740524
; GENERAL INFORMATION:
; APPLICANT: Akuta, Teruo
; APPLICANT: Yokoi, Haruhiko
; APPLICANT: Okuyama, Hajime
; APPLICANT: Takeda, Katsuo
; APPLICANT: Hasegawa, Mamoru
; APPLICANT: Nakanishi, Mahito
; TITLE OF INVENTION: Nucleic Acid Transfer Phage
; FILE REFERENCE: 50026/026001
; CURRENT APPLICATION NUMBER: US/09/720,003C
; CURRENT FILING DATE: 2001-09-04
; PRIOR APPLICATION NUMBER: PCT/JP99/03272
; PRIOR FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: JP 10-189845
; PRIOR FILING DATE: 1998-06-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificially synthesized peptide sequence
US-09-720-003C-5

Query Match 77.5%; Score 69; DB 2; Length 30;
Best Local Similarity 76.5%; Pred. No. 0.0038;
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 YISGGSGTYYSDSVKG 17
Db 3 YISRGGVSTYYSDTVKG 19

RESULT 40
US-10-144-549-21
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US-09-497-997C-23  
: Sequence 23. Application US/09497997C



; LENGTH: 89  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-840-459-49

Query Match 76.4%; Score 68; DB 2; Length 89;  
Best Local Similarity 87.5%; Pred. No. 0.016;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 ISSGGSGTYSDSVKVG 17  
||||| ||| ||| |||  
DB 42 ISSGGSYTYPPDSVKVG 57

RESULT 48  
US-09-497-625A-49  
; Sequence 49, Application US/09497625A  
; Patent No. 6727349  
; GENERAL INFORMATION:  
; APPLICANT: Larosa, Gregory J.  
; APPLICANT: Horvath, Christopher  
; APPLICANT: Newman, Walter  
; APPLICANT: Jones, S. Tarran  
; APPLICANT: O'Brien, Siobhan H.  
; APPLICANT: O'Keefe, Theresa  
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND  
; TITLE OF INVENTION: METHODS OF USE THEREFOR  
; FILE REFERENCE: 1855.1052-004  
; CURRENT APPLICATION NUMBER: US/09/497,625A  
; CURRENT FILING DATE: 2000-02-03  
; PRIOR APPLICATION NUMBER: 09/359,193  
; PRIOR FILING DATE: 1999-07-22  
; PRIOR APPLICATION NUMBER: 09/121,781  
; PRIOR FILING DATE: 1998-07-23  
; NUMBER OF SEQ ID NOS: 106  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 49  
; LENGTH: 89  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-497-625A-49

Query Match 76.4%; Score 68; DB 2; Length 89;  
Best Local Similarity 87.5%; Pred. No. 0.016;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 ISSGGSGTYSDSVKVG 17  
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DB 42 ISSGGSYTYPPDSVKVG 57

RESULT 49  
US-09-840-459-38  
; Sequence 38, Application US/09840459  
; Patent No. 6696550  
; GENERAL INFORMATION:  
; APPLICANT: Larosa, Gregory J.  
; APPLICANT: Horvath, Christopher  
; APPLICANT: Newman, Walter  
; APPLICANT: Jones, S. Tarran  
; APPLICANT: O'Brien, Siobhan H.  
; APPLICANT: O'Keefe, Theresa  
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND  
; TITLE OF INVENTION: METHODS OF USE THEREFOR  
; FILE REFERENCE: 1855.1052-012  
; CURRENT APPLICATION NUMBER: US/09/840,459  
; CURRENT FILING DATE: 2001-02-02  
; PRIOR APPLICATION NUMBER: PCT/US01/03537  
; PRIOR FILING DATE: 2001-02-02  
; PRIOR APPLICATION NUMBER: 09/497,625  
; PRIOR FILING DATE: 2000-02-03  
; PRIOR APPLICATION NUMBER: 09/359,193  
; PRIOR FILING DATE: 1999-07-22

; PRIOR APPLICATION NUMBER: 09/121,781  
; PRIOR FILING DATE: 1998-07-23  
; NUMBER OF SEQ ID NOS: 107  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 38  
; LENGTH: 98  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-840-459-38

Query Match 76.4%; Score 68; DB 2; Length 98;  
Best Local Similarity 87.5%; Pred. No. 0.017;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 ISSGGSGTYSDSVKVG 17  
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DB 51 ISSGGSYTYPPDSVKVG 66

RESULT 50  
US-09-840-459-39  
; Sequence 39, Application US/09840459  
; Patent No. 6696550  
; GENERAL INFORMATION:  
; APPLICANT: Larosa, Gregory J.  
; APPLICANT: Horvath, Christopher  
; APPLICANT: Newman, Walter  
; APPLICANT: Jones, S. Tarran  
; APPLICANT: O'Brien, Siobhan H.  
; APPLICANT: O'Keefe, Theresa  
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND  
; TITLE OF INVENTION: METHODS OF USE THEREFOR  
; FILE REFERENCE: 1855.1052-012  
; CURRENT APPLICATION NUMBER: US/09/840,459  
; CURRENT FILING DATE: 2001-02-02  
; PRIOR APPLICATION NUMBER: PCT/US01/03537  
; PRIOR FILING DATE: 2001-02-02  
; PRIOR APPLICATION NUMBER: 09/497,625  
; PRIOR FILING DATE: 2000-02-03  
; PRIOR APPLICATION NUMBER: 09/359,193  
; PRIOR FILING DATE: 1999-07-22  
; PRIOR APPLICATION NUMBER: 09/121,781  
; PRIOR FILING DATE: 1998-07-23  
; NUMBER OF SEQ ID NOS: 107  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 39  
; LENGTH: 98  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-840-459-39

Query Match 76.4%; Score 68; DB 2; Length 98;  
Best Local Similarity 87.5%; Pred. No. 0.017;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 ISSGGSGTYSDSVKVG 17  
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DB 51 ISSGGSYTYPPDSVKVG 66

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Job time : 25.7627 secs

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OM protein - protein search, using sw model

Run on: April 6, 2006, 09:13:24 ; Search time 137.441 Seconds  
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Title: US-10-089-500-4

Perfect score: 89

Sequence: 1 YISSGSGTYYSDSVKG 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Published Applications AA Main:  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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5	82	92.1	130	4	US-10-265-713-8
6	82	92.1	130	4	US-10-166-626-8
7	74	83.1	240	4	US-10-779-461-23
8	73	82.0	120	4	US-10-383-447-6
9	72	80.9	237	3	US-09-880-748-1906
10	72	80.9	237	3	US-09-880-748-2039
11	72	80.9	237	4	US-10-293-418-1906
12	72	80.9	237	4	US-10-293-418-2039
13	72	80.9	240	3	US-09-880-748-1905
14	72	80.9	240	4	US-10-293-418-1905
15	72	80.9	246	5	US-10-935-290-45
16	71	79.8	249	6	US-11-093-103-86
17	71	79.8	249	6	US-11-093-103-88
18	71	79.8	294	6	US-11-093-103-100
19	71	79.8	325	6	US-11-093-103-92
20	71	79.8	732	6	US-11-093-103-90
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22	70	78.7	121	4	US-10-447-331-4
23	70	78.7	449	6	US-11-056-776-5
24	70	78.7	468	6	US-11-056-776-6
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26	69	77.5	21	4	US-10-460-471-19
27	69	77.5	22	4	US-10-460-471-4

28	69	77.5	22	4	US-10-460-471-20	Sequence 20, Appl
29	69	77.5	30	4	US-10-460-471-7	Sequence 7, Appl
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31	69	77.5	30	4	US-10-368-280-4	Sequence 4, Appl
32	69	77.5	30	4	US-10-374-035-4	Sequence 4, Appl
33	69	77.5	30	5	US-10-694-243-14	Sequence 14, Appl
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35	69	77.5	31	4	US-10-460-471-9	Sequence 9, Appl
36	69	77.5	33	4	US-10-460-471-23	Sequence 23, Appl
37	69	77.5	49	4	US-10-460-471-10	Sequence 10, Appl
38	69	77.5	107	5	US-10-460-471-26	Sequence 26, Appl
39	69	77.5	120	5	US-10-493-668-117	Sequence 117, Appl
40	69	77.5	123	5	US-09-892-613C-2	Sequence 2, Appl
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43	69	77.5	140	4	US-10-006-773A-4	Sequence 4, Appl
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45	68	76.4	17	4	US-10-275-180A-26	Sequence 26, Appl
46	68	76.4	17	4	US-10-286-132A-26	Sequence 26, Appl
47	68	76.4	17	4	US-10-477-377-9	Sequence 9, Appl
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51	68	76.4	87	4	US-10-733-563-53	Sequence 53, Appl
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55	68	76.4	89	3	US-09-840-459-38	Sequence 38, Appl
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57	68	76.4	98	3	US-09-840-459-41	Sequence 41, Appl
58	68	76.4	98	4	US-10-766-773-38	Sequence 38, Appl
59	68	76.4	98	4	US-10-766-773-39	Sequence 39, Appl
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61	68	76.4	98	4	US-10-766-610-38	Sequence 38, Appl
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63	68	76.4	98	4	US-10-766-610-41	Sequence 41, Appl
64	68	76.4	98	4	US-10-733-563-38	Sequence 38, Appl
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67	68	76.4	118	3	US-09-423-800-46	Sequence 46, Appl
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79	68	76.4	118	6	US-11-047-996-88	Sequence 88, Appl
80	68	76.4	118	6	US-11-047-996-90	Sequence 90, Appl
81	68	76.4	119	4	US-10-281-479A-31	Sequence 31, Appl
82	68	76.4	119	4	US-10-281-479A-56	Sequence 56, Appl
83	68	76.4	119	4	US-10-281-479A-59	Sequence 59, Appl
84	68	76.4	119	4	US-10-281-479A-60	Sequence 60, Appl
85	68	76.4	119	4	US-10-281-479A-61	Sequence 61, Appl
86	68	76.4	119	4	US-10-275-180A-31	Sequence 31, Appl
87	68	76.4	119	4	US-10-275-180A-56	Sequence 56, Appl
88	68	76.4	119	4	US-10-275-180A-59	Sequence 59, Appl
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91	68	76.4	119	4	US-10-286-132A-31	Sequence 31, Appl
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93	68	76.4	119	4	US-10-286-132A-59	Sequence 59, Appl
94	68	76.4	119	4	US-10-286-132A-60	Sequence 60, Appl
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96	68	76.4	123	3	US-09-144-886-61	Sequence 61, Appl
97	68	76.4	123	3	US-10-632-706-58	Sequence 58, Appl
98	68	76.4	124	3	US-09-518-737-2	Sequence 2, Appl
99	68	76.4	124	5	US-10-723-748-2	Sequence 2, Appl
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101	68	76.4	134	4	US-10-477-377-3	Sequence 3, Appli	174	66	74.2	237	3	US-09-880-748-2019	Sequence 2019, Ap
102	68	76.4	137	3	US-09-423-800-76	Sequence 76, Appl	175	66	74.2	237	3	US-09-880-748-2020	Sequence 2020, Ap
103	68	76.4	137	3	US-09-423-800-77	Sequence 76, Appl	176	66	74.2	237	3	US-09-880-748-2027	Sequence 2027, Ap
104	68	76.4	137	4	US-10-337-981-76	Sequence 76, Appl	177	66	74.2	237	3	US-09-880-748-2028	Sequence 2028, Ap
105	68	76.4	137	4	US-10-337-981-77	Sequence 76, Appl	178	66	74.2	237	3	US-09-880-748-2036	Sequence 2036, Ap
106	68	76.4	137	6	US-11-047-996-76	Sequence 77, Appl	179	66	74.2	237	3	US-09-880-748-2040	Sequence 2040, Ap
107	68	76.4	137	6	US-11-047-996-77	Sequence 77, Appl	180	66	74.2	237	3	US-09-880-748-2043	Sequence 2043, Ap
108	68	76.4	462	4	US-10-281-479A-23	Sequence 23, Appl	181	66	74.2	237	3	US-09-880-748-2104	Sequence 2104, Ap
109	68	76.4	462	4	US-10-286-132A-23	Sequence 23, Appl	182	66	74.2	237	3	US-09-880-748-2110	Sequence 2110, Ap
110	68	76.4	464	4	US-10-275-180A-23	Sequence 23, Appl	183	66	74.2	237	3	US-09-880-748-2111	Sequence 2111, Ap
111	67	75.3	17	3	US-09-286-240-21	Sequence 21, Appl	184	66	74.2	237	3	US-09-880-748-2112	Sequence 2112, Ap
112	67	75.3	17	4	US-10-327-598-471	Sequence 471, App	185	66	74.2	237	3	US-09-880-748-2115	Sequence 2115, Ap
113	67	75.3	98	3	US-09-840-459-44	Sequence 44, Appl	186	66	74.2	237	3	US-09-880-748-2118	Sequence 2118, Ap
114	67	75.3	98	4	US-10-766-773-44	Sequence 44, Appl	187	66	74.2	237	3	US-09-880-748-2118	Sequence 2118, Ap
115	67	75.3	98	4	US-10-766-610-44	Sequence 44, Appl	188	66	74.2	237	4	US-10-293-418-2003	Sequence 2003, Ap
116	67	75.3	98	4	US-10-733-563-44	Sequence 44, Appl	189	66	74.2	237	4	US-10-293-418-2005	Sequence 2005, Ap
117	67	75.3	117	4	US-10-300-215-244	Sequence 244, App	190	66	74.2	237	4	US-10-293-418-2006	Sequence 2006, Ap
118	67	75.3	117	4	US-10-300-215-246	Sequence 246, App	191	66	74.2	237	4	US-10-293-418-2017	Sequence 2017, Ap
119	67	75.3	117	4	US-10-300-215-248	Sequence 248, App	192	66	74.2	237	4	US-10-293-418-2019	Sequence 2019, Ap
120	67	75.3	117	4	US-10-300-215-250	Sequence 250, App	193	66	74.2	237	4	US-10-293-418-2020	Sequence 2020, Ap
121	67	75.3	140	3	US-09-286-240-4	Sequence 4, Appli	194	66	74.2	237	4	US-10-293-418-2027	Sequence 2027, Ap
122	67	75.3	245	3	US-09-956-086-5	Sequence 5, Appli	195	66	74.2	237	4	US-10-293-418-2028	Sequence 2028, Ap
123	67	75.3	245	3	US-09-956-087-5	Sequence 5, Appli	196	66	74.2	237	4	US-10-293-418-2036	Sequence 2036, Ap
124	67	75.3	246	3	US-09-880-748-1314	Sequence 1314, Ap	197	66	74.2	237	4	US-10-293-418-2040	Sequence 2040, Ap
125	67	75.3	246	4	US-10-293-418-1314	Sequence 1314, Ap	198	66	74.2	237	4	US-10-293-418-2043	Sequence 2043, Ap
126	67	75.3	265	3	US-09-983-580-5	Sequence 5, Appli	199	66	74.2	237	4	US-10-293-418-2104	Sequence 2104, Ap
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128	66	74.2	17	4	US-10-031-874A-116	Sequence 116, App	201	66	74.2	237	4	US-10-293-418-2111	Sequence 2111, Ap
129	66	74.2	17	4	US-10-632-706-177	Sequence 177, App	202	66	74.2	237	4	US-10-293-418-2112	Sequence 2112, Ap
130	66	74.2	17	5	US-10-726-332-79	Sequence 79, Appl	203	66	74.2	237	4	US-10-293-418-2114	Sequence 2114, Ap
131	66	74.2	17	5	US-10-726-332-97	Sequence 97, Appl	204	66	74.2	237	4	US-10-293-418-2115	Sequence 2115, Ap
132	66	74.2	17	5	US-10-893-576-100	Sequence 100, App	205	66	74.2	237	4	US-10-293-418-2118	Sequence 2118, Ap
133	66	74.2	22	5	US-10-778-394-16	Sequence 16, Appl	206	66	74.2	238	3	US-09-880-748-2024	Sequence 2024, Ap
134	66	74.2	98	4	US-10-066-895-4	Sequence 4, Appli	207	66	74.2	238	4	US-10-293-418-2024	Sequence 2024, Ap
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136	66	74.2	98	4	US-10-308-817-57	Sequence 57, Appl	209	66	74.2	239	4	US-10-293-418-2034	Sequence 2034, Ap
137	66	74.2	98	4	US-10-032-037B-63	Sequence 63, Appl	210	66	74.2	240	3	US-09-880-748-2037	Sequence 2037, Ap
138	66	74.2	98	4	US-10-032-037B-79	Sequence 79, Appl	211	66	74.2	240	3	US-09-880-748-2016	Sequence 2016, Ap
139	66	74.2	98	4	US-10-029-988B-63	Sequence 63, Appl	212	66	74.2	240	3	US-09-880-748-2025	Sequence 2025, Ap
140	66	74.2	98	4	US-10-029-988B-79	Sequence 79, Appl	213	66	74.2	240	3	US-09-880-748-2029	Sequence 2029, Ap
141	66	74.2	98	4	US-10-032-423A-63	Sequence 63, Appl	214	66	74.2	240	3	US-09-880-748-2030	Sequence 2030, Ap
142	66	74.2	98	4	US-10-032-423A-79	Sequence 79, Appl	215	66	74.2	240	3	US-09-880-748-2041	Sequence 2041, Ap
143	66	74.2	98	4	US-10-453-698-57	Sequence 57, Appl	216	66	74.2	240	3	US-09-880-748-2044	Sequence 2044, Ap
144	66	74.2	98	4	US-10-029-926B-63	Sequence 63, Appl	217	66	74.2	240	3	US-09-880-748-2045	Sequence 2045, Ap
145	66	74.2	98	4	US-10-029-926B-79	Sequence 79, Appl	218	66	74.2	240	3	US-09-880-748-2048	Sequence 2048, Ap
146	66	74.2	98	4	US-10-038-591-30	Sequence 30, Appl	219	66	74.2	240	3	US-09-880-748-2105	Sequence 2105, Ap
147	66	74.2	98	4	US-10-379-392-16	Sequence 16, Appl	220	66	74.2	240	3	US-09-880-748-2108	Sequence 2108, Ap
148	66	74.2	98	5	US-10-775-444A-30	Sequence 30, Appl	221	66	74.2	240	3	US-09-880-748-2113	Sequence 2113, Ap
149	66	74.2	98	5	US-10-884-830-601	Sequence 601, App	222	66	74.2	240	3	US-09-880-748-2117	Sequence 2117, Ap
150	66	74.2	98	5	US-10-884-830-639	Sequence 639, App	223	66	74.2	240	4	US-10-293-418-2007	Sequence 2007, Ap
151	66	74.2	98	5	US-10-887-954-4	Sequence 4, Appli	224	66	74.2	240	4	US-10-293-418-2016	Sequence 2016, Ap
152	66	74.2	98	5	US-10-461-576-6	Sequence 6, Appli	225	66	74.2	240	4	US-10-293-418-2025	Sequence 2025, Ap
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154	66	74.2	109	5	US-10-727-155-288	Sequence 288, App	227	66	74.2	240	4	US-10-293-418-2030	Sequence 2030, Ap
155	66	74.2	114	5	US-10-938-353-115	Sequence 115, App	228	66	74.2	240	4	US-10-293-418-2041	Sequence 2041, Ap
156	66	74.2	114	6	US-11-136-538-1	Sequence 1, Appli	229	66	74.2	240	4	US-10-293-418-2044	Sequence 2044, Ap
157	66	74.2	115	5	US-10-938-353-108	Sequence 108, App	230	66	74.2	240	4	US-10-293-418-2045	Sequence 2045, Ap
158	66	74.2	115	5	US-10-938-353-116	Sequence 116, App	231	66	74.2	240	4	US-10-293-418-2048	Sequence 2048, Ap
159	66	74.2	117	5	US-10-938-353-106	Sequence 106, App	232	66	74.2	240	4	US-10-293-418-2105	Sequence 2105, Ap
160	66	74.2	120	5	US-10-893-576-186	Sequence 186, App	233	66	74.2	240	4	US-10-293-418-2108	Sequence 2108, Ap
161	66	74.2	122	4	US-10-269-805-7	Sequence 7, Appli	234	66	74.2	240	4	US-10-293-418-2113	Sequence 2113, Ap
162	66	74.2	122	4	US-10-269-805-11	Sequence 11, Appl	235	66	74.2	240	4	US-10-293-418-2117	Sequence 2117, Ap
163	66	74.2	122	4	US-10-269-805-53	Sequence 53, Appl	236	66	74.2	240	6	US-11-090-847-88	Sequence 88, Appl
164	66	74.2	122	5	US-10-888-959-5	Sequence 5, Appli	237	66	74.2	245	5	US-10-778-394-73	Sequence 73, Appl
165	66	74.2	131	3	US-09-988-115A-53	Sequence 53, Appl	238	66	74.2	248	3	US-09-880-748-1965	Sequence 1965, Ap
166	66	74.2	131	5	US-10-705-519-53	Sequence 53, Appl	239	66	74.2	248	3	US-09-880-748-1974	Sequence 1974, Ap
167	66	74.2	141	6	US-10-893-576-25	Sequence 25, Appl	240	66	74.2	248	4	US-10-293-418-1965	Sequence 1965, Ap
168	66	74.2	236	3	US-09-880-748-2010	Sequence 2010, Ap	241	66	74.2	248	4	US-10-293-418-1974	Sequence 1974, Ap
169	66	74.2	236	4	US-10-293-418-2010	Sequence 2010, Ap	242	66	74.2	250	3	US-09-880-748-1179	Sequence 1179, Ap
170	66	74.2	237	3	US-09-880-748-2003	Sequence 2003, Ap	243	66	74.2	250	3	US-09-880-748-1179	Sequence 1179, Ap
171	66	74.2	237	3	US-09-880-748-2005	Sequence 2005, Ap	244	66	74.2	250	3	US-09-880-748-1179	Sequence 1179, Ap
172	66	74.2	237	3	US-09-880-748-2006	Sequence 2006, Ap	245	66	74.2	444	4	US-10-150-475A-6	Sequence 6, Appli
173	66	74.2	237	3	US-09-880-748-2017	Sequence 2017, Ap	246	66	74.2	444	4	US-10-704-522-6	Sequence 6, Appli
												US-10-645-215-6	Sequence 6, Appli

247	66	74.2	444	6	US-11-136-538-7	Sequence 7, Appli	320	64	71.9	17	4	US-10-632-706-141	Sequence 141, App
248	66	74.2	460	5	US-10-938-353-14	Sequence 14, Appl	321	64	71.9	17	4	US-10-632-706-145	Sequence 145, App
249	66	74.2	460	5	US-10-938-353-26	Sequence 26, Appl	322	64	71.9	17	4	US-10-632-706-149	Sequence 149, App
250	66	74.2	460	5	US-10-938-353-74	Sequence 74, Appl	323	64	71.9	17	4	US-10-632-706-153	Sequence 153, App
251	66	74.2	461	5	US-10-938-353-34	Sequence 34, Appl	324	64	71.9	17	4	US-10-632-706-157	Sequence 157, App
252	66	74.2	461	5	US-10-938-353-38	Sequence 38, Appl	325	64	71.9	98	3	US-09-840-459-45	Sequence 45, Appl
253	66	74.2	461	5	US-10-938-353-54	Sequence 54, Appl	326	64	71.9	98	4	US-10-766-773-45	Sequence 45, Appl
254	66	74.2	461	5	US-10-938-353-66	Sequence 66, Appl	327	64	71.9	98	4	US-10-766-610-45	Sequence 45, Appl
255	66	74.2	461	5	US-10-938-353-70	Sequence 70, Appl	328	64	71.9	98	4	US-10-733-563-45	Sequence 45, Appl
256	66	74.2	461	5	US-10-938-353-78	Sequence 78, Appl	329	64	71.9	117	5	US-10-492-228-15	Sequence 15, Appl
257	66	74.2	461	5	US-10-938-353-82	Sequence 82, Appl	330	64	71.9	117	5	US-10-492-228-19	Sequence 19, Appl
258	66	74.2	462	5	US-10-938-353-46	Sequence 46, Appl	331	64	71.9	118	3	US-09-144-886-62	Sequence 62, Appl
259	66	74.2	462	5	US-10-938-353-50	Sequence 50, Appl	332	64	71.9	118	3	US-09-144-886-63	Sequence 63, Appl
260	66	74.2	462	5	US-10-938-353-86	Sequence 86, Appl	333	64	71.9	118	4	US-10-632-706-59	Sequence 59, Appl
261	66	74.2	464	5	US-10-938-353-102	Sequence 102, App	334	64	71.9	118	4	US-10-632-706-60	Sequence 60, Appl
262	66	74.2	473	4	US-10-038-591-50	Sequence 50, Appl	335	64	71.9	120	4	US-10-229-335-1	Sequence 1, Appl
263	66	74.2	473	4	US-10-775-444A-50	Sequence 50, Appl	336	64	71.9	120	4	US-10-229-335-2	Sequence 2, Appl
264	66	74.2	473	5	US-10-917-073A-4	Sequence 4, Appli	337	64	71.9	120	4	US-10-229-335-3	Sequence 3, Appl
265	65	73.0	17	4	US-10-384-060-55	Sequence 55, Appl	338	64	71.9	120	4	US-10-412-406-2	Sequence 2, Appl
266	65	73.0	17	4	US-10-436-782-39	Sequence 39, Appl	339	64	71.9	120	4	US-10-412-406-10	Sequence 10, Appl
267	65	73.0	17	4	US-10-436-782-7	Sequence 7, Appli	340	64	71.9	120	4	US-10-412-406-12	Sequence 12, Appl
268	65	73.0	17	4	US-10-470-045-50	Sequence 50, Appl	341	64	71.9	120	4	US-10-412-406-14	Sequence 14, Appl
269	65	73.0	17	4	US-10-327-598-472	Sequence 472, App	342	64	71.9	120	4	US-10-412-406-16	Sequence 16, Appl
270	65	73.0	17	4	US-10-327-598-481	Sequence 481, App	343	64	71.9	120	4	US-10-291-265-333	Sequence 333, App
271	65	73.0	17	5	US-10-994-129-7	Sequence 7, Appli	344	64	71.9	249	5	US-10-492-228-12	Sequence 12, Appl
272	65	73.0	17	6	US-11-004-795A-39	Sequence 39, Appl	345	64	71.9	249	5	US-10-492-228-71	Sequence 71, Appl
273	65	73.0	17	6	US-11-004-794A-39	Sequence 39, Appl	346	64	71.9	352	3	US-09-203-958A-2	Sequence 2, Appl
274	65	73.0	115	4	US-10-436-782-37	Sequence 37, Appl	347	64	71.9	352	5	US-10-764-131-2	Sequence 2, Appl
275	65	73.0	115	4	US-10-436-783-5	Sequence 5, Appli	348	64	71.9	444	5	US-10-492-228-57	Sequence 57, Appl
276	65	73.0	115	5	US-10-994-129-5	Sequence 5, Appli	349	64	71.9	495	4	US-10-108-260A-4114	Sequence 4114, Ap
277	65	73.0	115	6	US-11-004-795A-37	Sequence 37, Appl	350	64	71.9	663	4	US-10-412-406-32	Sequence 32, Appl
278	65	73.0	120	4	US-10-258-728-18	Sequence 18, Appl	351	63	70.8	4852	4	US-10-412-406-33	Sequence 33, Appl
279	65	73.0	120	4	US-10-258-728-19	Sequence 19, Appl	352	63	70.8	17	4	US-10-226-795-34	Sequence 34, Appl
280	65	73.0	120	4	US-10-258-728-20	Sequence 20, Appl	353	63	70.8	17	4	US-10-128-520-358	Sequence 358, App
281	65	73.0	120	4	US-10-258-728-21	Sequence 21, Appl	354	63	70.8	17	4	US-10-844-424-72	Sequence 72, Appl
282	65	73.0	120	4	US-10-258-728-22	Sequence 22, Appl	355	63	70.8	17	4	US-10-844-424-88	Sequence 88, Appl
283	65	73.0	120	4	US-10-258-728-22	Sequence 22, Appl	356	63	70.8	17	5	US-10-505-313-164	Sequence 164, App
284	65	73.0	121	4	US-10-300-215-90	Sequence 90, Appl	357	63	70.8	17	5	US-10-505-313-205	Sequence 205, App
285	65	73.0	121	4	US-10-300-215-92	Sequence 92, Appl	358	63	70.8	89	3	US-09-840-459-50	Sequence 50, Appl
286	65	73.0	121	4	US-10-300-215-113	Sequence 113, App	359	63	70.8	89	4	US-10-766-773-50	Sequence 50, Appl
287	65	73.0	121	4	US-10-300-215-125	Sequence 125, App	360	63	70.8	89	4	US-10-766-610-50	Sequence 50, Appl
288	65	73.0	121	4	US-10-300-215-126	Sequence 126, App	361	63	70.8	89	4	US-10-733-563-50	Sequence 50, Appl
289	65	73.0	121	4	US-10-300-215-133	Sequence 133, App	362	63	70.8	89	4	US-10-032-037B-72	Sequence 72, Appl
290	65	73.0	121	4	US-10-309-762-130	Sequence 130, App	363	63	70.8	98	4	US-10-029-988B-72	Sequence 72, Appl
291	65	73.0	121	4	US-10-258-728-3	Sequence 3, Appli	364	63	70.8	98	4	US-10-032-423A-72	Sequence 72, Appl
292	65	73.0	122	4	US-10-016-986-80	Sequence 80, Appl	365	63	70.8	98	4	US-10-029-926B-72	Sequence 72, Appl
293	65	73.0	125	3	US-09-910-358D-4	Sequence 4, Appli	366	63	70.8	98	5	US-10-884-830-620	Sequence 620, App
294	65	73.0	125	3	US-09-910-358D-8	Sequence 8, Appli	367	63	70.8	98	5	US-10-884-830-621	Sequence 621, App
295	65	73.0	127	4	US-10-154-971-8	Sequence 8, Appli	368	63	70.8	98	5	US-10-884-830-633	Sequence 633, App
296	65	73.0	127	4	US-10-154-971-16	Sequence 16, Appl	369	63	70.8	98	5	US-10-884-830-634	Sequence 634, App
297	65	73.0	127	5	US-10-638-723A-17	Sequence 17, Appl	370	63	70.8	111	3	US-09-899-896-7	Sequence 7, Appli
298	65	73.0	143	4	US-10-469-304-17	Sequence 17, Appl	371	63	70.8	121	4	US-10-371-942-38	Sequence 38, Appl
299	65	73.0	144	3	US-09-881-823-12	Sequence 12, Appl	372	63	70.8	121	4	US-10-844-424-26	Sequence 26, Appl
300	65	73.0	155	4	US-10-077-624-7	Sequence 7, Appli	373	63	70.8	125	5	US-10-492-668-153	Sequence 153, App
301	65	73.0	155	4	US-10-706-391-4	Sequence 4, Appli	374	63	70.8	126	5	US-10-451-585A-92	Sequence 92, Appl
302	65	73.0	165	4	US-10-077-624-4	Sequence 4, Appli	375	63	70.8	130	5	US-10-683-451-21	Sequence 21, Appl
303	65	73.0	165	4	US-10-706-391-2	Sequence 2, Appli	376	63	70.8	131	4	US-10-148-737-3	Sequence 3, Appli
304	65	73.0	182	4	US-10-309-762-246	Sequence 246, App	377	63	70.8	131	6	US-11-054-041-3	Sequence 3, Appli
305	65	73.0	217	4	US-10-698-041-5	Sequence 5, Appli	378	63	70.8	132	5	US-10-451-585A-86	Sequence 86, Appl
306	65	73.0	247	3	US-09-880-748-1652	Sequence 1652, Ap	379	63	70.8	132	5	US-10-451-585A-87	Sequence 87, Appl
307	65	73.0	247	4	US-10-293-418-1852	Sequence 1852, Ap	380	63	70.8	132	5	US-10-451-585A-88	Sequence 88, Appl
308	65	73.0	249	6	US-11-093-103-84	Sequence 84, Appli	381	63	70.8	132	5	US-10-451-585A-89	Sequence 89, Appl
309	65	73.0	256	3	US-09-880-748-2119	Sequence 2119, Ap	382	63	70.8	132	5	US-10-451-585A-90	Sequence 90, Appl
310	65	73.0	256	4	US-10-293-418-2119	Sequence 2119, Ap	383	63	70.8	132	5	US-10-451-585A-91	Sequence 91, Appl
311	65	73.0	384	4	US-10-291-265-804	Sequence 804, App	384	63	70.8	158	4	US-10-226-795-32	Sequence 32, Appl
312	65	73.0	384	4	US-10-291-265-805	Sequence 805, App	385	63	70.8	183	3	US-10-124-903-2	Sequence 2, Appli
313	65	73.0	384	4	US-10-291-265-806	Sequence 806, App	386	63	70.8	243	3	US-09-880-748-1929	Sequence 1929, Ap
314	65	73.0	384	4	US-10-291-265-807	Sequence 807, App	387	63	70.8	243	3	US-09-880-748-1942	Sequence 1942, Ap
315	65	73.0	702	6	US-11-035-599-52	Sequence 52, Appl	388	63	70.8	243	3	US-09-880-748-1944	Sequence 1944, Ap
316	65	73.0	702	6	US-11-035-599-53	Sequence 53, Appl	389	63	70.8	243	3	US-09-880-748-1945	Sequence 1945, Ap
317	65	73.0	731	6	US-11-035-599-51	Sequence 51, Appl	390	63	70.8	243	4	US-10-293-418-1929	Sequence 1929, Ap
318	65	73.0	734	6	US-11-035-599-50	Sequence 50, Appl	391	63	70.8	243	4	US-10-293-418-1942	Sequence 1942, Ap
319	64	71.9	17	3	US-09-977-797A-106	Sequence 106, App	392	63	70.8	243	4	US-10-293-418-1944	Sequence 1944, Ap

393	63	70.8	243	4	US-10-293-418-1945	Sequence 1945, Ap	466	61	68.5	639	5	US-10-792-498-17	Sequence 17, Appl
394	63	70.8	254	3	US-09-880-748-1295	Sequence 1295, Ap	467	60.5	68.0	88	3	US-09-840-459-51	Sequence 51, Appl
395	63	70.8	254	4	US-10-293-418-1295	Sequence 1295, Ap	468	60.5	68.0	88	4	US-10-766-773-51	Sequence 51, Appl
396	63	70.8	268	3	US-09-976-118-1	Sequence 1, Appl	469	60.5	68.0	88	4	US-10-766-610-51	Sequence 51, Appl
397	63	70.8	268	4	US-10-703-277-1	Sequence 1, Appl	470	60.5	68.0	88	4	US-10-733-563-51	Sequence 51, Appl
398	63	70.8	686	4	US-10-072-012-795	Sequence 795, Appl	471	60.5	68.0	119	5	US-10-815-449-1	Sequence 1, Appl
399	62	69.7	17	4	US-10-031-874A-112	Sequence 112, Appl	472	60.5	68.0	119	5	US-10-815-449-3	Sequence 3, Appl
400	62	69.7	17	4	US-10-276-939-9	Sequence 9, Appl	473	60.5	68.0	119	5	US-10-815-449-5	Sequence 5, Appl
401	62	69.7	17	5	US-10-726-332-52	Sequence 52, Appl	474	60.5	68.0	122	4	US-10-806-419-20	Sequence 20, Appl
402	62	69.7	17	5	US-10-476-265-5	Sequence 5, Appl	475	60	67.4	17	4	US-10-031-874A-103	Sequence 103, Appl
403	62	69.7	17	5	US-10-492-228-2	Sequence 2, Appl	476	60	67.4	17	5	US-10-798-380-141	Sequence 141, Appl
404	62	69.7	117	5	US-10-492-228-7	Sequence 7, Appl	477	60	67.4	17	5	US-10-783-311-100	Sequence 100, Appl
405	62	69.7	117	5	US-10-492-228-17	Sequence 17, Appl	478	60	67.4	17	5	US-10-783-311-212	Sequence 212, Appl
406	62	69.7	117	5	US-10-492-228-18	Sequence 18, Appl	479	60	67.4	98	4	US-10-194-975-28	Sequence 28, Appl
407	62	69.7	119	5	US-10-476-265-8	Sequence 8, Appl	480	60	67.4	98	4	US-10-308-817-68	Sequence 68, Appl
408	62	69.7	119	5	US-10-476-265-10	Sequence 10, Appl	481	60	67.4	98	4	US-10-032-037B-82	Sequence 82, Appl
409	62	69.7	120	4	US-10-628-109-230	Sequence 230, Appl	482	60	67.4	98	4	US-10-029-988B-82	Sequence 82, Appl
410	62	69.7	120	5	US-10-835-641-4	Sequence 4, Appl	483	60	67.4	98	4	US-10-032-423A-82	Sequence 82, Appl
411	62	69.7	120	5	US-10-014-012-230	Sequence 230, Appl	484	60	67.4	98	4	US-10-453-698-68	Sequence 68, Appl
412	62	69.7	121	4	US-10-276-939-3	Sequence 3, Appl	485	60	67.4	98	4	US-10-029-926B-82	Sequence 82, Appl
413	62	69.7	124	4	US-10-251-085B-104	Sequence 104, Appl	486	60	67.4	98	4	US-10-379-392-31	Sequence 31, Appl
414	62	69.7	124	4	US-10-251-085B-105	Sequence 105, Appl	487	60	67.4	98	5	US-10-884-830-656	Sequence 656, Appl
415	62	69.7	124	4	US-10-737-252-104	Sequence 104, Appl	488	60	67.4	98	5	US-10-884-830-660	Sequence 660, Appl
416	62	69.7	124	4	US-10-737-252-105	Sequence 105, Appl	489	60	67.4	109	5	US-10-727-155-296	Sequence 296, Appl
417	62	69.7	133	4	US-10-006-773-9	Sequence 9, Appl	490	60	67.4	114	4	US-10-309-762-145	Sequence 145, Appl
418	62	69.7	138	4	US-10-010-942B-8	Sequence 8, Appl	491	60	67.4	114	5	US-10-805-177-59	Sequence 59, Appl
419	62	69.7	138	4	US-10-010-942B-8	Sequence 8, Appl	492	60	67.4	114	5	US-10-938-353-113	Sequence 113, Appl
420	62	69.7	138	4	US-10-010-942B-12	Sequence 12, Appl	493	60	67.4	118	3	US-09-144-886-64	Sequence 64, Appl
421	62	69.7	138	4	US-10-388-389-4	Sequence 4, Appl	494	60	67.4	118	3	US-09-144-886-65	Sequence 65, Appl
422	62	69.7	138	4	US-10-388-389-8	Sequence 8, Appl	495	60	67.4	118	3	US-09-144-886-66	Sequence 66, Appl
423	62	69.7	138	4	US-10-388-389-12	Sequence 12, Appl	496	60	67.4	118	3	US-09-144-886-67	Sequence 67, Appl
424	62	69.7	138	4	US-10-703-713-4	Sequence 4, Appl	497	60	67.4	118	4	US-10-632-706-61	Sequence 61, Appl
425	62	69.7	138	4	US-10-703-713-8	Sequence 8, Appl	498	60	67.4	118	4	US-10-632-706-62	Sequence 62, Appl
426	62	69.7	138	4	US-10-703-713-12	Sequence 12, Appl	499	60	67.4	118	4	US-10-632-706-63	Sequence 63, Appl
427	62	69.7	138	4	US-10-704-070-4	Sequence 4, Appl	500	60	67.4	118	4	US-10-632-706-64	Sequence 64, Appl
428	62	69.7	138	4	US-10-704-070-8	Sequence 8, Appl	501	60	67.4	119	4	US-10-309-762-146	Sequence 146, Appl
429	62	69.7	138	4	US-10-704-070-12	Sequence 12, Appl	502	60	67.4	119	4	US-10-309-762-146	Sequence 146, Appl
430	62	69.7	138	5	US-10-232-030-4	Sequence 4, Appl	503	60	67.4	121	5	US-10-798-380-137	Sequence 137, Appl
431	62	69.7	138	5	US-10-232-030-8	Sequence 8, Appl	504	60	67.4	121	5	US-10-798-380-137	Sequence 137, Appl
432	62	69.7	138	5	US-10-232-030-12	Sequence 12, Appl	505	60	67.4	124	4	US-10-308-817-190	Sequence 190, Appl
433	62	69.7	142	5	US-10-492-228-58	Sequence 58, Appl	506	60	67.4	124	4	US-10-453-698-190	Sequence 190, Appl
434	62	69.7	241	6	US-11-090-847-50	Sequence 50, Appl	507	60	67.4	126	5	US-10-492-668-150	Sequence 150, Appl
435	62	69.7	256	3	US-09-880-748-1604	Sequence 1604, Ap	508	60	67.4	130	4	US-10-118-100-51	Sequence 51, Appl
436	62	69.7	256	4	US-10-293-418-1604	Sequence 1604, Ap	509	60	67.4	132	5	US-10-783-311-95	Sequence 95, Appl
437	62	69.7	367	4	US-10-291-265-899	Sequence 899, Appl	510	60	67.4	132	5	US-10-783-311-207	Sequence 207, Appl
438	62	69.7	449	5	US-10-476-265-12	Sequence 12, Appl	511	60	67.4	136	5	US-10-910-901-24	Sequence 24, Appl
439	62	69.7	461	5	US-10-938-353-2	Sequence 2, Appl	512	60	67.4	138	4	US-10-309-764-127	Sequence 127, Appl
440	62	69.7	468	5	US-10-476-265-20	Sequence 20, Appl	513	60	67.4	171	4	US-10-309-762-169	Sequence 169, Appl
441	61	68.5	16	4	US-10-031-874A-166	Sequence 166, Appl	514	60	67.4	243	3	US-09-880-748-2102	Sequence 2102, Ap
442	61	68.5	17	4	US-10-031-874A-105	Sequence 105, Appl	515	60	67.4	243	4	US-10-293-418-2102	Sequence 2102, Ap
443	61	68.5	17	5	US-10-726-332-70	Sequence 70, Appl	516	60	67.4	244	5	US-10-610-452-16	Sequence 16, Appl
444	61	68.5	17	5	US-10-496-869-7	Sequence 7, Appl	517	60	67.4	244	5	US-10-610-452-16	Sequence 16, Appl
445	61	68.5	32	3	US-09-956-206A-35	Sequence 35, Appl	518	60	67.4	247	3	US-09-880-748-1953	Sequence 1953, Ap
446	61	68.5	32	5	US-10-965-616-35	Sequence 35, Appl	519	60	67.4	247	4	US-10-293-418-1953	Sequence 1953, Ap
447	61	68.5	116	5	US-10-727-155-84	Sequence 84, Appl	520	60	67.4	247	5	US-10-798-380-139	Sequence 139, Appl
448	61	68.5	116	5	US-10-727-155-140	Sequence 140, Appl	521	60	67.4	248	6	US-11-090-847-60	Sequence 60, Appl
449	61	68.5	116	5	US-10-727-155-148	Sequence 148, Appl	522	60	67.4	248	6	US-11-090-847-60	Sequence 60, Appl
450	61	68.5	121	5	US-10-915-490-18	Sequence 18, Appl	523	59.5	66.9	295	4	US-10-406-830-21	Sequence 21, Appl
451	61	68.5	121	5	US-10-496-869-30	Sequence 30, Appl	524	59	66.3	312	4	US-10-291-255-334	Sequence 334, Appl
452	61	68.5	123	3	US-09-144-886-60	Sequence 60, Appl	525	59	66.3	17	3	US-09-968-561A-14	Sequence 14, Appl
453	61	68.5	123	4	US-10-632-706-57	Sequence 57, Appl	526	59	66.3	17	3	US-09-968-561A-38	Sequence 38, Appl
454	61	68.5	124	5	US-10-733-532-130	Sequence 130, Appl	527	59	66.3	17	3	US-09-968-561A-68	Sequence 68, Appl
455	61	68.5	124	5	US-10-492-668-157	Sequence 157, Appl	528	59	66.3	17	3	US-09-968-561A-74	Sequence 74, Appl
456	61	68.5	125	4	US-10-251-085B-161	Sequence 161, Appl	529	59	66.3	17	3	US-09-968-561A-80	Sequence 80, Appl
457	61	68.5	125	4	US-10-737-252-161	Sequence 161, Appl	530	59	66.3	17	3	US-09-968-561A-86	Sequence 86, Appl
458	61	68.5	126	4	US-10-353-721-7	Sequence 7, Appl	531	59	66.3	17	3	US-09-968-561A-92	Sequence 92, Appl
459	61	68.5	130	5	US-10-885-492-5	Sequence 5, Appl	532	59	66.3	17	3	US-09-968-561A-122	Sequence 122, Appl
460	61	68.5	147	4	US-10-353-721-10	Sequence 10, Appl	533	59	66.3	17	3	US-09-968-561A-128	Sequence 128, Appl
461	61	68.5	250	6	US-11-090-847-75	Sequence 75, Appl	534	59	66.3	17	3	US-09-968-561A-134	Sequence 134, Appl
462	61	68.5	409	4	US-10-353-721-14	Sequence 14, Appl	535	59	66.3	17	3	US-09-968-561A-140	Sequence 140, Appl
463	61	68.5	456	4	US-10-634-862-11	Sequence 11, Appl	536	59	66.3	17	3	US-09-968-561A-146	Sequence 146, Appl
464	61	68.5	472	5	US-10-072-012-796	Sequence 796, Appl	537	59	66.3	17	3	US-09-968-561A-188	Sequence 188, Appl
465	61	68.5	639	5	US-10-792-498-16	Sequence 16, Appl	538	59	66.3	17	3	US-09-968-561A-194	Sequence 194, Appl



539	59	66.3	17	3	US-09-968-561A-212	Sequence 212, App	612	59	66.3	17	5	US-10-891-972-56	Sequence 56, Appl
540	59	66.3	17	3	US-09-968-561A-218	Sequence 218, App	613	59	66.3	17	5	US-10-891-972-142	Sequence 142, App
541	59	66.3	17	3	US-09-968-561A-236	Sequence 236, App	614	59	66.3	17	5	US-10-891-972-148	Sequence 148, App
542	59	66.3	17	3	US-09-968-561A-260	Sequence 260, App	615	59	66.3	17	5	US-10-891-972-154	Sequence 154, App
543	59	66.3	17	3	US-09-968-561A-266	Sequence 266, App	616	59	66.3	17	5	US-10-505-313-100	Sequence 100, App
544	59	66.3	17	3	US-09-968-561A-272	Sequence 272, App	617	59	66.3	17	5	US-10-505-313-147	Sequence 147, App
545	59	66.3	17	3	US-09-968-561A-284	Sequence 284, App	618	59	66.3	17	5	US-10-505-313-215	Sequence 215, App
546	59	66.3	17	3	US-09-968-561A-296	Sequence 296, App	619	59	66.3	17	6	US-11-074-803-57	Sequence 57, Appl
547	59	66.3	17	3	US-09-968-561A-308	Sequence 308, App	620	59	66.3	17	6	US-11-074-803-63	Sequence 63, Appl
548	59	66.3	17	3	US-09-968-561A-314	Sequence 314, App	621	59	66.3	17	6	US-11-115-682-14	Sequence 14, Appl
549	59	66.3	17	3	US-09-977-797A-94	Sequence 94, Appl	622	59	66.3	17	6	US-11-115-682-38	Sequence 38, Appl
550	59	66.3	17	3	US-09-972-656-45	Sequence 45, Appl	623	59	66.3	17	6	US-11-115-682-68	Sequence 68, Appl
551	59	66.3	17	3	US-09-968-744A-14	Sequence 14, Appl	624	59	66.3	17	6	US-11-115-682-74	Sequence 74, Appl
552	59	66.3	17	3	US-09-968-744A-38	Sequence 38, Appl	625	59	66.3	17	6	US-11-115-682-80	Sequence 80, Appl
553	59	66.3	17	3	US-09-968-744A-68	Sequence 68, Appl	626	59	66.3	17	6	US-11-115-682-86	Sequence 86, Appl
554	59	66.3	17	3	US-09-968-744A-74	Sequence 74, Appl	627	59	66.3	17	6	US-11-115-682-92	Sequence 92, Appl
555	59	66.3	17	3	US-09-968-744A-80	Sequence 80, Appl	628	59	66.3	17	6	US-11-115-682-122	Sequence 122, App
556	59	66.3	17	3	US-09-968-744A-86	Sequence 86, Appl	629	59	66.3	17	6	US-11-115-682-138	Sequence 138, App
557	59	66.3	17	3	US-09-968-744A-92	Sequence 92, Appl	630	59	66.3	17	6	US-11-115-682-194	Sequence 194, App
558	59	66.3	17	3	US-09-968-744A-122	Sequence 122, App	631	59	66.3	17	6	US-11-115-682-140	Sequence 140, App
559	59	66.3	17	3	US-09-968-744A-128	Sequence 128, App	632	59	66.3	17	6	US-11-115-682-146	Sequence 146, App
560	59	66.3	17	3	US-09-968-744A-134	Sequence 134, App	633	59	66.3	17	6	US-11-115-682-188	Sequence 188, App
561	59	66.3	17	3	US-09-968-744A-140	Sequence 140, App	634	59	66.3	17	6	US-11-115-682-212	Sequence 212, App
562	59	66.3	17	3	US-09-968-744A-146	Sequence 146, App	635	59	66.3	17	6	US-11-115-682-218	Sequence 218, App
563	59	66.3	17	3	US-09-968-744A-158	Sequence 158, App	636	59	66.3	17	6	US-11-115-682-236	Sequence 236, App
564	59	66.3	17	3	US-09-968-744A-184	Sequence 184, App	637	59	66.3	17	6	US-11-115-682-260	Sequence 260, App
565	59	66.3	17	3	US-09-968-744A-212	Sequence 212, App	638	59	66.3	17	6	US-11-115-682-286	Sequence 286, App
566	59	66.3	17	3	US-09-968-744A-218	Sequence 218, App	639	59	66.3	17	6	US-11-115-682-272	Sequence 272, App
567	59	66.3	17	3	US-09-968-744A-236	Sequence 236, App	640	59	66.3	17	6	US-11-115-682-284	Sequence 284, App
568	59	66.3	17	3	US-09-968-744A-260	Sequence 260, App	641	59	66.3	17	6	US-11-115-682-296	Sequence 296, App
569	59	66.3	17	3	US-09-968-744A-266	Sequence 266, App	642	59	66.3	17	6	US-11-115-682-308	Sequence 308, App
570	59	66.3	17	3	US-09-968-744A-272	Sequence 272, App	643	59	66.3	17	6	US-11-115-682-314	Sequence 314, App
571	59	66.3	17	3	US-09-968-744A-284	Sequence 284, App	644	59	66.3	17	6	US-10-387-955-62	Sequence 62, Appl
572	59	66.3	17	3	US-09-968-744A-296	Sequence 296, App	645	59	66.3	19	4	US-10-387-955-68	Sequence 68, Appl
573	59	66.3	17	3	US-09-968-744A-308	Sequence 308, App	646	59	66.3	19	4	US-10-387-955-68	Sequence 68, Appl
574	59	66.3	17	3	US-09-968-744A-314	Sequence 314, App	647	59	66.3	21	5	US-10-492-228-61	Sequence 61, Appl
575	59	66.3	17	3	US-09-791-551-88	Sequence 88, Appl	648	59	66.3	98	3	US-09-823-698A-18	Sequence 18, Appl
576	59	66.3	17	3	US-09-968-561A-14	Sequence 14, Appl	649	59	66.3	98	4	US-10-194-975-22	Sequence 22, Appl
577	59	66.3	17	3	US-09-968-561A-38	Sequence 38, Appl	650	59	66.3	98	4	US-10-194-975-30	Sequence 30, Appl
578	59	66.3	17	3	US-09-968-561A-68	Sequence 68, Appl	651	59	66.3	98	4	US-10-125-687-19	Sequence 19, Appl
579	59	66.3	17	3	US-09-968-561A-74	Sequence 74, Appl	652	59	66.3	98	4	US-10-010-942B-10	Sequence 10, Appl
580	59	66.3	17	3	US-09-968-561A-80	Sequence 80, Appl	653	59	66.3	98	4	US-10-308-817-62	Sequence 62, Appl
581	59	66.3	17	3	US-09-968-561A-86	Sequence 86, Appl	654	59	66.3	98	4	US-10-032-037B-77	Sequence 77, Appl
582	59	66.3	17	3	US-09-968-561A-92	Sequence 92, Appl	655	59	66.3	98	4	US-10-029-988B-77	Sequence 77, Appl
583	59	66.3	17	3	US-09-968-561A-122	Sequence 122, App	656	59	66.3	98	4	US-10-032-43A-77	Sequence 77, Appl
584	59	66.3	17	3	US-09-968-561A-128	Sequence 128, App	657	59	66.3	98	4	US-10-453-698-62	Sequence 62, Appl
585	59	66.3	17	3	US-09-968-561A-134	Sequence 134, App	658	59	66.3	98	4	US-10-029-926B-77	Sequence 77, Appl
586	59	66.3	17	3	US-09-968-561A-140	Sequence 140, App	659	59	66.3	98	4	US-10-038-591-32	Sequence 32, Appl
587	59	66.3	17	3	US-09-968-561A-146	Sequence 146, App	660	59	66.3	98	4	US-10-388-389-10	Sequence 10, Appl
588	59	66.3	17	3	US-09-968-561A-188	Sequence 188, App	661	59	66.3	98	4	US-10-379-392-23	Sequence 23, Appl
589	59	66.3	17	3	US-09-968-561A-194	Sequence 194, App	662	59	66.3	98	4	US-10-703-713-10	Sequence 10, Appl
590	59	66.3	17	3	US-09-968-561A-212	Sequence 212, App	663	59	66.3	98	4	US-10-704-070-10	Sequence 10, Appl
591	59	66.3	17	3	US-09-968-561A-218	Sequence 218, App	664	59	66.3	98	4	US-10-775-444A-32	Sequence 32, Appl
592	59	66.3	17	3	US-09-968-561A-236	Sequence 236, App	665	59	66.3	98	5	US-10-884-830-619	Sequence 619, App
593	59	66.3	17	3	US-09-968-561A-260	Sequence 260, App	666	59	66.3	98	5	US-10-232-030-10	Sequence 10, Appl
594	59	66.3	17	3	US-09-968-561A-266	Sequence 266, App	667	59	66.3	98	5	US-10-863-355-12	Sequence 12, Appl
595	59	66.3	17	3	US-09-968-561A-272	Sequence 272, App	668	59	66.3	98	5	US-10-492-668-158	Sequence 158, App
596	59	66.3	17	3	US-09-968-561A-284	Sequence 284, App	669	59	66.3	98	5	US-10-911-838-20	Sequence 20, Appl
597	59	66.3	17	3	US-09-968-561A-296	Sequence 296, App	670	59	66.3	98	5	US-10-996-191-19	Sequence 19, Appl
598	59	66.3	17	3	US-09-968-561A-308	Sequence 308, App	671	59	66.3	98	5	US-10-831-459-48	Sequence 48, Appl
599	59	66.3	17	3	US-09-968-561A-314	Sequence 314, App	672	59	66.3	109	4	US-10-309-784-17	Sequence 17, Appl
600	59	66.3	17	4	US-10-305-231-104	Sequence 104, App	673	59	66.3	109	4	US-10-779-461-154	Sequence 154, App
601	59	66.3	17	4	US-10-401-344-10	Sequence 10, Appl	674	59	66.3	109	4	US-10-800-197-149	Sequence 149, App
602	59	66.3	17	4	US-10-128-520-357	Sequence 357, App	675	59	66.3	109	5	US-10-727-155-279	Sequence 279, App
603	59	66.3	17	4	US-10-688-925-44	Sequence 44, Appl	676	59	66.3	109	5	US-10-877-773-8	Sequence 8, Appl
604	59	66.3	17	4	US-10-327-598-476	Sequence 476, App	677	59	66.3	109	5	US-10-877-774-8	Sequence 8, Appl
605	59	66.3	17	4	US-10-396-578-57	Sequence 57, Appl	678	59	66.3	115	4	US-10-447-331-5	Sequence 5, Appl
606	59	66.3	17	4	US-10-396-578-63	Sequence 63, Appl	679	59	66.3	116	3	US-09-840-459-80	Sequence 80, Appl
607	59	66.3	17	4	US-10-844-424-107	Sequence 107, App	680	59	66.3	116	4	US-10-766-773-80	Sequence 80, Appl
608	59	66.3	17	4	US-10-741-481-51	Sequence 51, Appl	681	59	66.3	116	4	US-10-766-610-80	Sequence 80, Appl
609	59	66.3	17	5	US-10-798-380-123	Sequence 123, App	682	59	66.3	116	4	US-10-733-563-80	Sequence 80, Appl
610	59	66.3	17	5	US-10-726-332-64	Sequence 64, Appl	683	59	66.3	116	4	US-10-403-814A-2	Sequence 2, Appl
611	59	66.3	17	5	US-10-726-332-85	Sequence 85, Appl	684	59	66.3	116	5	US-10-744-774-5	Sequence 5, Appl

685	59	66.3	116	6	US-11-031-485-114	Sequence 114, App	758	59	66.3	128	4	US-10-766-773-78	Sequence 78, Appl
686	59	66.3	117	3	US-09-840-459-83	Sequence 83, Appl	759	59	66.3	128	4	US-10-766-773-79	Sequence 79, Appl
687	59	66.3	117	4	US-10-766-773-83	Sequence 83, Appl	760	59	66.3	128	4	US-10-766-773-77	Sequence 77, Appl
688	59	66.3	117	4	US-10-766-610-83	Sequence 83, Appl	761	59	66.3	128	4	US-10-766-610-78	Sequence 78, Appl
689	59	66.3	117	4	US-10-733-563-83	Sequence 83, Appl	762	59	66.3	128	4	US-10-766-610-79	Sequence 79, Appl
690	59	66.3	118	4	US-10-001-934-39	Sequence 39, Appl	763	59	66.3	128	4	US-10-733-563-77	Sequence 77, Appl
691	59	66.3	118	4	US-10-309-763-129	Sequence 129, App	764	59	66.3	128	4	US-10-733-563-78	Sequence 78, Appl
692	59	66.3	118	4	US-10-275-046-68	Sequence 68, Appl	765	59	66.3	128	4	US-10-733-563-79	Sequence 79, Appl
693	59	66.3	118	5	US-10-798-380-119	Sequence 119, App	766	59	66.3	130	4	US-10-118-100-54	Sequence 54, Appl
694	59	66.3	119	4	US-10-401-344-6	Sequence 6, Appl	767	59	66.3	134	4	US-10-327-598-886	Sequence 886, Appl
695	59	66.3	119	4	US-10-309-764-25	Sequence 25, Appl	768	59	66.3	136	3	US-09-837-306-184	Sequence 184, App
696	59	66.3	119	6	US-11-021-438-6	Sequence 6, Appl	769	59	66.3	136	4	US-10-045-674-487	Sequence 487, App
697	59	66.3	120	3	US-09-840-459-85	Sequence 85, Appl	770	59	66.3	136	4	US-10-309-764-131	Sequence 131, App
698	59	66.3	120	4	US-10-125-687-4	Sequence 4, Appl	771	59	66.3	143	3	US-09-791-551-117	Sequence 117, App
699	59	66.3	120	4	US-10-275-046-80	Sequence 80, Appl	772	59	66.3	147	5	US-10-473-287-60	Sequence 60, Appl
700	59	66.3	120	4	US-10-766-773-85	Sequence 85, Appl	773	59	66.3	156	5	US-10-473-287-59	Sequence 59, Appl
701	59	66.3	120	4	US-10-766-610-85	Sequence 85, Appl	774	59	66.3	177	4	US-10-693-629-64	Sequence 64, Appl
702	59	66.3	120	4	US-10-733-563-85	Sequence 85, Appl	775	59	66.3	217	4	US-10-128-520-140	Sequence 140, App
703	59	66.3	120	4	US-10-779-461-140	Sequence 140, App	776	59	66.3	217	4	US-10-128-520-141	Sequence 141, App
704	59	66.3	120	5	US-10-938-353-104	Sequence 104, App	777	59	66.3	217	4	US-10-128-520-142	Sequence 142, App
705	59	66.3	120	5	US-10-891-972-23	Sequence 23, Appl	778	59	66.3	217	4	US-10-128-520-146	Sequence 146, App
706	59	66.3	120	5	US-10-996-191-4	Sequence 4, Appl	779	59	66.3	220	4	US-10-128-520-144	Sequence 144, App
707	59	66.3	121	3	US-09-920-171-4	Sequence 4, Appl	780	59	66.3	220	4	US-10-128-520-154	Sequence 154, App
708	59	66.3	121	3	US-09-822-698A-3	Sequence 3, Appl	781	59	66.3	220	4	US-10-128-520-156	Sequence 156, App
709	59	66.3	121	3	US-09-840-459-92	Sequence 92, Appl	782	59	66.3	221	4	US-10-128-520-143	Sequence 143, App
710	59	66.3	121	4	US-10-113-996-4	Sequence 4, Appl	783	59	66.3	221	4	US-10-128-520-171	Sequence 171, App
711	59	66.3	121	4	US-10-010-942B-9	Sequence 9, Appl	784	59	66.3	222	4	US-10-128-520-145	Sequence 145, App
712	59	66.3	121	4	US-10-275-046-78	Sequence 78, Appl	785	59	66.3	222	4	US-10-128-520-152	Sequence 152, App
713	59	66.3	121	4	US-10-388-389-9	Sequence 9, Appl	786	59	66.3	223	3	US-09-972-656-86	Sequence 86, Appl
714	59	66.3	121	4	US-10-766-773-92	Sequence 92, Appl	787	59	66.3	223	3	US-09-972-656-68	Sequence 68, Appl
715	59	66.3	121	4	US-10-766-610-92	Sequence 92, Appl	788	59	66.3	224	4	US-10-128-520-148	Sequence 148, App
716	59	66.3	121	4	US-10-733-563-92	Sequence 92, Appl	789	59	66.3	224	4	US-10-128-520-150	Sequence 150, App
717	59	66.3	121	4	US-10-703-713-9	Sequence 9, Appl	790	59	66.3	238	4	US-10-779-461-1	Sequence 1, Appl
718	59	66.3	121	4	US-10-704-070-9	Sequence 9, Appl	791	59	66.3	239	3	US-09-880-748-1922	Sequence 1922, Ap
719	59	66.3	121	4	US-10-800-197-128	Sequence 128, App	792	59	66.3	239	3	US-09-880-748-2018	Sequence 2018, Ap
720	59	66.3	121	5	US-10-791-619-4	Sequence 4, Appl	793	59	66.3	239	3	US-09-880-748-2022	Sequence 2022, Ap
721	59	66.3	121	5	US-10-232-030-9	Sequence 9, Appl	794	59	66.3	239	3	US-09-880-748-2023	Sequence 2023, Ap
722	59	66.3	121	6	US-11-031-485-118	Sequence 118, App	795	59	66.3	239	3	US-09-880-748-2035	Sequence 2035, Ap
723	59	66.3	122	4	US-10-800-197-134	Sequence 134, App	796	59	66.3	239	4	US-10-293-418-1922	Sequence 1922, Ap
724	59	66.3	122	5	US-10-727-153-262	Sequence 262, App	797	59	66.3	239	4	US-10-293-418-2018	Sequence 2018, Ap
725	59	66.3	122	5	US-10-891-973-33	Sequence 33, Appl	798	59	66.3	239	4	US-10-293-418-2022	Sequence 2022, Ap
726	59	66.3	122	5	US-10-505-313-4	Sequence 4, Appl	799	59	66.3	239	4	US-10-293-418-2023	Sequence 2023, Ap
727	59	66.3	123	4	US-10-269-805-1	Sequence 1, Appl	800	59	66.3	239	4	US-10-293-418-2035	Sequence 2035, Ap
728	59	66.3	123	4	US-10-269-805-23	Sequence 23, Appl	801	59	66.3	240	3	US-09-192-854-2	Sequence 2, Appl
729	59	66.3	123	4	US-10-269-805-59	Sequence 59, Appl	802	59	66.3	240	3	US-09-968-561A-2	Sequence 2, Appl
730	59	66.3	124	3	US-09-840-459-89	Sequence 89, Appl	803	59	66.3	240	3	US-09-880-748-1930	Sequence 1930, Ap
731	59	66.3	124	3	US-10-040-244-16	Sequence 16, Appl	804	59	66.3	240	3	US-09-880-748-2047	Sequence 2047, Ap
732	59	66.3	124	4	US-10-766-773-89	Sequence 89, Appl	805	59	66.3	240	3	US-09-968-744A-2	Sequence 2, Appl
733	59	66.3	124	4	US-10-766-610-89	Sequence 89, Appl	806	59	66.3	240	3	US-09-968-561A-2	Sequence 2, Appl
734	59	66.3	124	4	US-10-688-925-4	Sequence 4, Appl	807	59	66.3	240	4	US-10-293-418-1930	Sequence 1930, Ap
735	59	66.3	124	4	US-10-733-563-89	Sequence 89, Appl	808	59	66.3	240	4	US-10-293-418-2047	Sequence 2047, Ap
736	59	66.3	124	5	US-10-505-313-8	Sequence 8, Appl	809	59	66.3	240	4	US-10-450-012-2	Sequence 2, Appl
737	59	66.3	125	3	US-09-840-459-76	Sequence 76, Appl	810	59	66.3	240	5	US-10-744-774-1	Sequence 1, Appl
738	59	66.3	125	3	US-09-840-459-84	Sequence 84, Appl	811	59	66.3	240	6	US-11-115-682-2	Sequence 2, Appl
739	59	66.3	125	3	US-09-850-165-107	Sequence 107, App	812	59	66.3	241	4	US-09-880-748-2060	Sequence 2060, Ap
740	59	66.3	125	4	US-10-766-773-76	Sequence 76, Appl	813	59	66.3	241	4	US-10-293-418-2060	Sequence 2060, Ap
741	59	66.3	125	4	US-10-766-773-84	Sequence 84, Appl	814	59	66.3	242	4	US-10-779-461-9	Sequence 9, Appl
742	59	66.3	125	4	US-10-766-610-76	Sequence 76, Appl	815	59	66.3	242	6	US-11-017-030-58	Sequence 58, Appl
743	59	66.3	125	4	US-10-766-610-84	Sequence 84, Appl	816	59	66.3	242	6	US-11-017-030-66	Sequence 66, Appl
744	59	66.3	125	4	US-10-733-563-76	Sequence 76, Appl	817	59	66.3	243	3	US-09-880-748-1969	Sequence 1969, Ap
745	59	66.3	125	4	US-10-733-563-84	Sequence 84, Appl	818	59	66.3	243	3	US-09-880-748-2056	Sequence 2056, Ap
746	59	66.3	125	4	US-10-741-481-47	Sequence 47, Appl	819	59	66.3	243	4	US-10-322-673-51	Sequence 51, Appl
747	59	66.3	126	5	US-10-725-962-20	Sequence 20, Appl	820	59	66.3	243	4	US-10-322-673-55	Sequence 55, Appl
748	59	66.3	126	5	US-10-505-313-6	Sequence 6, Appl	821	59	66.3	243	4	US-10-293-418-1969	Sequence 1969, Ap
749	59	66.3	127	4	US-10-320-231A-36	Sequence 36, Appl	822	59	66.3	243	4	US-10-293-418-2056	Sequence 2056, Ap
750	59	66.3	127	4	US-10-800-197-124	Sequence 124, App	823	59	66.3	243	4	US-10-779-461-46	Sequence 46, Appl
751	59	66.3	127	5	US-10-725-962-6	Sequence 6, Appl	824	59	66.3	243	5	US-10-935-290-69	Sequence 69, Appl
752	59	66.3	127	5	US-10-867-506-36	Sequence 36, Appl	825	59	66.3	243	5	US-10-981-465-51	Sequence 51, Appl
753	59	66.3	127	5	US-10-505-313-235	Sequence 235, App	826	59	66.3	243	5	US-10-981-465-55	Sequence 55, Appl
754	59	66.3	128	3	US-09-840-459-77	Sequence 77, Appl	827	59	66.3	243	5	US-10-981-621-51	Sequence 51, Appl
755	59	66.3	128	3	US-09-840-459-78	Sequence 78, Appl	828	59	66.3	243	5	US-10-981-621-55	Sequence 55, Appl
756	59	66.3	128	3	US-09-840-459-79	Sequence 79, Appl	829	59	66.3	243	5	US-10-981-673-51	Sequence 51, Appl
757	59	66.3	128	4	US-10-766-773-77	Sequence 77, Appl	830	59	66.3	243	5	US-10-981-673-55	Sequence 55, Appl

831	59	66.3	243	5	US-10-981-691-51	Sequence 51, Appl	904	59	66.3	249	5	US-10-986-376-53	Sequence 53, Appl
832	59	66.3	243	5	US-10-981-691-55	Sequence 55, Appl	905	59	66.3	249	6	US-11-017-030-15	Sequence 15, Appl
833	59	66.3	243	6	US-11-021-438-26	Sequence 26, Appl	906	59	66.3	249	6	US-11-017-030-54	Sequence 54, Appl
834	59	66.3	243	6	US-11-021-438-28	Sequence 28, Appl	907	59	66.3	249	6	US-11-017-030-62	Sequence 62, Appl
835	59	66.3	244	4	US-10-120-414-77	Sequence 77, Appl	908	59	66.3	249	6	US-11-090-847-132	Sequence 132, Appl
836	59	66.3	244	4	US-10-322-673-45	Sequence 45, Appl	909	59	66.3	250	3	US-09-880-748-1420	Sequence 1420, Ap
837	59	66.3	244	5	US-10-935-290-121	Sequence 121, App	910	59	66.3	250	4	US-10-120-414-72	Sequence 72, Appl
838	59	66.3	244	5	US-10-981-465-45	Sequence 45, Appl	911	59	66.3	250	4	US-10-293-418-1420	Sequence 1420, Ap
839	59	66.3	244	5	US-10-981-621-45	Sequence 45, Appl	912	59	66.3	250	4	US-10-779-461-8	Sequence 8, Appl
840	59	66.3	244	5	US-10-981-673-45	Sequence 45, Appl	913	59	66.3	250	5	US-10-992-195-72	Sequence 72, Appl
841	59	66.3	244	5	US-10-981-691-45	Sequence 45, Appl	914	59	66.3	250	6	US-11-090-847-74	Sequence 74, Appl
842	59	66.3	244	5	US-10-992-195-77	Sequence 77, Appl	915	59	66.3	250	6	US-11-090-847-82	Sequence 82, Appl
843	59	66.3	244	6	US-11-017-030-49	Sequence 49, Appl	916	59	66.3	250	6	US-11-090-847-136	Sequence 136, App
844	59	66.3	244	6	US-11-090-847-142	Sequence 142, App	917	59	66.3	251	3	US-09-880-748-908	Sequence 908, App
845	59	66.3	244	6	US-11-090-847-147	Sequence 147, App	918	59	66.3	251	3	US-09-880-748-1605	Sequence 1605, Ap
846	59	66.3	245	4	US-10-322-673-43	Sequence 43, Appl	919	59	66.3	251	3	US-09-880-748-1708	Sequence 1708, Ap
847	59	66.3	245	4	US-10-779-461-24	Sequence 24, Appl	920	59	66.3	251	3	US-09-880-748-1740	Sequence 1740, Ap
848	59	66.3	245	4	US-10-779-461-59	Sequence 59, Appl	921	59	66.3	251	4	US-10-293-418-908	Sequence 908, App
849	59	66.3	245	4	US-10-779-461-11	Sequence 11, Appl	922	59	66.3	251	4	US-10-293-418-1605	Sequence 1605, Ap
850	59	66.3	245	4	US-10-800-197-11	Sequence 11, Appl	923	59	66.3	251	4	US-10-293-418-1708	Sequence 1708, Ap
851	59	66.3	245	5	US-10-798-380-121	Sequence 121, App	924	59	66.3	251	4	US-10-293-418-1740	Sequence 1740, Ap
852	59	66.3	245	5	US-10-981-465-43	Sequence 43, Appl	925	59	66.3	251	4	US-10-800-197-15	Sequence 15, Appl
853	59	66.3	245	5	US-10-981-621-43	Sequence 43, Appl	926	59	66.3	251	6	US-11-017-030-55	Sequence 55, Appl
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856	59	66.3	245	6	US-11-017-030-48	Sequence 48, Appl	929	59	66.3	252	3	US-10-293-418-1431	Sequence 1431, Ap
857	59	66.3	245	6	US-11-017-030-53	Sequence 53, Appl	930	59	66.3	252	6	US-11-017-030-12	Sequence 12, Appl
858	59	66.3	245	6	US-11-017-030-65	Sequence 65, Appl	931	59	66.3	253	3	US-09-880-748-989	Sequence 989, App
859	59	66.3	245	6	US-11-090-847-137	Sequence 137, App	932	59	66.3	253	4	US-10-120-414-76	Sequence 76, Appl
860	59	66.3	246	3	US-09-880-748-1324	Sequence 1324, Ap	933	59	66.3	253	4	US-10-293-418-989	Sequence 989, App
861	59	66.3	246	3	US-09-880-748-1975	Sequence 1975, Ap	934	59	66.3	253	4	US-10-800-197-9	Sequence 9, Appl
862	59	66.3	246	4	US-10-120-414-80	Sequence 80, Appl	935	59	66.3	253	5	US-10-992-195-76	Sequence 76, Appl
863	59	66.3	246	4	US-10-293-418-1324	Sequence 1324, Ap	936	59	66.3	253	6	US-11-017-030-17	Sequence 17, Appl
864	59	66.3	246	4	US-10-293-418-1975	Sequence 1975, Ap	937	59	66.3	253	6	US-11-017-030-20	Sequence 20, Appl
865	59	66.3	246	4	US-10-779-461-45	Sequence 45, Appl	938	59	66.3	253	6	US-11-017-030-57	Sequence 57, Appl
866	59	66.3	246	4	US-10-779-461-47	Sequence 47, Appl	939	59	66.3	253	6	US-11-090-847-135	Sequence 135, App
867	59	66.3	246	5	US-10-992-195-80	Sequence 80, Appl	940	59	66.3	253	6	US-11-090-847-148	Sequence 148, App
868	59	66.3	246	6	US-11-090-847-144	Sequence 144, App	941	59	66.3	254	3	US-09-880-748-1701	Sequence 1701, Ap
869	59	66.3	246	6	US-11-090-847-145	Sequence 145, App	942	59	66.3	254	3	US-09-880-748-1739	Sequence 1739, Ap
870	59	66.3	247	3	US-09-880-748-996	Sequence 996, App	943	59	66.3	254	4	US-10-293-418-1701	Sequence 1701, Ap
871	59	66.3	247	3	US-09-880-748-1294	Sequence 1294, Ap	944	59	66.3	254	4	US-10-293-418-1739	Sequence 1739, Ap
872	59	66.3	247	3	US-09-880-748-1923	Sequence 1923, Ap	945	59	66.3	254	6	US-11-017-030-1	Sequence 1, Appl
873	59	66.3	247	4	US-10-120-414-81	Sequence 81, Appl	946	59	66.3	254	6	US-11-017-030-45	Sequence 45, Appl
874	59	66.3	247	4	US-10-293-418-996	Sequence 996, App	947	59	66.3	254	6	US-11-017-030-52	Sequence 52, Appl
875	59	66.3	247	4	US-10-293-418-1294	Sequence 1294, Ap	948	59	66.3	255	6	US-11-017-030-3	Sequence 3, Appl
876	59	66.3	247	4	US-10-293-418-1923	Sequence 1923, Ap	949	59	66.3	255	6	US-11-090-847-139	Sequence 139, App
877	59	66.3	247	5	US-10-992-195-81	Sequence 81, Appl	950	59	66.3	255	6	US-11-090-847-143	Sequence 143, App
878	59	66.3	247	6	US-11-017-030-16	Sequence 16, Appl	951	59	66.3	256	3	US-09-880-748-1183	Sequence 1183, Ap
879	59	66.3	247	6	US-11-017-030-50	Sequence 50, Appl	952	59	66.3	256	4	US-10-293-418-1183	Sequence 1183, Ap
880	59	66.3	247	6	US-11-017-030-60	Sequence 60, Appl	953	59	66.3	256	6	US-11-090-847-66	Sequence 66, Appl
881	59	66.3	247	6	US-11-017-030-67	Sequence 67, Appl	954	59	66.3	256	6	US-11-090-847-140	Sequence 140, App
882	59	66.3	247	6	US-11-090-847-138	Sequence 138, App	955	59	66.3	262	4	US-10-688-925-2	Sequence 2, Appl
883	59	66.3	247	6	US-11-090-847-141	Sequence 141, App	956	59	66.3	288	3	US-09-818-247-22	Sequence 22, Appl
884	59	66.3	248	3	US-09-880-748-921	Sequence 921, App	957	59	66.3	288	6	US-11-038-956-22	Sequence 22, Appl
885	59	66.3	248	3	US-09-880-748-1456	Sequence 1456, Ap	958	59	66.3	290	3	US-09-969-748C-2	Sequence 2, Appl
886	59	66.3	248	4	US-10-120-414-78	Sequence 78, Appl	959	59	66.3	290	3	US-09-949-039-2	Sequence 2, Appl
887	59	66.3	248	4	US-10-293-418-921	Sequence 921, App	960	59	66.3	290	5	US-10-470-987-42	Sequence 42, Appl
888	59	66.3	248	4	US-10-293-418-1456	Sequence 1456, Ap	961	59	66.3	291	4	US-10-406-830-9	Sequence 9, Appl
889	59	66.3	248	5	US-10-981-692-32	Sequence 32, Appl	962	59	66.3	291	4	US-10-406-830-10	Sequence 10, Appl
890	59	66.3	248	5	US-10-992-195-78	Sequence 78, Appl	963	59	66.3	296	3	US-09-969-748C-12	Sequence 12, Appl
891	59	66.3	248	6	US-11-017-030-4	Sequence 4, Appl	964	59	66.3	296	3	US-09-949-039-75	Sequence 75, Appl
892	59	66.3	248	6	US-11-017-030-11	Sequence 11, Appl	965	59	66.3	313	4	US-10-291-285-427	Sequence 427, App
893	59	66.3	248	6	US-11-017-030-18	Sequence 18, Appl	966	59	66.3	367	4	US-10-045-674-453	Sequence 453, App
894	59	66.3	248	6	US-11-017-030-46	Sequence 46, Appl	967	59	66.3	368	3	US-09-837-606-196	Sequence 196, App
895	59	66.3	248	6	US-11-017-030-47	Sequence 47, Appl	968	59	66.3	381	3	US-09-823-698A-5	Sequence 5, Appl
896	59	66.3	248	6	US-11-017-030-51	Sequence 51, Appl	969	59	66.3	445	4	US-10-320-231A-79	Sequence 79, Appl
897	59	66.3	248	6	US-11-017-030-56	Sequence 56, Appl	970	59	66.3	445	5	US-10-867-506-79	Sequence 79, Appl
898	59	66.3	248	6	US-11-017-030-63	Sequence 63, Appl	971	59	66.3	451	3	US-09-822-698A-26	Sequence 26, Appl
899	59	66.3	248	6	US-11-017-030-64	Sequence 64, Appl	972	59	66.3	465	4	US-10-401-344-2	Sequence 2, Appl
900	59	66.3	249	4	US-10-139-785-53	Sequence 53, Appl	973	59	66.3	470	4	US-10-038-591-46	Sequence 46, Appl
901	59	66.3	249	5	US-10-986-046-53	Sequence 53, Appl	974	59	66.3	470	4	US-10-775-444A-46	Sequence 46, Appl
902	59	66.3	249	5	US-10-986-047-53	Sequence 53, Appl	975	59	66.3	638	5	US-10-505-313-254	Sequence 254, App
903	59	66.3	249	5	US-10-986-349-53	Sequence 53, Appl	976	59.5	65.7	115	5	US-10-727-155-120	Sequence 120, App

Sequence 102, App  
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Sequence 122, App  
Sequence 222, App  
Sequence 5, Appl  
Sequence 36, Appl  
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Sequence 48, Appl  
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Sequence 71, Appl  
Sequence 71, Appl  
Sequence 34, Appl  
Sequence 622, App  
Sequence 623, App  
Sequence 9, Appl  
Sequence 25, Appl  
Sequence 11, Appl  
Sequence 6, Appl  
Sequence 6, Appl

# ALIGNMENTS

RESULT 1  
US-09-764-304-18  
; Sequence 18, Application US/09764304  
; Patent No. US2002026036A1  
; GENERAL INFORMATION:  
; APPLICANT: SHITARA, KENYA  
; APPLICANT: HANAI, NOBUO  
; APPLICANT: HASEGAWA, MAMORU  
; APPLICANT: MIYAJI, HIROMASA  
; APPLICANT: KUWANA, YOSHIHISA  
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY  
; FILE REFERENCE: 249-101  
; CURRENT APPLICATION NUMBER: US/09/764,304  
; EARLIER FILING DATE: 2001-01-19  
; EARLIER FILING DATE: 1999-01-05  
; EARLIER FILING DATE: 1999-01-05  
; EARLIER FILING DATE: 1995-05-31  
; EARLIER FILING DATE: 1995-03-21  
; EARLIER FILING DATE: 1992-09-17  
; EARLIER FILING DATE: 1991-09-18  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 18  
; LENGTH: 130  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: cDNA KM-641  
US-09-764-304-18

Query Match 100.0%; Score 89; DB 3; Length 130;  
Best Local Similarity 100.0%; Pred. No. 9.3e-05;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 YISGGSGTYYSDSVKG 17  
Db 60 YISGGSGTYYSDSVKG 76

RESULT 2  
US-10-265-713-18  
; Sequence 18, Application US/10265713  
; Publication No. US20030095964A1  
; GENERAL INFORMATION:  
; APPLICANT: SHITARA, KENYA  
; APPLICANT: HANAI, NOBUO  
; APPLICANT: HASEGAWA, MAMORU  
; APPLICANT: MIYAJI, HIROMASA  
; APPLICANT: KUWANA, YOSHIHISA  
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY  
; FILE REFERENCE: 249-101  
; CURRENT APPLICATION NUMBER: US/10/265,713  
; CURRENT FILING DATE: 2002-10-08  
; PRIOR FILING DATE: 1999-01-05  
; PRIOR FILING DATE: US 08/454,680  
; PRIOR FILING DATE: 1995-05-31  
; PRIOR FILING DATE: US 08/408,133  
; PRIOR FILING DATE: 1995-03-21  
; PRIOR FILING DATE: US 08/292,178  
; PRIOR FILING DATE: 1994-08-17  
; PRIOR FILING DATE: US07/947,674  
; PRIOR FILING DATE: 1992-09-17  
; PRIOR FILING DATE: JP 3-238375  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 18  
; LENGTH: 130  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: cDNA KM-641  
US-10-265-713-18

Query Match 100.0%; Score 89; DB 4; Length 130;  
Best Local Similarity 100.0%; Pred. No. 9.3e-05;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 YISGGSGTYYSDSVKG 17  
Db 60 YISGGSGTYYSDSVKG 76

RESULT 3  
US-10-166-626-18  
; Sequence 18, Application US/10166626  
; Publication No. US20030166876A1  
; GENERAL INFORMATION:  
; APPLICANT: SHITARA, KENYA  
; APPLICANT: HANAI, NOBUO  
; APPLICANT: HASEGAWA, MAMORU  
; APPLICANT: MIYAJI, HIROMASA  
; APPLICANT: KUWANA, YOSHIHISA  
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY  
; FILE REFERENCE: 249-101  
; CURRENT APPLICATION NUMBER: US/10/166,626  
; CURRENT FILING DATE: 2002-06-12  
; PRIOR FILING DATE: US/09/225,322B  
; PRIOR FILING DATE: 1999-01-05  
; PRIOR FILING DATE: US 08/454,680  
; PRIOR FILING DATE: 1995-05-31  
; PRIOR FILING DATE: US 08/408,133  
; PRIOR FILING DATE: 1995-03-21  
; PRIOR FILING DATE: US 08/292,178  
; PRIOR FILING DATE: 1994-08-17  
; PRIOR FILING DATE: US07/947,674  
; PRIOR FILING DATE: 1992-09-17  
; PRIOR FILING DATE: JP 3-238375  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 18  
; LENGTH: 130  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: cDNA KM-641  
US-10-166-626-18



Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ISSGGSGTYSDSVKG 17  
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Db 61 ISSGGSGTYSDSVKG 76

RESULT 7  
US-10-779-461-23  
; Sequence 23, Application US/10779461  
; Publication No. US20040166544A1  
; GENERAL INFORMATION:  
; APPLICANT: Morton, Philip A  
; TITLE OF INVENTION: ANTIBODIES TO C-MET FOR THE TREATMENT OF CANCERS  
; CURRENT APPLICATION NUMBER: US/10/779,461  
; CURRENT FILING DATE: 2004-02-13  
; PRIOR APPLICATION NUMBER: 60/447,073  
; PRIOR FILING DATE: 2003-02-13  
; NUMBER OF SEQ ID NOS: 161  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 23  
; LENGTH: 240  
; TYPE: PRT  
; ORGANISM: artificial  
; FEATURE:  
; OTHER INFORMATION: phage display generated human antibody  
US-10-779-461-23

Query Match 83.1%; Score 74; DB 4; Length 240;  
Best Local Similarity 82.4%; Pred. No. 0.022;  
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YISSGSGTYSDSVKG 17  
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Db 50 YISSGSGTYSDSVKG 66

RESULT 8  
US-10-383-447-6  
; Sequence 6, Application US/10383447  
; Publication No. US20040096392A1  
; GENERAL INFORMATION:  
; APPLICANT: Bhaskar, Vinay  
; APPLICANT: de la Calle, Agustin  
; APPLICANT: Law, Debbie  
; APPLICANT: Caras, Ingrid  
; APPLICANT: Ramakrishnan, Vanitha  
; APPLICANT: Murray, Richard  
; APPLICANT: Afar, Daniel  
; APPLICANT: Powers, David  
; TITLE OF INVENTION: Antibodies Against Cancer Antigen TWEFF2 and Uses Thereof  
; FILE REFERENCE: 05882.0138.NPUS00  
; CURRENT APPLICATION NUMBER: US/10/383,447  
; CURRENT FILING DATE: 2002-03-07  
; PRIOR APPLICATION NUMBER: US 60/362,837  
; PRIOR FILING DATE: 2002-03-08  
; PRIOR APPLICATION NUMBER: US 60/463,812  
; PRIOR FILING DATE: 2002-12-27  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 6  
; LENGTH: 120  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Heavy chain variable region  
US-10-383-447-6

Query Match 82.0%; Score 73; DB 4; Length 120;  
Best Local Similarity 76.5%; Pred. No. 0.015;  
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 YISSGSGTYSDSVKG 17  
|||||  
Db 50 YISNGGNTYSDTVKG 66

RESULT 9  
US-09-880-748-1906  
; Sequence 1906, Application US/09880748  
; Publication No. US2003005937A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
; FILE REFERENCE: PF523  
; CURRENT APPLICATION NUMBER: US/09/880,748  
; CURRENT FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/212,210  
; PRIOR FILING DATE: 2000-06-15  
; PRIOR APPLICATION NUMBER: 60/240,816  
; PRIOR FILING DATE: 2000-10-17  
; PRIOR APPLICATION NUMBER: 60/276,248  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/277,379  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/293,499  
; PRIOR FILING DATE: 2001-05-25  
; NUMBER OF SEQ ID NOS: 3239  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1906  
; LENGTH: 237  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-880-748-1906

Query Match 80.9%; Score 72; DB 3; Length 237;  
Best Local Similarity 82.4%; Pred. No. 0.04;  
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YISSGSGTYSDSVKG 17  
|||||  
Db 50 YISSGSGTYSDSVKG 66

RESULT 10  
US-09-880-748-2039  
; Sequence 2039, Application US/09880748  
; Publication No. US2003005937A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
; FILE REFERENCE: PF523  
; CURRENT APPLICATION NUMBER: US/09/880,748  
; CURRENT FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/212,210  
; PRIOR FILING DATE: 2000-06-15  
; PRIOR APPLICATION NUMBER: 60/240,816  
; PRIOR FILING DATE: 2000-10-17  
; PRIOR APPLICATION NUMBER: 60/276,248  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/277,379  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/293,499  
; PRIOR FILING DATE: 2001-05-25  
; NUMBER OF SEQ ID NOS: 3239  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2039  
; LENGTH: 237  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-880-748-2039

Query Match 80.9%; Score 72; DB 3; Length 237;  
Best Local Similarity 82.4%; Pred. No. 0.04;  
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YISSGGSGTYYSDSVKG 17  
|||||:|||||  
Db 50 YISSGGSTYYADSVKG 66

## RESULT 11

US-10-293-418-1906  
; Sequence 1906, Application US/10293418  
; Publication No. US20030223996A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS  
; FILE REFERENCE: PF523P2  
; CURRENT APPLICATION NUMBER: US/10/293,418  
; CURRENT FILING DATE: 2002-11-27  
; PRIOR APPLICATION NUMBER: 60/331,469  
; PRIOR FILING DATE: 2001-11-16  
; PRIOR APPLICATION NUMBER: 60/340,817  
; PRIOR FILING DATE: 2001-12-19  
; PRIOR APPLICATION NUMBER: 09/880,748  
; PRIOR FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/293,499  
; PRIOR FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: 60/277,379  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/276,248  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/240,816  
; PRIOR FILING DATE: 2000-10-17  
; PRIOR APPLICATION NUMBER: 60/212,210  
; PRIOR FILING DATE: 2000-06-16  
; NUMBER OF SEQ ID NOS: 3247  
; SEQ ID NO 1906  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-293-418-1906

Query Match 80.9%; Score 72; DB 4; Length 237;  
Best Local Similarity 82.4%; Pred. No. 0.04;  
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YISSGGSGTYYSDSVKG 17  
|||||:|||||  
Db 50 YISSGGSTYYADSVKG 66

## RESULT 12

US-10-293-418-2039  
; Sequence 2039, Application US/10293418  
; Publication No. US20030223996A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS  
; FILE REFERENCE: PF523P2  
; CURRENT APPLICATION NUMBER: US/10/293,418  
; CURRENT FILING DATE: 2002-11-27  
; PRIOR APPLICATION NUMBER: 60/331,469  
; PRIOR FILING DATE: 2001-11-16  
; PRIOR APPLICATION NUMBER: 60/340,817  
; PRIOR FILING DATE: 2001-12-19  
; PRIOR APPLICATION NUMBER: 09/880,748  
; PRIOR FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/293,499  
; PRIOR FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: 60/277,379  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/276,248  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/240,816  
; PRIOR FILING DATE: 2000-10-17  
; PRIOR APPLICATION NUMBER: 60/212,210

; PRIOR FILING DATE: 2000-06-16  
; NUMBER OF SEQ ID NOS: 3247  
; SEQ ID NO 2039  
; LENGTH: 237  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-293-418-2039

Query Match 80.9%; Score 72; DB 4; Length 237;  
Best Local Similarity 82.4%; Pred. No. 0.04;  
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YISSGGSGTYYSDSVKG 17  
|||||:|||||  
Db 50 YISSGGSTYYADSVKG 66

## RESULT 13

US-09-880-748-1905  
; Sequence 1905, Application US/09880748  
; Publication No. US20030059937A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS  
; FILE REFERENCE: PF523  
; CURRENT APPLICATION NUMBER: US/09/880,748  
; CURRENT FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/212,210  
; PRIOR FILING DATE: 2000-06-15  
; PRIOR APPLICATION NUMBER: 60/240,816  
; PRIOR FILING DATE: 2000-10-17  
; PRIOR APPLICATION NUMBER: 60/276,248  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/277,379  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/293,499  
; PRIOR FILING DATE: 2001-05-25  
; NUMBER OF SEQ ID NOS: 3239  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1905  
; LENGTH: 240  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-880-748-1905

Query Match 80.9%; Score 72; DB 3; Length 240;  
Best Local Similarity 82.4%; Pred. No. 0.041;  
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YISSGGSGTYYSDSVKG 17  
|||||:|||||  
Db 50 YISSGGSTYYADSVKG 66

## RESULT 14

US-10-293-418-1905  
; Sequence 1905, Application US/10293418  
; Publication No. US20030223996A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS  
; FILE REFERENCE: PF523P2  
; CURRENT APPLICATION NUMBER: US/10/293,418  
; CURRENT FILING DATE: 2002-11-27  
; PRIOR APPLICATION NUMBER: 60/331,469  
; PRIOR FILING DATE: 2001-11-16  
; PRIOR APPLICATION NUMBER: 60/340,817  
; PRIOR FILING DATE: 2001-12-19  
; PRIOR APPLICATION NUMBER: 09/880,748  
; PRIOR FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/293,499  
; PRIOR FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: 60/277,379

; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/276,248  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/240,816  
; PRIOR FILING DATE: 2000-10-17  
; PRIOR APPLICATION NUMBER: 60/212,210  
; PRIOR FILING DATE: 2000-06-16  
; NUMBER OF SEQ ID NOS: 3247  
; SEQ ID NO 1905  
; LENGTH: 240  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-293-418-1905

Query Match 80.9%; Score 72; DB 4; Length 240;  
Best Local Similarity 82.4%; Pred. No. 0.041; 2; Indels 0; Gaps 0;  
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YISSGSGTYYSDSVK 17  
|||||:|||||  
Db 50 YISSGSGTYYADSVK 66

RESULT 15  
US-10-935-290-45  
; Sequence 45, Application US/10935290  
; Publication No. US20050069542A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker et al.  
; TITLE OF INVENTION: Antibodies that Specifically Bind to GMAD  
; FILE REFERENCE: PF594P1  
; CURRENT APPLICATION NUMBER: US/10/935,290  
; CURRENT FILING DATE: 2004-09-08  
; PRIOR APPLICATION NUMBER: PCT/US03/09625  
; PRIOR FILING DATE: 2003-03-28  
; PRIOR APPLICATION NUMBER: 60/368,813  
; PRIOR FILING DATE: 2002-04-01  
; NUMBER OF SEQ ID NOS: 234  
; SEQ ID NO 45  
; LENGTH: 246  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: scFv protein GMBC608  
US-10-935-290-45

Query Match 80.9%; Score 72; DB 5; Length 246;  
Best Local Similarity 82.4%; Pred. No. 0.042; 2; Indels 0; Gaps 0;  
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YISSGSGTYYSDSVK 17  
|||||:|||||  
Db 50 YISSGSGTYYTDSVK 66

RESULT 16  
US-11-093-103-86  
; Sequence 86, Application US/11093103  
; Publication No. US20050196397A1  
; GENERAL INFORMATION:  
; APPLICANT: Scheiflinger, Friedrich  
; APPLICANT: Kerschbaumer, Randolph  
; APPLICANT: Falkner, Falko-Guenter  
; APPLICANT: Dörner, Friedrich  
; APPLICANT: Baxter Aktiengesellschaft  
; TITLE OF INVENTION: Factor IX/Factor IXa Activating Antibodies and Antibody  
; TITLE OF INVENTION: Derivatives  
; FILE REFERENCE: 20695C-005900US  
; CURRENT APPLICATION NUMBER: US/11/093,103  
; CURRENT FILING DATE: 2005-03-28  
; PRIOR APPLICATION NUMBER: US/09/661,992  
; PRIOR FILING DATE: 2000-09-14  
; PRIOR APPLICATION NUMBER: AT A157600

; PRIOR FILING DATE: 1999-09-14  
; NUMBER OF SEQ ID NOS: 112  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 86  
; LENGTH: 249  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:scFv from  
; OTHER INFORMATION: hybridoma cell line 198/AB2 (subclone of 198/B1)  
US-11-093-103-86

Query Match 79.8%; Score 71; DB 6; Length 249;  
Best Local Similarity 87.5%; Pred. No. 0.059;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 ISSGSGTYYSDSVK 17  
|||||:|||||  
Db 51 ISSGSGSTYYPDVK 66

RESULT 17  
US-11-093-103-88  
; Sequence 88, Application US/11093103  
; Publication No. US20050196397A1  
; GENERAL INFORMATION:  
; APPLICANT: Scheiflinger, Friedrich  
; APPLICANT: Kerschbaumer, Randolph  
; APPLICANT: Falkner, Falko-Guenter  
; APPLICANT: Dörner, Friedrich  
; APPLICANT: Baxter Aktiengesellschaft  
; TITLE OF INVENTION: Factor IX/Factor IXa Activating Antibodies and Antibody  
; TITLE OF INVENTION: Derivatives  
; FILE REFERENCE: 20695C-005900US  
; CURRENT APPLICATION NUMBER: US/11/093,103  
; CURRENT FILING DATE: 2005-03-28  
; PRIOR APPLICATION NUMBER: US/09/661,992  
; PRIOR FILING DATE: 2000-09-14  
; PRIOR APPLICATION NUMBER: AT A157600  
; PRIOR FILING DATE: 1999-09-14  
; NUMBER OF SEQ ID NOS: 112  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 88  
; LENGTH: 249  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:scFv derived  
; OTHER INFORMATION: from hybridoma cell line 198/A1  
US-11-093-103-88

Query Match 79.8%; Score 71; DB 6; Length 249;  
Best Local Similarity 87.5%; Pred. No. 0.059;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 ISSGSGTYYSDSVK 17  
|||||:|||||  
Db 51 ISSGSGSTYYPDVK 66

RESULT 18  
US-11-093-103-100  
; Sequence 100, Application US/11093103  
; Publication No. US20050196397A1  
; GENERAL INFORMATION:  
; APPLICANT: Scheiflinger, Friedrich  
; APPLICANT: Kerschbaumer, Randolph  
; APPLICANT: Falkner, Falko-Guenter  
; APPLICANT: Dörner, Friedrich  
; APPLICANT: Baxter Aktiengesellschaft  
; TITLE OF INVENTION: Factor IX/Factor IXa Activating Antibodies and Antibody  
; TITLE OF INVENTION: Derivatives  
; FILE REFERENCE: 20695C-005900US



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; CURRENT APPLICATION NUMBER: US/11/093,103
; CURRENT FILING DATE: 2005-03-28
; PRIOR APPLICATION NUMBER: US/09/661,992
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: AT A157600
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 100
; LENGTH: 294
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:198AB2 scFv
; OTHER INFORMATION: linked to c-myc-tag and His6 tag (ORF of
; OTHER INFORMATION: expression vector pMyHis6-198AB2#102)
US-11-093-103-100

Query Match          79.8%; Score 71; DB 6; Length 294;
Best Local Similarity 87.5%; Pred. No. 0.069; 2; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 ISSGSGSTYYSDSVK 17
   ||||| ||| |||||
Db 73 ISSGSGSTYYSDSVK 88

RESULT 19
US-11-093-103-92
; Sequence 92, Application US/11093103
; Publication No. US20050196397A1
; GENERAL INFORMATION:
; APPLICANT: Scheiflinger, Friedrich
; APPLICANT: Kerschbaumer, RandoIf
; APPLICANT: Falkner, Falko-Guenter
; APPLICANT: Dörner, Friedrich
; APPLICANT: Baxter Aktiengesellschaft
; TITLE OF INVENTION: Factor IX/Factor IXa Activating Antibodies and Antibody
; FILE REFERENCE: 20695C-005900US
; CURRENT APPLICATION NUMBER: US/11/093,103
; CURRENT FILING DATE: 2005-03-28
; PRIOR APPLICATION NUMBER: US/09/661,992
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: AT A157600
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 92
; LENGTH: 325
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:plasmid
; OTHER INFORMATION: pZlp-198AB2#102
; NAME/KEY: MOD RES
; LOCATION: (166)
; OTHER INFORMATION: Xaa = Cys, Tyr, Ser or Phe
US-11-093-103-92

Query Match          79.8%; Score 71; DB 6; Length 325;
Best Local Similarity 87.5%; Pred. No. 0.076; 2; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 ISSGSGSTYYSDSVK 17
   ||||| ||| |||||
Db 73 ISSGSGSTYYSDSVK 88

RESULT 20
US-11-093-103-90
; Sequence 90, Application US/11093103
; Publication No. US20050196397A1
; GENERAL INFORMATION:
; APPLICANT: Scheiflinger, Friedrich
; APPLICANT: Kerschbaumer, RandoIf
; APPLICANT: Falkner, Falko-Guenter
; APPLICANT: Dörner, Friedrich
; APPLICANT: Baxter Aktiengesellschaft
; TITLE OF INVENTION: Factor IX/Factor IXa Activating Antibodies and Antibody
; FILE REFERENCE: 20695C-005900US
; CURRENT APPLICATION NUMBER: US/11/093,103
; CURRENT FILING DATE: 2005-03-28
; PRIOR APPLICATION NUMBER: US/09/661,992
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: AT A157600
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 90
; LENGTH: 732
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:198A2
; OTHER INFORMATION: scFv-alkaline phosphatase fusion protein (ORF of
; OTHER INFORMATION: expression vector pDAF2-198AB2#100)
US-11-093-103-90

Query Match          79.8%; Score 71; DB 6; Length 732;
Best Local Similarity 87.5%; Pred. No. 0.17; 2; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ISSGSGSTYYSDSVK 17
   ||||| ||| |||||
Db 73 ISSGSGSTYYSDSVK 88

RESULT 21
US-11-056-776-4
; Sequence 4, Application US/11056776
; Publication No. US20050232919A1
; GENERAL INFORMATION:
; APPLICANT: Grasso, Luigi
; APPLICANT: Nicolaides, Nicholas C.
; APPLICANT: Sasse, Philip M.
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES THAT SPECIFICALLY BLOCK BIOLOGICAL ACTIVITY
; TITLE OF INVENTION: OF A TUMOR ANTIGEN
; FILE REFERENCE: MOR-0373
; CURRENT APPLICATION NUMBER: US/11/056,776
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: US 60/544,364
; PRIOR FILING DATE: 2004-02-12
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-11-056-776-4

Query Match          78.7%; Score 70; DB 6; Length 119;
Best Local Similarity 87.5%; Pred. No. 0.039; 1; Indels 0; Gaps 0;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 ISSGSGSTYYSDSVK 17
   ||||| ||| |||||
Db 51 ISSGSGSTYYADSVK 66

RESULT 22
US-10-447-331-4
```

```
; Sequence 4, Application US/10447331
; Publication No. US20030219434A1
; GENERAL INFORMATION:
; APPLICANT: Carter, Paul J.
; APPLICANT: Ridgway, John B.
; TITLE OF INVENTION: ANTIBODIES FOR CANCER THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS
; FILE REFERENCE: GENENT.122A
; CURRENT APPLICATION NUMBER: US/10/447,331
; CURRENT FILING DATE: 2003-05-28
; PRIOR APPLICATION NUMBER: US/09/515,825
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: 60/122262
; PRIOR FILING DATE: 1999-03-01
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-447-331-4

Query Match      78.7%; Score 70; DB 4; Length 121;
Best Local Similarity 87.5%; Pred. No. 0.04;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY  2 ISSGGSGTYSDSVKG 17
Db  51 INSGGSYTYSDSVKG 66

RESULT 23
US-11-056-776-5
; Sequence 5, Application US/11056776
; Publication No. US20050232919A1
; GENERAL INFORMATION:
; APPLICANT: Grasso, Luigi
; APPLICANT: Nicolaides, Nicholas C.
; APPLICANT: Sass, Philip M.
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES THAT SPECIFICALLY BLOCK BIOLOGICAL ACTIVITY
; TITLE OF INVENTION: OF A TUMOR ANTIGEN
; FILE REFERENCE: MOR-0373
; CURRENT APPLICATION NUMBER: US/11/056,776
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: US 60/544,364
; PRIOR FILING DATE: 2004-02-12
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5
; LENGTH: 449
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-11-056-776-5

Query Match      78.7%; Score 70; DB 6; Length 449;
Best Local Similarity 87.5%; Pred. No. 0.15;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY  2 ISSGGSGTYSDSVKG 17
Db  51 INSGGSYTYADSVKG 66

RESULT 24
US-11-056-776-6
; Sequence 6, Application US/11056776
; Publication No. US20050232919A1
; GENERAL INFORMATION:
; APPLICANT: Grasso, Luigi
; APPLICANT: Nicolaides, Nicholas C.
; APPLICANT: Sass, Philip M.
```

```
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES THAT SPECIFICALLY BLOCK BIOLOGICAL ACTIVITY
; TITLE OF INVENTION: OF A TUMOR ANTIGEN
; FILE REFERENCE: MOR-0373
; CURRENT APPLICATION NUMBER: US/11/056,776
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: US 60/544,364
; PRIOR FILING DATE: 2004-02-12
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 6
; LENGTH: 468
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-11-056-776-6

Query Match      78.7%; Score 70; DB 6; Length 468;
Best Local Similarity 87.5%; Pred. No. 0.15;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY  2 ISSGGSGTYSDSVKG 17
Db  70 INSGGSYTYADSVKG 85

RESULT 25
US-10-460-471-31
; Sequence 31, Application US/10460471
; Publication No. US20030206900A1
; GENERAL INFORMATION:
; APPLICANT: TERNYNCK, THERESA
; APPLICANT: AVrameas, ALEXANDRE
; APPLICANT: BUTTIN, GERARD
; APPLICANT: AVrameas, STRAITIS
; APPLICANT: SARON, MARIE-FRANCOISE
; APPLICANT: BLONDEL, BRUNO
; APPLICANT: COUDERC, THERESA
; APPLICANT: MICHELSON, SUSAN
; APPLICANT: ZIPETO, DONATO
; TITLE OF INVENTION: VECTOR DERIVED FROM ANTIBODIES FOR TRANSFERRING SUBSTANCES INTO C
; FILE REFERENCE: 0660-0166-0XCONT
; CURRENT APPLICATION NUMBER: US/10/460,471
; CURRENT FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: US/09/497,997C
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: PCT/FR98/01740
; PRIOR FILING DATE: 1998-08-04
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SYNTHETIC PEPTIDE
US-10-460-471-31

Query Match      77.5%; Score 69; DB 4; Length 17;
Best Local Similarity 76.5%; Pred. No. 0.0078;
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY  1 YISSGGSGTYSDSVKG 17
Db  1 YISRGGSYTYSDTVKG 17

RESULT 26
US-10-460-471-19
; Sequence 19, Application US/10460471
; Publication No. US20030206900A1
; GENERAL INFORMATION:
; APPLICANT: TERNYNCK, THERESA
```

```
/ APPLICANT: AVAMEAS, ALEXANDRE
/ APPLICANT: BUTTIN, GERARD
/ APPLICANT: AVAMEAS, STRAITTIS
/ APPLICANT: SARON, MARIE-FRANCOISE
/ APPLICANT: BLONDEL, BRUNO
/ APPLICANT: COUDERC, THERESA
/ APPLICANT: MICHELSON, SUSAN
/ APPLICANT: ZIPETO, DONATO
/ TITLE OF INVENTION: VECTOR DERIVED FROM ANTIBODIES FOR TRANSFERRING SUBSTANCES INTO C
/ FILE REFERENCE: 0660-0166-OXCONT
/ CURRENT APPLICATION NUMBER: US/10/460,471
/ CURRENT FILING DATE: 2003-06-13
/ PRIOR APPLICATION NUMBER: US/09/497,997C
/ PRIOR FILING DATE: 2000-02-04
/ PRIOR APPLICATION NUMBER: PCT/FR98/01740
/ PRIOR FILING DATE: 1998-08-04
/ NUMBER OF SEQ ID NOS: 36
/ SOFTWARE: Patentin version 3.1
/ SEQ ID NO 19
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: SYNTHETIC PEPTIDE
US-10-460-471-19

Query Match          77.5%; Score 69; DB 4; Length 21;
Best Local Similarity 76.5%; Pred. No. 0.0096;
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 YISGGSGTYYSDSVKG 17
    ||| ||| ||| ||| |||
DB 3 YISGGSVTYSDTVKG 19

RESULT 27
US-10-460-471-4
/ Sequence 4, Application US/10460471
/ Publication No. US20030206900A1
/ GENERAL INFORMATION:
/ APPLICANT: TERNYNCK, THERESA
/ APPLICANT: AVAMEAS, ALEXANDRE
/ APPLICANT: BUTTIN, GERARD
/ APPLICANT: AVAMEAS, STRAITTIS
/ APPLICANT: SARON, MARIE-FRANCOISE
/ APPLICANT: BLONDEL, BRUNO
/ APPLICANT: COUDERC, THERESA
/ APPLICANT: MICHELSON, SUSAN
/ APPLICANT: ZIPETO, DONATO
/ TITLE OF INVENTION: VECTOR DERIVED FROM ANTIBODIES FOR TRANSFERRING SUBSTANCES INTO C
/ FILE REFERENCE: 0660-0166-OXCONT
/ CURRENT APPLICATION NUMBER: US/10/460,471
/ CURRENT FILING DATE: 2003-06-13
/ PRIOR APPLICATION NUMBER: US/09/497,997C
/ PRIOR FILING DATE: 2000-02-04
/ PRIOR APPLICATION NUMBER: PCT/FR98/01740
/ PRIOR FILING DATE: 1998-08-04
/ NUMBER OF SEQ ID NOS: 36
/ SOFTWARE: Patentin version 3.1
/ SEQ ID NO 4
/ LENGTH: 22
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: SYNTHETIC PEPTIDE
US-10-460-471-4

Query Match          77.5%; Score 69; DB 4; Length 22;
Best Local Similarity 76.5%; Pred. No. 0.01;
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 YISGGSGTYYSDSVKG 17
    ||| ||| ||| ||| |||
DB 3 YISGGSVTYSDTVKG 19
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```
DB 3 YISGGSVTYSDTVKG 19

RESULT 28
US-10-460-471-20
/ Sequence 20, Application US/10460471
/ Publication No. US20030206900A1
/ GENERAL INFORMATION:
/ APPLICANT: TERNYNCK, THERESA
/ APPLICANT: AVAMEAS, ALEXANDRE
/ APPLICANT: BUTTIN, GERARD
/ APPLICANT: AVAMEAS, STRAITTIS
/ APPLICANT: SARON, MARIE-FRANCOISE
/ APPLICANT: BLONDEL, BRUNO
/ APPLICANT: COUDERC, THERESA
/ APPLICANT: MICHELSON, SUSAN
/ APPLICANT: ZIPETO, DONATO
/ TITLE OF INVENTION: VECTOR DERIVED FROM ANTIBODIES FOR TRANSFERRING SUBSTANCES INTO C
/ FILE REFERENCE: 0660-0166-OXCONT
/ CURRENT APPLICATION NUMBER: US/10/460,471
/ CURRENT FILING DATE: 2003-06-13
/ PRIOR APPLICATION NUMBER: US/09/497,997C
/ PRIOR FILING DATE: 2000-02-04
/ PRIOR APPLICATION NUMBER: PCT/FR98/01740
/ PRIOR FILING DATE: 1998-08-04
/ NUMBER OF SEQ ID NOS: 36
/ SOFTWARE: Patentin version 3.1
/ SEQ ID NO 20
/ LENGTH: 22
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: SYNTHETIC PEPTIDE
US-10-460-471-20

Query Match          77.5%; Score 69; DB 4; Length 22;
Best Local Similarity 76.5%; Pred. No. 0.01;
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 YISGGSGTYYSDSVKG 17
    ||| ||| ||| ||| |||
DB 3 YISGGSVTYSDTVKG 19

RESULT 29
US-10-460-471-7
/ Sequence 7, Application US/10460471
/ Publication No. US20030206900A1
/ GENERAL INFORMATION:
/ APPLICANT: TERNYNCK, THERESA
/ APPLICANT: AVAMEAS, ALEXANDRE
/ APPLICANT: BUTTIN, GERARD
/ APPLICANT: AVAMEAS, STRAITTIS
/ APPLICANT: SARON, MARIE-FRANCOISE
/ APPLICANT: BLONDEL, BRUNO
/ APPLICANT: COUDERC, THERESA
/ APPLICANT: MICHELSON, SUSAN
/ APPLICANT: ZIPETO, DONATO
/ TITLE OF INVENTION: VECTOR DERIVED FROM ANTIBODIES FOR TRANSFERRING SUBSTANCES INTO C
/ FILE REFERENCE: 0660-0166-OXCONT
/ CURRENT APPLICATION NUMBER: US/10/460,471
/ CURRENT FILING DATE: 2003-06-13
/ PRIOR APPLICATION NUMBER: US/09/497,997C
/ PRIOR FILING DATE: 2000-02-04
/ PRIOR APPLICATION NUMBER: PCT/FR98/01740
/ PRIOR FILING DATE: 1998-08-04
/ NUMBER OF SEQ ID NOS: 36
/ SOFTWARE: Patentin version 3.1
/ SEQ ID NO 7
/ LENGTH: 30
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
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OTHER INFORMATION: SYNTHETIC PEPTIDE

US-10-460-471-7  
Query Match 77.5%; Score 69; DB 4; Length 30;  
Best Local Similarity 76.5%; Pred. No. 0.014;  
Matches 13; Conservative 1; Mismatches 0; Gaps 0;

QY 1 YISSGGSGTYYSDSVKG 17  
Db 3 YISRGVSTYYSDTVKG 19

RESULT 30  
US-10-144-549-21  
; Sequence 21, Application US/10144549  
; Publication No. US20030211590A1  
; GENERAL INFORMATION:  
; APPLICANT: Geneshuttle Biopharm, Inc.  
; TITLE OF INVENTION: A NEW FUSION PROTEIN FOR USE AS VECTOR  
; FILE REFERENCE: MBHB 02-340  
; CURRENT APPLICATION NUMBER: US/10/144,549  
; CURRENT FILING DATE: 2002-05-13  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 21  
; LENGTH: 30  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; OTHER INFORMATION: Membrane fusion sequence.  
; NAME/KEY: MISC\_FEATURE  
; OTHER INFORMATION: Synthetic membrane fusion sequence  
US-10-144-549-21

Query Match 77.5%; Score 69; DB 4; Length 30;  
Best Local Similarity 76.5%; Pred. No. 0.014;  
Matches 13; Conservative 1; Mismatches 0; Gaps 0;

QY 1 YISSGGSGTYYSDSVKG 17  
Db 3 YISRGVSTYYSDTVKG 19

RESULT 31  
US-10-368-280-4  
; Sequence 4, Application US/10368280  
; Publication No. US20030219375A1  
; GENERAL INFORMATION:  
; APPLICANT: Washington University, St. Louis  
; APPLICANT: Pivnicka-Worms, David  
; TITLE OF INVENTION: MEMBRANE-PERMEANT PEPTIDE COMPLEXES FOR MEDICAL IMAGING, DIAGNOSTIC  
; FILE REFERENCE: 60005161-0022  
; CURRENT APPLICATION NUMBER: US/10/368,280  
; CURRENT FILING DATE: 2003-02-18  
; PRIOR APPLICATION NUMBER: US 09/557,465  
; PRIOR FILING DATE: 2000-04-25  
; PRIOR APPLICATION NUMBER: US 09/336,093  
; PRIOR FILING DATE: 1999-06-20  
; PRIOR APPLICATION NUMBER: US 60/090,087  
; PRIOR FILING DATE: 1998-06-20  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 4  
; LENGTH: 30  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Peptide derivable from the heavy chain variable region of an antibody  
US-10-368-280-4

Query Match 77.5%; Score 69; DB 4; Length 30;  
Best Local Similarity 76.5%; Pred. No. 0.014;  
Matches 13; Conservative 1; Mismatches 0; Gaps 0;

QY 1 YISSGGSGTYYSDSVKG 17  
Db 3 YISRGVSTYYSDTVKG 19

RESULT 32  
US-10-374-035-4  
; Sequence 4, Application US/10374035  
; Publication No. US20030219378A1  
; GENERAL INFORMATION:  
; APPLICANT: Washington University, St. Louis  
; APPLICANT: Pivnicka-Worms, David  
; TITLE OF INVENTION: MEMBRANE-PERMEANT PEPTIDE COMPLEXES FOR MEDICAL IMAGING, DIAGNOSTIC  
; FILE REFERENCE: 09789280-0006  
; CURRENT APPLICATION NUMBER: US/10/374,035  
; CURRENT FILING DATE: 2003-02-25  
; PRIOR APPLICATION NUMBER: US 10/368,280  
; PRIOR FILING DATE: 2003-02-18  
; PRIOR APPLICATION NUMBER: US 09/557,465  
; PRIOR FILING DATE: 2000-04-25  
; PRIOR APPLICATION NUMBER: US 09/336,093  
; PRIOR FILING DATE: 1999-06-18  
; PRIOR APPLICATION NUMBER: US 60/090,087  
; PRIOR FILING DATE: 1998-06-20  
; NUMBER OF SEQ ID NOS: 39  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 4  
; LENGTH: 30  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Peptide derivable from the heavy chain variable region of an antibody  
US-10-374-035-4

Query Match 77.5%; Score 69; DB 4; Length 30;  
Best Local Similarity 76.5%; Pred. No. 0.014;  
Matches 13; Conservative 1; Mismatches 0; Gaps 0;

QY 1 YISSGGSGTYYSDSVKG 17  
Db 3 YISRGVSTYYSDTVKG 19

RESULT 33  
US-10-694-243-14  
; Sequence 14, Application US/10694243  
; Publication No. US20050130167A1  
; GENERAL INFORMATION:  
; APPLICANT: BAO, GANG  
; APPLICANT: NIE, SHUMING  
; APPLICANT: NIJIN, NIJIN  
; APPLICANT: LACONTE, LESLIE  
; TITLE OF INVENTION: MULTIFUNCTIONAL MAGNETIC NANOPARTICLE PROBES FOR  
; FILE REFERENCE: 17625-0058  
; CURRENT APPLICATION NUMBER: US/10/694,243  
; CURRENT FILING DATE: 2003-10-27  
; PRIOR APPLICATION NUMBER: 60/421,361  
; PRIOR FILING DATE: 2002-10-25  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 14  
; LENGTH: 30  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Peptide derivable from the heavy chain variable region of an antibody  
US-10-694-243-14

US-10-460-471-9

; PRIOR FILING DATE: 2000-02-04  
 ; PRIOR APPLICATION NUMBER: PCT/FR98/01740  
 ; PRIOR FILING DATE: 1998-08-04



Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 YISSGGSGTYTYPDSVKG 17  
||||| ||| :|||  
DB 50 YISSGGGTYYPDVKG 66

RESULT 42  
US-10-490-535-2  
; Sequence 2, Application US/10490535  
; Publication No. US20050118182A1  
; GENERAL INFORMATION:  
; APPLICANT: Paestan, Ira H.  
; APPLICANT: Salvatore, Giuliana  
; APPLICANT: Beers, Richard  
; APPLICANT: Kreitman, Robert J.  
; APPLICANT: The Government of the United States of America  
; APPLICANT: as represented by The Secretary of the  
; APPLICANT: Department of Health and Human Services  
; TITLE OF INVENTION: Mutated Anti-CD22 Antibodies With Increased Affinity to  
; TITLE OF INVENTION: CD22-Expressing Leukemia Cells  
; FILE REFERENCE: 015280-438100US  
; CURRENT APPLICATION NUMBER: US/10/490,535  
; CURRENT FILING DATE: 2004-03-24  
; PRIOR APPLICATION NUMBER: US 60/325,360  
; PRIOR FILING DATE: 2001-09-26  
; PRIOR APPLICATION NUMBER: WO PCT/US02/30316  
; PRIOR FILING DATE: 2002-09-25  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 123  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:RFB4 heavy  
; OTHER INFORMATION: chain variable region  
US-10-490-535-2

Query Match 77.5%; Score 69; DB 5; Length 123;  
Best Local Similarity 76.5%; Pred. No. 0.055;  
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 YISSGGSGTYTYPDSVKG 17  
||||| ||| :|||  
DB 50 YISSGGGTYYPDVKG 66

RESULT 43  
US-10-006-773-4  
; Sequence 4, Application US/10006773  
; Publication No. US20020132983A1  
; GENERAL INFORMATION:  
; APPLICANT: Jungmans, Richard P.  
; TITLE OF INVENTION: Antibodies as Chimeric Effector Cell Receptors Against Tumor Anti  
; FILE REFERENCE: 003  
; CURRENT APPLICATION NUMBER: US/10/006,773  
; CURRENT FILING DATE: 2001-12-10  
; PRIOR APPLICATION NUMBER: 60/250,089  
; PRIOR FILING DATE: 2000-11-30  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 4  
; LENGTH: 140  
; TYPE: PRT  
; ORGANISM: Mus sp.  
US-10-006-773-4

Query Match 77.5%; Score 69; DB 4; Length 140;  
Best Local Similarity 87.5%; Pred. No. 0.063;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 ISSGGSGTYTYPDSVKG 17

DB 70 ISSGGSHYYPDVKG 85  
||||| ||| :|||

RESULT 44  
US-10-281-479A-26  
; Sequence 26, Application US/10281479A  
; Publication No. US20030133932A1  
; GENERAL INFORMATION:  
; APPLICANT: The UAB Research Foundation  
; APPLICANT: Zhou, Tong  
; APPLICANT: Ichikawa, Kimihisa  
; APPLICANT: Kimberly, Robert P.  
; APPLICANT: Koopman, William J.  
; APPLICANT: Oshumi, Jun  
; APPLICANT: LoBuglio, Albert S.  
; APPLICANT: Buchsbaum, Donald J.  
; TITLE OF INVENTION: COMBINATIONS OF ANTIBODIES SELECTIVE FOR A TUMOR NECROSIS  
; TITLE OF INVENTION: FACTOR-RELATED APOPTOSIS-INDUCING LIGAND RECEPTOR AND OTHER THERE  
; TITLE OF INVENTION: AGENTS  
; FILE REFERENCE: 21085.0029U6  
; CURRENT APPLICATION NUMBER: US/10/281,479A  
; CURRENT FILING DATE: 2003-01-28  
; PRIOR APPLICATION NUMBER: 60/391,478  
; PRIOR FILING DATE: 2002-06-24  
; PRIOR APPLICATION NUMBER: 60/346,402  
; PRIOR FILING DATE: 2001-11-01  
; PRIOR APPLICATION NUMBER: PCT/US01/14151  
; PRIOR FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: 60/201,344  
; PRIOR FILING DATE: 2000-05-02  
; NUMBER OF SEQ ID NOS: 102  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 26  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:/No. US20030133932A1e = Synthe  
US-10-281-479A-26

Query Match 76.4%; Score 68; DB 4; Length 17;  
Best Local Similarity 87.5%; Pred. No. 0.011;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 ISSGGSGTYTYPDSVKG 17  
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DB 2 ISSGGSHYYPDVKG 17

RESULT 45  
US-10-275-180A-26  
; Sequence 26, Application US/10275180A  
; Publication No. US20030190687A1  
; GENERAL INFORMATION:  
; APPLICANT: The UAB Research Foundation  
; APPLICANT: Zhou, Tong  
; APPLICANT: Ichikawa, Kimihisa  
; APPLICANT: Kimberly, Robert P.  
; APPLICANT: Koopman, William J.  
; TITLE OF INVENTION: AN ANTIBODY SELECTIVE FOR A TUMOR NECROSIS FACTOR-RELATED APOPTOS  
; TITLE OF INVENTION: INDUCING LIGAND RECEPTOR AND USES THEREOF  
; FILE REFERENCE: 21085.0029U5  
; CURRENT APPLICATION NUMBER: US/10/275,180A  
; CURRENT FILING DATE: 2002-10-31  
; NUMBER OF SEQ ID NOS: 102  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 26  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:/No. US20030190687A1e =

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; TYPE: PRT
; ORGANISM: Mus musculus
US-10-477-377-9

Query Match 76.4%; Score 68; DB 4; Length 17;
Best Local Similarity 87.5%; Pred. No. 0.011;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 ISSGGSTYSDSVKG 17
   ||||| |||||
Db 2 ISSGGSTYYPDSVKG 17
   ||||| |||||

RESULT 48
US-09-840-459-53
; Sequence 53, Application US/09840459
; Patent No. US20020150576A1
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 53
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-840-459-53

Query Match 76.4%; Score 68; DB 3; Length 87;
Best Local Similarity 70.6%; Pred. No. 0.054;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 YISSGGSTYSDSVKG 17
   ||||| |||||
Db 39 YISNGGSTYYPDSVKG 55
   ||||| |||||

RESULT 49
US-10-766-773-53
; Sequence 53, Application US/10766773
; Publication No. US20040126851A1
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-028
; CURRENT APPLICATION NUMBER: US/10/766,773
; CURRENT FILING DATE: 2004-01-27
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193

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;  
; PRIOR FILING DATE: 1999-07-22  
; PRIOR APPLICATION NUMBER: 09/121,781  
; PRIOR FILING DATE: 1998-07-23  
; NUMBER OF SEQ ID NOS: 106  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 53  
; LENGTH: 87  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-766-773-53

Query Match 76.4%; Score 68; DB 4; Length 87;  
Best Local Similarity 70.6%; Pred. No. 0.054;  
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 YISSGGSTYYSDSVKG 17  
|||:| | | | | | | | |  
Db 39 YISNGGGSTYYPDVTKG 55

RESULT 50  
US-10-766-610-53  
; Sequence 53, Application US/10766610  
; Publication No. US20040132980A1  
; GENERAL INFORMATION:  
; APPLICANT: Larosa, Gregory J.  
; APPLICANT: Horvath, Christopher  
; APPLICANT: Newman, Walter  
; APPLICANT: Jones, S. Tarran  
; APPLICANT: O'Brien, Siobhan H.  
; APPLICANT: O'Keefe, Theresa  
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND  
; FILE REFERENCE: 1855.1052-029  
; CURRENT APPLICATION NUMBER: US/10/766,610  
; CURRENT FILING DATE: 2004-01-27  
; PRIOR APPLICATION NUMBER: 09/840,459  
; PRIOR FILING DATE: 2001-04-23  
; PRIOR APPLICATION NUMBER: PCT/US01/03537  
; PRIOR FILING DATE: 2001-02-02  
; PRIOR APPLICATION NUMBER: 09/497,625  
; PRIOR FILING DATE: 2000-02-03  
; PRIOR APPLICATION NUMBER: 09/359,193  
; PRIOR FILING DATE: 1999-07-22  
; PRIOR APPLICATION NUMBER: 09/121,781  
; PRIOR FILING DATE: 1998-07-23  
; NUMBER OF SEQ ID NOS: 107  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 53  
; LENGTH: 87  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-766-610-53

Query Match 76.4%; Score 68; DB 4; Length 87;  
Best Local Similarity 70.6%; Pred. No. 0.054;  
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 YISSGGSTYYSDSVKG 17  
|||:| | | | | | | | |  
Db 39 YISNGGGSTYYPDVTKG 55

Search completed: April 6, 2006, 09:22:24  
Job time : 142.441 secs

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OM protein - protein search, using sw model

Run on: April 6, 2006, 09:13:32 ; Search time 17.2881 Seconds  
(without alignments)  
30.672 Million cell updates/sec

Title: US-10-089-500-4

Perfect score: 89

Sequence: 1 YISGSGSYRYSVKG 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 184161 seqs, 31191982 residues

Total number of hits satisfying chosen parameters: 184161

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Published Applications AA New.\*

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2: /SIDSS/ptodata/2/pubppa/US06\_NEW\_PUB.pep.\*

3: /SIDSS/ptodata/2/pubppa/US07\_NEW\_PUB.pep.\*

4: /SIDSS/ptodata/2/pubppa/PCT\_NEW\_PUB.pep.\*

5: /SIDSS/ptodata/2/pubppa/US05\_NEW\_PUB.pep.\*

6: /SIDSS/ptodata/2/pubppa/US10\_NEW\_PUB.pep.\*

7: /SIDSS/ptodata/2/pubppa/US11\_NEW\_PUB.pep.\*

8: /SIDSS/ptodata/2/pubppa/US60\_NEW\_PUB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	89	100.0	17	6	US-10-473-037-4
2	89	100.0	119	6	US-10-473-037-9
3	89	100.0	119	6	US-10-473-037-49
4	89	100.0	130	7	US-11-228-293-18
5	89	100.0	130	7	US-11-228-319-18
6	89	100.0	138	6	US-10-473-037-1
7	86	96.6	118	6	US-10-325-366A-208
8	82	92.1	130	7	US-11-228-293-8
9	82	92.1	130	7	US-11-228-319-8
10	73	82.0	116	7	US-11-102-512-24
11	72	80.9	237	7	US-11-054-515-1906
12	72	80.9	237	7	US-11-054-515-2039
13	72	80.9	237	7	US-11-266-444-1906
14	72	80.9	237	7	US-11-266-444-2039
15	72	80.9	240	7	US-11-054-515-1905
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246	7	US-11-266-444-1314	Sequence 1314, Ap
17	6	US-10-982-440-111	Sequence 111, App
22	7	US-11-149-943-16	Sequence 16, Appl
98	7	US-11-144-248-30	Sequence 30, Appl
98	7	US-11-054-669-17	Sequence 17, Appl
98	7	US-11-084-554-27	Sequence 27, Appl
98	7	US-11-144-222-30	Sequence 30, Appl
98	7	US-11-004-590-16	Sequence 16, Appl
98	7	US-11-136-250-27	Sequence 27, Appl
98	7	US-11-182-343-30	Sequence 30, Appl
116	7	US-11-102-512-62	Sequence 62, Appl
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122	6	US-10-982-440-7	Sequence 7, Appli
122	6	US-10-982-440-11	Sequence 11, Appl
122	6	US-10-982-440-53	Sequence 53, Appl
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236	7	US-11-266-444-2010	Sequence 2010, Ap
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237	7	US-11-266-444-2118	Sequence 2118, Ap
238	7	US-11-054-515-2024	Sequence 2024, Ap
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239	7	US-11-054-515-2034	Sequence 2034, Ap
239	7	US-11-266-444-2034	Sequence 2034, Ap
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240	7	US-11-054-515-2045	Sequence 2045, Ap
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240	7	US-11-054-515-2048	Sequence 2105, Ap
240	7	US-11-054-515-2108	Sequence 2108, Ap
240	7	US-11-054-515-2113	Sequence 2113, Ap
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101	66	74.2	240	7	US-11-266-444-2016	Sequence 2016, Ap	174	63	70.8	254	7	US-11-266-444-1295	Sequence 1295, Ap
102	66	74.2	240	7	US-11-266-444-2035	Sequence 2025, Ap	175	62	68.7	112	6	US-10-771-257-3	Sequence 3, Appl
103	66	74.2	240	7	US-11-266-444-2039	Sequence 2039, Ap	176	62	68.7	112	6	US-10-771-257-3	Sequence 3, Appl
104	66	74.2	240	7	US-11-266-444-2030	Sequence 2030, Ap	177	62	68.7	112	7	US-11-127-932-1	Sequence 1, Appl
105	66	74.2	240	7	US-11-266-444-2041	Sequence 2041, Ap	178	62	68.7	112	7	US-11-127-932-1	Sequence 1, Appl
106	66	74.2	240	7	US-11-266-444-2044	Sequence 2044, Ap	179	62	68.7	112	7	US-11-102-512-33	Sequence 33, Appl
107	66	74.2	240	7	US-11-266-444-2045	Sequence 2045, Ap	180	62	68.7	116	7	US-11-102-512-80	Sequence 80, Appl
108	66	74.2	240	7	US-11-266-444-2048	Sequence 2048, Ap	181	62	68.7	123	7	US-11-127-903-48	Sequence 48, Appl
109	66	74.2	240	7	US-11-266-444-2105	Sequence 2105, Ap	182	62	68.7	125	7	US-11-127-903-46	Sequence 46, Appl
110	66	74.2	240	7	US-11-266-444-2108	Sequence 2108, Ap	183	62	68.7	125	7	US-11-127-903-46	Sequence 46, Appl
111	66	74.2	240	7	US-11-266-444-2113	Sequence 2113, Ap	184	62	68.7	138	6	US-10-789-273-8	Sequence 8, Appl
112	66	74.2	240	7	US-11-266-444-2117	Sequence 2117, Ap	185	62	68.7	138	6	US-10-789-273-12	Sequence 12, Appl
113	66	74.2	248	7	US-11-054-515-1965	Sequence 1965, Ap	186	62	68.7	256	7	US-11-054-515-1604	Sequence 1604, Ap
114	66	74.2	248	7	US-11-054-515-1974	Sequence 1974, Ap	187	62	68.7	256	7	US-11-266-444-1604	Sequence 1604, Ap
115	66	74.2	248	7	US-11-266-444-1965	Sequence 1965, Ap	188	62	68.7	367	7	US-11-000-463-899	Sequence 899, App
116	66	74.2	248	7	US-11-266-444-1974	Sequence 1974, Ap	189	61	68.5	17	7	US-11-097-812-167	Sequence 167, App
117	66	74.2	250	7	US-11-054-515-1179	Sequence 1179, Ap	190	61	68.5	115	7	US-11-127-932-2	Sequence 2, Appl
118	66	74.2	250	7	US-11-266-444-1179	Sequence 1179, Ap	191	61	68.5	115	7	US-11-127-932-3	Sequence 3, Appl
119	66	74.2	444	7	US-11-172-320-6	Sequence 6, Appl	192	61	68.5	115	7	US-11-127-932-6	Sequence 6, Appl
120	66	74.2	444	7	US-11-173-969-6	Sequence 6, Appl	193	61	68.5	115	7	US-11-127-932-7	Sequence 7, Appl
121	66	74.2	473	7	US-11-144-248-50	Sequence 50, Appl	194	61	68.5	115	7	US-11-127-932-8	Sequence 8, Appl
122	66	74.2	473	7	US-11-144-222-50	Sequence 50, Appl	195	61	68.5	115	7	US-11-127-932-9	Sequence 9, Appl
123	66	74.2	473	7	US-11-182-343-50	Sequence 50, Appl	196	61	68.5	115	7	US-11-127-932-10	Sequence 10, Appl
124	65	73.0	17	7	US-11-097-812-95	Sequence 95, Appl	197	61	68.5	115	7	US-11-097-812-22	Sequence 22, Appl
125	65	73.0	17	7	US-11-097-812-161	Sequence 161, App	198	61	68.5	115	7	US-11-097-812-26	Sequence 26, Appl
126	65	73.0	17	7	US-11-097-812-164	Sequence 164, App	199	61	68.5	115	7	US-11-127-903-2	Sequence 2, Appl
127	65	73.0	113	7	US-11-097-812-82	Sequence 82, Appl	200	61	68.5	115	7	US-11-127-903-3	Sequence 3, Appl
128	65	73.0	115	7	US-11-097-812-28	Sequence 28, Appl	201	61	68.5	115	7	US-11-127-903-6	Sequence 6, Appl
129	65	73.0	115	7	US-11-097-812-35	Sequence 35, Appl	202	61	68.5	115	7	US-11-127-903-7	Sequence 7, Appl
130	65	73.0	116	6	US-10-925-366A-214	Sequence 214, App	203	61	68.5	115	7	US-11-127-903-8	Sequence 8, Appl
131	65	73.0	118	6	US-10-771-257-15	Sequence 15, Appl	204	61	68.5	115	7	US-11-127-903-9	Sequence 9, Appl
132	65	73.0	118	7	US-11-127-677-15	Sequence 15, Appl	205	61	68.5	115	7	US-11-127-903-10	Sequence 10, Appl
133	65	73.0	119	7	US-11-097-812-133	Sequence 133, App	206	61	68.5	116	7	US-11-102-512-67	Sequence 67, Appl
134	65	73.0	119	7	US-11-097-812-134	Sequence 134, App	207	61	68.5	117	7	US-11-097-812-23	Sequence 23, Appl
135	65	73.0	119	7	US-11-097-812-137	Sequence 137, App	208	61	68.5	117	7	US-11-097-812-29	Sequence 29, Appl
136	65	73.0	119	7	US-11-097-812-139	Sequence 139, App	209	61	68.5	117	7	US-11-097-812-33	Sequence 33, Appl
137	65	73.0	119	7	US-11-097-812-140	Sequence 140, App	210	61	68.5	117	7	US-11-165-023-30	Sequence 30, Appl
138	65	73.0	119	7	US-11-097-812-146	Sequence 146, App	211	61	68.5	119	7	US-11-097-812-142	Sequence 142, App
139	65	73.0	119	7	US-11-097-812-147	Sequence 147, App	212	61	68.5	119	7	US-11-097-812-149	Sequence 149, App
140	65	73.0	119	7	US-11-097-812-148	Sequence 148, App	213	61	68.5	119	7	US-11-097-812-150	Sequence 150, App
141	65	73.0	119	7	US-11-097-812-151	Sequence 151, App	214	61	68.5	137	6	US-10-993-543-100	Sequence 100, App
142	65	73.0	119	7	US-11-097-812-152	Sequence 152, App	215	60.5	68.0	16	6	US-10-507-662-5	Sequence 5, Appl
143	65	73.0	119	7	US-11-097-812-154	Sequence 154, App	216	60.5	68.0	120	6	US-10-507-662-23	Sequence 23, Appl
144	65	73.0	119	7	US-11-097-812-203	Sequence 203, App	217	60	67.4	22	7	US-11-149-943-30	Sequence 30, Appl
145	65	73.0	129	6	US-10-771-257-61	Sequence 61, Appl	218	60	67.4	98	7	US-11-054-669-28	Sequence 28, Appl
146	65	73.0	127	7	US-11-127-677-59	Sequence 59, Appl	219	60	67.4	98	7	US-11-084-554-39	Sequence 39, Appl
147	65	73.0	129	7	US-11-054-515-1652	Sequence 1652, Ap	220	60	67.4	98	7	US-11-004-590-30	Sequence 30, Appl
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150	65	73.0	256	7	US-11-266-444-2119	Sequence 2119, Ap	223	60	67.4	116	7	US-11-103-512-9	Sequence 9, Appl
151	65	73.0	384	7	US-11-000-463-804	Sequence 804, App	224	60	67.4	123	6	US-10-925-366A-216	Sequence 216, App
152	65	73.0	384	7	US-11-000-463-805	Sequence 805, App	225	60	67.4	123	6	US-10-771-257-59	Sequence 59, Appl
153	65	73.0	384	7	US-11-000-463-806	Sequence 806, App	226	60	67.4	123	7	US-11-127-677-57	Sequence 57, Appl
154	65	73.0	384	7	US-11-000-463-807	Sequence 807, App	227	60	67.4	123	7	US-11-127-903-45	Sequence 45, Appl
155	64	71.9	17	7	US-11-097-812-90	Sequence 90, Appl	228	60	67.4	123	7	US-11-127-903-47	Sequence 47, Appl
156	64	71.9	118	7	US-11-097-812-69	Sequence 69, Appl	229	60	67.4	124	7	US-11-102-512-61	Sequence 61, Appl
157	64	71.9	159	7	US-11-000-463-333	Sequence 333, App	230	60	67.4	130	7	US-11-103-284-51	Sequence 51, Appl
158	63	70.8	98	7	US-11-084-554-42	Sequence 42, Appl	231	60	67.4	243	7	US-11-054-515-2102	Sequence 2102, Ap
159	63	70.8	98	7	US-11-136-250-42	Sequence 42, Appl	232	60	67.4	243	7	US-11-266-444-2102	Sequence 2102, Ap
160	63	70.8	121	6	US-10-771-257-7	Sequence 7, Appl	233	60	67.4	247	7	US-11-054-515-1953	Sequence 1953, Ap
161	63	70.8	121	7	US-11-127-677-7	Sequence 7, Appl	234	60	67.4	247	7	US-11-266-444-1953	Sequence 1953, Ap
162	63	70.8	125	6	US-10-771-257-6	Sequence 6, Appl	235	59.5	68.9	312	7	US-11-000-463-334	Sequence 334, App
163	63	70.8	125	7	US-11-127-677-6	Sequence 6, Appl	236	59	66.3	17	6	US-10-982-440-105	Sequence 105, App
164	63	70.8	125	7	US-11-127-903-43	Sequence 43, Appl	237	59	66.3	17	7	US-11-201-825-39	Sequence 39, Appl
165	63	70.8	243	7	US-11-054-515-1929	Sequence 1929, Ap	238	59	66.3	19	7	US-11-167-872-62	Sequence 62, Appl
166	63	70.8	243	7	US-11-054-515-1942	Sequence 1942, Ap	239	59	66.3	19	7	US-11-167-872-68	Sequence 68, Appl
167	63	70.8	243	7	US-11-054-515-1944	Sequence 1944, Ap	240	59	66.3	22	7	US-11-149-943-23	Sequence 23, Appl
168	63	70.8	243	7	US-11-054-515-1945	Sequence 1945, Ap	241	59	66.3	85	6	US-10-925-366A-350	Sequence 350, App
169	63	70.8	243	7	US-11-266-444-1929	Sequence 1929, Ap	242	59	66.3	86	6	US-10-925-366A-357	Sequence 357, App
170	63	70.8	243	7	US-11-266-444-1942	Sequence 1942, Ap	243	59	66.3	89	6	US-10-925-366A-367	Sequence 367, App
171	63	70.8	243	7	US-11-266-444-1944	Sequence 1944, Ap	244	59	66.3	96	6	US-10-993-543-287	Sequence 287, App



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392	58	65.2	119	7	US-11-143-386-9	Sequence 9, Appli	465	56	62.9	17	7	US-11-224-623-16	Sequence 16, Appl
393	58	65.2	119	7	US-11-187-364-9	Sequence 9, Appli	466	56	62.9	17	7	US-11-217-919-80	Sequence 80, Appl
394	58	65.2	120	7	US-11-149-943-57	Sequence 57, Appl	467	56	62.9	116	7	US-11-102-512-13	Sequence 13, Appl
395	58	65.2	123	7	US-11-127-903-40	Sequence 40, Appl	468	56	62.9	116	7	US-11-102-512-21	Sequence 21, Appl
396	58	65.2	123	7	US-11-102-512-15	Sequence 15, Appl	469	56	62.9	116	7	US-11-102-512-45	Sequence 45, Appl
397	58	65.2	123	7	US-11-102-512-85	Sequence 85, Appl	470	56	62.9	116	7	US-11-102-512-59	Sequence 59, Appl
398	58	65.2	124	7	US-11-049-536-310	Sequence 310, Appl	471	56	62.9	117	6	US-10-834-397-24	Sequence 24, Appl
399	58	65.2	124	7	US-11-199-739-310	Sequence 310, Appl	472	56	62.9	117	7	US-11-049-536-698	Sequence 698, Appl
400	58	65.2	241	7	US-11-102-512-88	Sequence 88, Appl	473	56	62.9	121	6	US-11-199-739-698	Sequence 698, Appl
401	58	65.2	250	7	US-11-054-515-1851	Sequence 1851, Ap	474	56	62.9	121	6	US-10-925-366A-212	Sequence 212, Appl
402	58	65.2	250	7	US-11-266-444-1851	Sequence 1851, Ap	475	56	62.9	122	7	US-11-144-248-24	Sequence 24, Appl
403	58	65.2	251	7	US-11-054-515-1411	Sequence 1411, Ap	476	56	62.9	122	7	US-11-144-222-4	Sequence 24, Appl
404	58	65.2	251	7	US-11-266-444-1411	Sequence 1411, Ap	477	56	62.9	122	7	US-11-182-343-24	Sequence 24, Appl
405	58	65.2	16	7	US-11-149-309-23	Sequence 23, Appl	478	56	62.9	124	6	US-10-771-257-19	Sequence 19, Appl
406	57.5	64.6	17	7	US-11-171-567-166	Sequence 166, Appl	479	56	62.9	124	6	US-11-127-677-19	Sequence 19, Appl
407	57.5	64.6	97	7	US-11-054-669-48	Sequence 48, Appl	480	56	62.9	129	6	US-10-993-543-160	Sequence 160, Appl
408	57.5	64.6	97	7	US-11-093-274-32	Sequence 32, Appl	481	56	62.9	135	6	US-10-993-543-36	Sequence 36, Appl
409	57.5	64.6	116	7	US-11-125-837-35	Sequence 35, Appl	482	56	62.9	174	7	US-11-144-248-4	Sequence 4, Appli
410	57.5	64.6	116	7	US-11-125-837-38	Sequence 38, Appl	483	56	62.9	174	7	US-11-144-222-4	Sequence 4, Appli
411	57.5	64.6	118	7	US-11-149-309-13	Sequence 13, Appl	484	56	62.9	174	7	US-11-182-343-4	Sequence 4, Appli
412	57.5	64.6	118	7	US-11-149-309-14	Sequence 14, Appl	485	56	62.9	240	7	US-11-054-515-2013	Sequence 2013, Ap
413	57.5	64.6	118	7	US-11-149-309-15	Sequence 15, Appl	486	56	62.9	240	7	US-11-266-444-2013	Sequence 2013, Ap
414	57.5	64.6	118	7	US-11-149-309-16	Sequence 16, Appl	487	56	62.9	241	7	US-11-054-515-1911	Sequence 1911, Ap
415	57.5	64.6	118	7	US-11-149-309-36	Sequence 36, Appl	488	56	62.9	241	7	US-11-266-444-1911	Sequence 1911, Ap
416	57	64.0	116	7	US-11-102-512-7	Sequence 7, Appli	489	56	62.9	242	7	US-11-054-515-1949	Sequence 1949, Ap
417	57	64.0	116	7	US-11-102-512-10	Sequence 10, Appl	490	56	62.9	242	7	US-11-266-444-1949	Sequence 1949, Ap
418	57	64.0	116	7	US-11-102-512-22	Sequence 22, Appl	491	56	62.9	249	7	US-11-054-515-963	Sequence 963, App
419	57	64.0	116	7	US-11-102-512-28	Sequence 28, Appl	492	56	62.9	249	7	US-11-266-444-963	Sequence 963, App
420	57	64.0	116	7	US-11-102-512-29	Sequence 29, Appl	493	56	62.9	251	7	US-11-054-515-951	Sequence 951, App
421	57	64.0	116	7	US-11-102-512-34	Sequence 34, Appl	494	56	62.9	251	7	US-11-266-444-951	Sequence 951, App
422	57	64.0	116	7	US-11-102-512-63	Sequence 63, Appl	495	56	62.9	255	7	US-11-054-515-1819	Sequence 1819, Ap
423	57	64.0	116	7	US-11-102-512-65	Sequence 65, Appl	496	56	62.9	255	7	US-11-266-444-1819	Sequence 1819, Ap
424	57	64.0	116	7	US-11-102-512-81	Sequence 81, Appl	497	56	62.9	470	7	US-11-144-248-49	Sequence 49, Appl
425	57	64.0	118	7	US-11-049-536-198	Sequence 198, App	498	56	62.9	470	7	US-11-144-222-49	Sequence 49, Appl
426	57	64.0	118	7	US-11-199-739-198	Sequence 198, App	499	56	62.9	524	7	US-11-182-343-49	Sequence 49, Appl
427	57	64.0	119	6	US-10-925-366A-210	Sequence 210, App	500	56	62.9	524	7	US-11-041-095-58	Sequence 58, Appl
428	57	64.0	121	7	US-11-037-199-19	Sequence 19, Appl	501	55.5	62.4	16	7	US-11-171-567-164	Sequence 164, App
429	57	64.0	125	6	US-10-771-257-43	Sequence 43, Appl	502	55.5	62.4	118	7	US-11-049-536-334	Sequence 334, App
430	57	64.0	125	6	US-11-127-677-41	Sequence 41, Appl	503	55.5	62.4	118	7	US-11-199-739-334	Sequence 334, App
431	57	64.0	129	7	US-11-049-536-554	Sequence 554, App	504	55	61.8	22	7	US-11-149-943-29	Sequence 29, Appl
432	57	64.0	129	7	US-11-199-739-554	Sequence 554, App	505	55	61.8	99	7	US-11-054-669-27	Sequence 27, Appl
433	57	64.0	248	7	US-11-054-515-1876	Sequence 1876, Ap	506	55	61.8	99	7	US-11-084-554-38	Sequence 38, Appl
434	57	64.0	248	7	US-11-266-444-1876	Sequence 1876, Ap	507	55	61.8	99	7	US-11-084-554-38	Sequence 38, Appl
435	57	64.0	250	7	US-11-054-515-1341	Sequence 1341, Ap	508	55	61.8	112	7	US-11-136-250-38	Sequence 38, Appl
436	57	64.0	250	7	US-11-266-444-1341	Sequence 1341, Ap	509	55	61.8	112	7	US-11-195-095-12	Sequence 12, Appl
437	57	64.0	253	7	US-11-054-515-1432	Sequence 1432, Ap	510	55	61.8	115	7	US-11-127-903-27	Sequence 27, Appl
438	57	64.0	253	7	US-11-266-444-1432	Sequence 1432, Ap	511	55	61.8	116	6	US-10-925-366A-209	Sequence 209, App
439	57	64.0	254	7	US-11-054-515-1735	Sequence 1735, Ap	512	55	61.8	117	7	US-11-127-903-42	Sequence 42, Appl
440	57	64.0	254	7	US-11-266-444-1735	Sequence 1735, Ap	513	55	61.8	119	6	US-10-771-257-10	Sequence 10, Appl
441	56.5	63.5	16	7	US-11-171-567-163	Sequence 163, Appl	514	55	61.8	119	6	US-11-127-677-10	Sequence 10, Appl
442	56.5	63.5	21	7	US-11-149-943-32	Sequence 32, Appl	515	55	61.8	125	7	US-11-144-248-16	Sequence 16, Appl
443	56.5	63.5	21	7	US-11-149-943-34	Sequence 34, Appl	516	55	61.8	125	7	US-11-144-222-16	Sequence 16, Appl
444	56.5	63.5	97	7	US-11-054-669-29	Sequence 29, Appl	517	55	61.8	125	7	US-11-182-343-16	Sequence 16, Appl
445	56.5	63.5	97	7	US-11-054-669-31	Sequence 31, Appl	518	55	61.8	131	7	US-11-049-536-24	Sequence 24, Appl
446	56.5	63.5	97	7	US-11-084-554-41	Sequence 41, Appl	519	55	61.8	131	7	US-11-199-739-24	Sequence 24, Appl
447	56.5	63.5	97	7	US-11-004-590-32	Sequence 32, Appl	520	55	61.8	150	7	US-11-267-310-9	Sequence 9, Appli
448	56.5	63.5	97	7	US-11-004-590-34	Sequence 34, Appl	521	55	61.8	150	7	US-11-267-131-9	Sequence 9, Appli
449	56.5	63.5	97	7	US-11-136-250-41	Sequence 41, Appl	522	55	61.8	153	7	US-11-267-310-11	Sequence 11, Appl
450	56.5	63.5	116	7	US-11-054-669-101	Sequence 101, App	523	55	61.8	153	7	US-11-267-191-11	Sequence 11, Appl
451	56.5	63.5	120	7	US-11-171-567-200	Sequence 200, App	524	55	61.8	205	7	US-11-128-440-9	Sequence 9, Appli
452	56.5	63.5	125	6	US-10-771-257-49	Sequence 49, Appl	525	55	61.8	239	7	US-11-054-515-1882	Sequence 1882, Ap
453	56.5	63.5	125	7	US-11-127-677-47	Sequence 47, Appl	526	55	61.8	239	7	US-11-266-444-1882	Sequence 1882, Ap
454	56.5	63.5	247	7	US-11-054-515-1177	Sequence 1177, Ap	527	55	61.8	241	7	US-11-054-515-1888	Sequence 1888, Ap
455	56.5	63.5	247	7	US-11-266-444-1177	Sequence 1177, Ap	528	55	61.8	241	7	US-11-266-444-1888	Sequence 1888, Ap
456	56.5	63.5	249	7	US-11-054-515-1335	Sequence 1335, Ap	529	55	61.8	242	7	US-11-054-515-1884	Sequence 1884, Ap
457	56.5	63.5	249	7	US-11-266-444-1335	Sequence 1335, Ap	530	55	61.8	242	7	US-11-266-444-1884	Sequence 1884, Ap
458	56.5	63.5	252	7	US-11-054-515-1311	Sequence 1311, Ap	531	55	61.8	243	7	US-11-054-515-1940	Sequence 1940, Ap
459	56.5	63.5	252	7	US-11-266-444-1311	Sequence 1311, Ap	532	55	61.8	243	7	US-11-266-444-1940	Sequence 1940, Ap
460	56.5	63.5	253	7	US-11-054-515-1449	Sequence 1449, Ap	533	55	61.8	247	7	US-11-054-515-1892	Sequence 1892, Ap
461	56.5	63.5	253	7	US-11-054-515-1814	Sequence 1814, Ap	534	55	61.8	247	7	US-11-266-444-1892	Sequence 1892, Ap
462	56.5	63.5	253	7	US-11-266-444-1449	Sequence 1449, Ap	535	55	61.8	249	7	US-11-054-515-941	Sequence 941, App
463	56.5	63.5	253	7	US-11-266-444-1814	Sequence 1814, Ap	536	55	61.8	249	7	US-11-054-515-1956	Sequence 1956, App

537	55	61.8	249	7	US-11-266-444-941	Sequence 941, App	610	54	60.7	239	6	US-10-952-535A-6	Sequence 6, Appl1
538	55	61.8	249	7	US-11-266-444-1956	Sequence 1956, App	611	54	60.7	241	7	US-11-054-515-2055	Sequence 2055, App
539	55	61.8	251	7	US-11-054-515-3245	Sequence 3245, App	612	54	60.7	241	7	US-11-266-444-2055	Sequence 2055, App
540	55	61.8	254	7	US-11-054-515-1441	Sequence 1441, App	613	54	60.7	244	7	US-11-054-515-1924	Sequence 1924, App
541	55	61.8	254	7	US-11-266-444-1441	Sequence 1441, App	614	54	60.7	244	7	US-11-266-444-1924	Sequence 1924, App
542	55	61.8	255	7	US-11-054-515-1608	Sequence 1608, App	615	54	60.7	245	7	US-11-054-515-3241	Sequence 3241, App
543	55	61.8	255	7	US-11-266-444-1608	Sequence 1608, App	616	54	60.7	247	7	US-11-054-515-994	Sequence 924, App
544	54.5	61.2	17	6	US-10-507-178-2	Sequence 2, Appl1	617	54	60.7	247	7	US-11-054-515-1330	Sequence 1330, App
545	54.5	61.2	119	7	US-11-049-536-370	Sequence 370, App	618	54	60.7	247	7	US-11-266-444-924	Sequence 924, App
546	54.5	61.2	119	7	US-11-199-739-370	Sequence 370, App	619	54	60.7	247	7	US-11-266-444-1330	Sequence 1330, App
547	54.5	61.2	120	7	US-11-049-536-482	Sequence 482, App	620	54	60.7	248	7	US-11-054-515-1421	Sequence 1421, App
548	54.5	61.2	120	7	US-11-199-739-482	Sequence 482, App	621	54	60.7	248	7	US-11-266-444-1421	Sequence 1421, App
549	54.5	61.2	238	7	US-11-193-561-10	Sequence 10, Appl1	622	54	60.7	249	7	US-11-054-515-5	Sequence 5, Appl1
550	54.5	61.2	238	7	US-11-193-771-10	Sequence 10, Appl1	623	54	60.7	249	7	US-11-054-515-397	Sequence 397, App
551	54.5	61.2	238	7	US-11-193-789-10	Sequence 10, Appl1	624	54	60.7	249	7	US-11-054-515-512	Sequence 512, App
552	54.5	61.2	238	7	US-11-193-806-10	Sequence 10, Appl1	625	54	60.7	249	7	US-11-054-515-892	Sequence 892, App
553	54.5	61.2	238	7	US-11-193-857-10	Sequence 10, Appl1	626	54	60.7	249	7	US-11-054-515-911	Sequence 911, App
554	54.5	61.2	246	7	US-11-054-515-1980	Sequence 1980, App	627	54	60.7	249	7	US-11-054-515-1102	Sequence 1102, App
555	54.5	61.2	246	7	US-11-266-444-1980	Sequence 1980, App	628	54	60.7	249	7	US-11-054-515-1105	Sequence 1105, App
556	54.5	61.2	307	7	US-11-000-463-332	Sequence 332, App	629	54	60.7	249	7	US-11-054-515-1108	Sequence 1108, App
557	54.5	61.2	363	7	US-11-000-463-335	Sequence 335, App	630	54	60.7	249	7	US-11-054-515-1110	Sequence 1110, App
558	54	60.7	17	6	US-10-982-440-116	Sequence 116, App	631	54	60.7	249	7	US-11-054-515-1111	Sequence 1111, App
559	54	60.7	22	7	US-11-149-943-24	Sequence 24, App1	632	54	60.7	249	7	US-11-054-515-1113	Sequence 1113, App
560	54	60.7	22	7	US-11-149-943-37	Sequence 37, App1	633	54	60.7	249	7	US-11-054-515-1115	Sequence 1115, App
561	54	60.7	22	7	US-11-054-669-23	Sequence 23, App1	634	54	60.7	249	7	US-11-054-515-1117	Sequence 1117, App
562	54	60.7	98	7	US-11-054-669-23	Sequence 23, App1	635	54	60.7	249	7	US-11-054-515-1119	Sequence 1119, App
563	54	60.7	98	7	US-11-054-669-24	Sequence 24, App1	636	54	60.7	249	7	US-11-054-515-1724	Sequence 1724, App
564	54	60.7	98	7	US-11-054-669-25	Sequence 25, App1	637	54	60.7	249	7	US-11-054-515-1725	Sequence 1725, App
565	54	60.7	98	7	US-11-054-669-33	Sequence 33, App1	638	54	60.7	249	7	US-11-266-444-5	Sequence 5, Appl1
566	54	60.7	98	7	US-11-084-554-34	Sequence 34, App1	639	54	60.7	249	7	US-11-266-444-397	Sequence 397, App
567	54	60.7	98	7	US-11-084-554-47	Sequence 47, App1	640	54	60.7	249	7	US-11-266-444-512	Sequence 512, App
568	54	60.7	98	7	US-11-004-590-24	Sequence 24, App1	641	54	60.7	249	7	US-11-266-444-892	Sequence 892, App
569	54	60.7	98	7	US-11-004-590-25	Sequence 25, App1	642	54	60.7	249	7	US-11-266-444-911	Sequence 911, App
570	54	60.7	98	7	US-11-004-590-37	Sequence 37, App1	643	54	60.7	249	7	US-11-266-444-1102	Sequence 1102, App
571	54	60.7	98	7	US-11-136-250-34	Sequence 34, App1	644	54	60.7	249	7	US-11-266-444-1105	Sequence 1105, App
572	54	60.7	98	7	US-11-136-250-47	Sequence 47, App1	645	54	60.7	249	7	US-11-266-444-1108	Sequence 1108, App
573	54	60.7	115	6	US-10-952-535A-2	Sequence 2, Appl1	646	54	60.7	249	7	US-11-266-444-1110	Sequence 1110, App
574	54	60.7	116	6	US-10-925-368A-228	Sequence 228, App	647	54	60.7	249	7	US-11-266-444-1111	Sequence 1111, App
575	54	60.7	116	6	US-11-102-512-16	Sequence 16, App1	648	54	60.7	249	7	US-11-266-444-1113	Sequence 1113, App
576	54	60.7	116	6	US-11-102-512-73	Sequence 73, App1	649	54	60.7	249	7	US-11-266-444-1115	Sequence 1115, App
577	54	60.7	117	6	US-10-771-257-9	Sequence 9, Appl1	650	54	60.7	249	7	US-11-266-444-1117	Sequence 1117, App
578	54	60.7	117	6	US-10-771-257-18	Sequence 18, App1	651	54	60.7	249	7	US-11-266-444-1119	Sequence 1119, App
579	54	60.7	117	6	US-10-771-257-81	Sequence 81, App1	652	54	60.7	249	7	US-11-266-444-1724	Sequence 1724, App
580	54	60.7	117	6	US-10-771-257-82	Sequence 82, App1	653	54	60.7	249	7	US-11-266-444-1725	Sequence 1725, App
581	54	60.7	117	6	US-10-771-257-83	Sequence 83, App1	654	54	60.7	252	7	US-11-054-515-1201	Sequence 1201, App
582	54	60.7	117	6	US-10-771-257-87	Sequence 87, App1	655	54	60.7	252	7	US-11-054-515-1394	Sequence 1394, App
583	54	60.7	117	6	US-10-771-257-89	Sequence 89, App1	656	54	60.7	252	7	US-11-054-515-1519	Sequence 1519, App
584	54	60.7	117	6	US-10-771-257-92	Sequence 92, App1	657	54	60.7	252	7	US-11-054-515-1627	Sequence 1627, App
585	54	60.7	117	6	US-10-771-257-93	Sequence 93, App1	658	54	60.7	252	7	US-11-054-515-1731	Sequence 1731, App
586	54	60.7	117	6	US-10-771-257-94	Sequence 94, App1	659	54	60.7	252	7	US-11-266-444-1201	Sequence 1201, App
587	54	60.7	117	6	US-10-771-257-96	Sequence 96, App1	660	54	60.7	252	7	US-11-266-444-1394	Sequence 1394, App
588	54	60.7	117	7	US-11-127-677-9	Sequence 9, Appl1	661	54	60.7	252	7	US-11-266-444-1519	Sequence 1519, App
589	54	60.7	117	7	US-11-127-677-18	Sequence 18, App1	662	54	60.7	252	7	US-11-266-444-1627	Sequence 1627, App
590	54	60.7	117	7	US-11-127-903-44	Sequence 44, App1	663	54	60.7	252	7	US-11-266-444-1731	Sequence 1731, App
591	54	60.7	119	7	US-11-102-512-42	Sequence 42, App1	664	54	60.7	253	7	US-11-054-515-1337	Sequence 1337, App
592	54	60.7	120	6	US-10-771-257-12	Sequence 12, App1	665	54	60.7	253	7	US-11-054-515-1835	Sequence 1835, App
593	54	60.7	120	7	US-11-127-677-12	Sequence 12, App1	666	54	60.7	253	7	US-11-266-444-1337	Sequence 1337, App
594	54	60.7	120	7	US-11-049-536-590	Sequence 590, App	667	54	60.7	253	7	US-11-266-444-1835	Sequence 1835, App
595	54	60.7	120	6	US-11-199-739-590	Sequence 590, App	668	54	60.7	254	7	US-11-054-515-977	Sequence 977, App
596	54	60.7	121	6	US-10-771-257-20	Sequence 20, App1	669	54	60.7	254	7	US-11-054-515-981	Sequence 981, App
597	54	60.7	121	7	US-11-127-677-20	Sequence 20, App1	670	54	60.7	254	7	US-11-054-515-983	Sequence 983, App
598	54	60.7	123	6	US-10-982-440-21	Sequence 21, App1	671	54	60.7	254	7	US-11-054-515-1673	Sequence 1673, App
599	54	60.7	123	7	US-11-127-903-39	Sequence 39, App1	672	54	60.7	254	7	US-11-266-444-977	Sequence 977, App
600	54	60.7	124	6	US-10-771-257-50	Sequence 50, App1	673	54	60.7	254	7	US-11-266-444-981	Sequence 981, App
601	54	60.7	124	7	US-11-127-677-48	Sequence 48, App1	674	54	60.7	254	7	US-11-266-444-983	Sequence 983, App
602	54	60.7	126	6	US-10-771-257-45	Sequence 45, App1	675	54	60.7	256	7	US-11-266-444-1673	Sequence 1673, App
603	54	60.7	126	7	US-11-127-677-43	Sequence 43, App1	676	54	60.7	256	7	US-11-054-515-839	Sequence 839, App
604	54	60.7	128	6	US-10-982-440-29	Sequence 29, App1	677	54	60.7	256	7	US-11-266-444-839	Sequence 839, App
605	54	60.7	130	7	US-11-109-264-53	Sequence 53, App1	678	53.5	60.1	243	7	US-11-054-515-995	Sequence 995, App
606	54	60.7	130	7	US-11-109-264-53	Sequence 53, App1	679	53.5	60.1	243	7	US-11-266-444-995	Sequence 995, App
607	54	60.7	132	6	US-10-993-543-176	Sequence 176, App	680	53.5	60.1	255	7	US-11-054-515-1137	Sequence 1137, App
608	54	60.7	238	7	US-11-054-515-1931	Sequence 1931, App	681	53.5	60.1	255	7	US-11-266-444-1137	Sequence 1137, App
609	54	60.7	238	7	US-11-266-444-1931	Sequence 1931, App	682	53.6	59.6	17	7	US-11-224-623-5	Sequence 5, Appl1

683	53	59.6	112	7	US-11-224-623-10	Sequence 10, Appl	756	52	58.4	119	6	US-10-771-257-14	Sequence 14, Appl
684	53	59.6	116	7	US-11-102-513-25	Sequence 25, Appl	757	52	58.4	119	6	US-10-771-257-21	Sequence 21, Appl
685	53	59.6	116	7	US-11-102-513-60	Sequence 60, Appl	758	52	58.4	119	7	US-11-127-677-14	Sequence 14, Appl
686	53	59.6	117	7	US-11-127-903-32	Sequence 32, Appl	759	52	58.4	119	7	US-11-127-677-21	Sequence 21, Appl
687	53	59.6	118	7	US-11-102-513-14	Sequence 14, Appl	760	52	58.4	119	7	US-11-049-536-470	Sequence 470, Appl
688	53	59.6	119	6	US-10-925-366A-364	Sequence 364, Appl	761	52	58.4	119	7	US-11-049-536-534	Sequence 534, Appl
689	53	59.6	119	6	US-11-217-913-183	Sequence 183, Appl	762	52	58.4	119	7	US-11-199-739-470	Sequence 470, Appl
690	53	59.6	122	6	US-10-771-257-57	Sequence 57, Appl	763	52	58.4	119	7	US-11-199-739-534	Sequence 534, Appl
691	53	59.6	122	6	US-11-127-677-55	Sequence 55, Appl	764	52	58.4	120	6	US-10-771-257-46	Sequence 46, Appl
692	53	59.6	123	6	US-10-771-257-5	Sequence 5, Appl	765	52	58.4	120	6	US-11-127-677-44	Sequence 44, Appl
693	53	59.6	123	6	US-11-127-677-5	Sequence 5, Appl	766	52	58.4	122	7	US-11-049-536-574	Sequence 574, Appl
694	53	59.6	124	7	US-11-144-248-8	Sequence 8, Appl	767	52	58.4	122	7	US-11-199-739-574	Sequence 574, Appl
695	53	59.6	124	7	US-11-144-222-8	Sequence 8, Appl	768	52	58.4	122	7	US-11-102-512-75	Sequence 75, Appl
696	53	59.6	124	7	US-11-182-343-8	Sequence 8, Appl	769	52	58.4	123	6	US-10-925-366A-217	Sequence 217, Appl
697	53	59.6	127	6	US-10-771-257-48	Sequence 48, Appl	770	52	58.4	123	6	US-10-771-257-86	Sequence 86, Appl
698	53	59.6	127	7	US-11-127-677-46	Sequence 46, Appl	771	52	58.4	123	6	US-10-993-543-112	Sequence 112, Appl
699	53	59.6	139	6	US-10-721-763-33	Sequence 33, Appl	772	52	58.4	123	6	US-11-102-512-18	Sequence 18, Appl
700	53	59.6	204	7	US-11-128-440-15	Sequence 15, Appl	773	52	58.4	123	7	US-11-102-512-58	Sequence 58, Appl
701	53	59.6	217	7	US-11-128-440-11	Sequence 11, Appl	774	52	58.4	123	7	US-11-102-512-70	Sequence 70, Appl
702	53	59.6	244	7	US-11-054-515-1991	Sequence 1991, Ap	775	52	58.4	125	7	US-11-049-536-478	Sequence 478, Appl
703	53	59.6	244	7	US-11-266-444-1991	Sequence 1991, Ap	776	52	58.4	125	7	US-11-199-739-478	Sequence 478, Appl
704	53	59.6	246	7	US-11-054-515-1002	Sequence 1002, Ap	777	52	58.4	127	7	US-11-049-536-64	Sequence 64, Appl
705	53	59.6	246	7	US-11-266-444-1002	Sequence 1002, Ap	778	52	58.4	127	7	US-11-199-739-64	Sequence 64, Appl
706	53	59.6	248	7	US-11-054-515-913	Sequence 913, Appl	779	52	58.4	128	7	US-11-049-536-76	Sequence 76, Appl
707	53	59.6	248	7	US-11-266-444-913	Sequence 913, Appl	780	52	58.4	128	7	US-11-199-739-76	Sequence 76, Appl
708	53	59.6	251	7	US-11-054-515-1171	Sequence 1171, Ap	781	52	58.4	129	7	US-11-064-174-143	Sequence 143, Appl
709	53	59.6	251	7	US-11-266-444-1171	Sequence 1171, Ap	782	52	58.4	132	6	US-10-993-543-152	Sequence 152, Appl
710	53	59.6	254	7	US-11-054-515-971	Sequence 971, Appl	783	52	58.4	148	7	US-11-049-536-20	Sequence 20, Appl
711	53	59.6	254	7	US-11-054-515-1195	Sequence 1195, Ap	784	52	58.4	148	7	US-11-199-739-20	Sequence 20, Appl
712	53	59.6	254	7	US-11-054-515-1625	Sequence 1625, Ap	785	52	58.4	237	7	US-11-054-515-1941	Sequence 1941, Ap
713	53	59.6	254	7	US-11-266-444-971	Sequence 971, Appl	786	52	58.4	237	7	US-11-266-444-1941	Sequence 1941, Ap
714	53	59.6	254	7	US-11-266-444-1195	Sequence 1195, Ap	787	52	58.4	241	7	US-11-054-515-1937	Sequence 1937, Ap
715	53	59.6	254	7	US-11-266-444-1625	Sequence 1625, Ap	788	52	58.4	241	7	US-11-266-444-1937	Sequence 1937, Ap
716	53	59.6	256	7	US-11-054-515-1209	Sequence 1209, Ap	789	52	58.4	247	7	US-11-054-515-1703	Sequence 1703, Ap
717	53	59.6	256	7	US-11-054-515-1392	Sequence 1392, Ap	790	52	58.4	247	7	US-11-054-515-1764	Sequence 1764, Ap
718	53	59.6	256	7	US-11-266-444-1209	Sequence 1209, Ap	791	52	58.4	247	7	US-11-054-515-1928	Sequence 1928, Ap
719	53	59.6	256	7	US-11-266-444-1392	Sequence 1392, Ap	792	52	58.4	247	7	US-11-054-515-1934	Sequence 1934, Ap
720	53	59.6	258	7	US-11-054-515-1841	Sequence 1841, Ap	793	52	58.4	247	7	US-11-054-515-1978	Sequence 1978, Ap
721	53	59.6	258	7	US-11-266-444-1841	Sequence 1841, Ap	794	52	58.4	247	7	US-11-266-444-1703	Sequence 1703, Ap
722	53	59.6	442	7	US-11-224-623-12	Sequence 12, Appl	795	52	58.4	247	7	US-11-266-444-1764	Sequence 1764, Ap
723	53	59.6	470	7	US-11-144-248-45	Sequence 45, Appl	796	52	58.4	247	7	US-11-266-444-1928	Sequence 1928, Ap
724	53	59.6	470	7	US-11-144-222-45	Sequence 45, Appl	797	52	58.4	247	7	US-11-266-444-1934	Sequence 1934, Ap
725	53	59.6	470	7	US-11-182-343-45	Sequence 45, Appl	798	52	58.4	247	7	US-11-266-444-1978	Sequence 1978, Ap
726	53	59.6	533	7	US-11-072-513-3224	Sequence 3224, Ap	799	52	58.4	248	7	US-11-054-515-914	Sequence 914, Appl
727	52.5	59.0	119	6	US-10-771-257-58	Sequence 58, Appl	800	52	58.4	248	7	US-11-054-515-916	Sequence 916, Appl
728	52.5	59.0	119	7	US-11-127-677-56	Sequence 56, Appl	801	52	58.4	248	7	US-11-054-515-1323	Sequence 1323, Ap
729	52.5	59.0	121	7	US-11-049-536-346	Sequence 346, Appl	802	52	58.4	248	7	US-11-266-444-514	Sequence 514, Appl
730	52.5	59.0	121	7	US-11-199-739-346	Sequence 346, Appl	803	52	58.4	248	7	US-11-266-444-916	Sequence 916, Appl
731	52.5	59.0	126	7	US-11-049-536-422	Sequence 422, Appl	804	52	58.4	248	7	US-11-266-444-1323	Sequence 1323, Ap
732	52.5	59.0	126	7	US-11-199-739-422	Sequence 422, Appl	805	52	58.4	249	7	US-11-054-515-974	Sequence 974, Appl
733	52	58.4	19	7	US-11-167-872-50	Sequence 50, Appl	806	52	58.4	249	7	US-11-054-515-1856	Sequence 1856, Ap
734	52	58.4	22	7	US-11-149-943-20	Sequence 20, Appl	807	52	58.4	249	7	US-11-266-444-974	Sequence 974, Appl
735	52	58.4	22	7	US-11-149-943-22	Sequence 22, Appl	808	52	58.4	249	7	US-11-266-444-1856	Sequence 1856, Ap
736	52	58.4	22	7	US-11-149-943-27	Sequence 27, Appl	809	52	58.4	250	7	US-11-054-515-1613	Sequence 1613, Ap
737	52	58.4	98	7	US-11-054-669-21	Sequence 21, Appl	810	52	58.4	250	7	US-11-266-444-1613	Sequence 1613, Ap
738	52	58.4	98	7	US-11-084-554-32	Sequence 32, Appl	811	52	58.4	251	7	US-11-054-515-952	Sequence 952, Appl
739	52	58.4	98	7	US-11-084-554-36	Sequence 36, Appl	812	52	58.4	251	7	US-11-054-515-982	Sequence 982, Appl
740	52	58.4	98	7	US-11-004-590-20	Sequence 20, Appl	813	52	58.4	251	7	US-11-054-515-1114	Sequence 1114, Ap
741	52	58.4	98	7	US-11-004-590-22	Sequence 22, Appl	814	52	58.4	251	7	US-11-266-444-952	Sequence 952, Appl
742	52	58.4	98	7	US-11-004-590-27	Sequence 27, Appl	815	52	58.4	251	7	US-11-266-444-982	Sequence 982, Appl
743	52	58.4	98	7	US-11-136-250-32	Sequence 32, Appl	816	52	58.4	251	7	US-11-266-444-1114	Sequence 1114, Ap
744	52	58.4	98	7	US-11-136-250-36	Sequence 36, Appl	817	52	58.4	252	7	US-11-054-515-956	Sequence 956, Appl
745	52	58.4	112	7	US-11-224-623-8	Sequence 8, Appl	818	52	58.4	252	7	US-11-054-515-1634	Sequence 1634, Ap
746	52	58.4	115	7	US-11-127-903-23	Sequence 23, Appl	819	52	58.4	252	7	US-11-054-515-1637	Sequence 1637, Ap
747	52	58.4	116	7	US-11-127-932-4	Sequence 4, Appl	820	52	58.4	252	7	US-11-266-444-956	Sequence 956, Appl
748	52	58.4	116	7	US-11-127-903-4	Sequence 4, Appl	821	52	58.4	252	7	US-11-266-444-1634	Sequence 1634, Ap
749	52	58.4	117	7	US-11-049-536-602	Sequence 602, Appl	822	52	58.4	252	7	US-11-266-444-1637	Sequence 1637, Ap
750	52	58.4	117	7	US-11-199-739-602	Sequence 602, Appl	823	52	58.4	253	7	US-11-054-515-854	Sequence 854, Appl
751	52	58.4	118	6	US-10-886-383-1	Sequence 1, Appl	824	52	58.4	253	7	US-11-054-515-880	Sequence 880, Appl
752	52	58.4	118	7	US-11-049-536-266	Sequence 266, Appl	825	52	58.4	253	7	US-11-054-515-885	Sequence 885, Appl
753	52	58.4	118	7	US-11-049-536-338	Sequence 338, Appl	826	52	58.4	253	7	US-11-054-515-1044	Sequence 1044, Ap
754	52	58.4	118	7	US-11-199-739-266	Sequence 266, Appl	827	52	58.4	253	7	US-11-054-515-1089	Sequence 1089, Ap
755	52	58.4	118	7	US-11-199-739-338	Sequence 338, Appl	828	52	58.4	253	7	US-11-054-515-1091	Sequence 1091, Ap



829	52	58.4	253	7	US-11-054-515-1093	Sequence 1093, Ap	902	50.5	56.7	119	7	US-11-049-536-638	Sequence 638, App
830	52	58.4	253	7	US-11-054-515-1094	Sequence 1094, Ap	903	50.5	56.7	119	7	US-11-199-739-330	Sequence 330, App
831	52	58.4	253	7	US-11-054-515-1096	Sequence 1096, Ap	904	50.5	56.7	119	7	US-11-199-739-402	Sequence 402, App
832	52	58.4	253	7	US-11-054-515-1097	Sequence 1097, Ap	905	50.5	56.7	119	7	US-11-199-739-538	Sequence 538, App
833	52	58.4	253	7	US-11-054-515-1098	Sequence 1098, Ap	906	50.5	56.7	119	7	US-11-199-739-562	Sequence 562, App
834	52	58.4	253	7	US-11-054-515-1100	Sequence 1100, Ap	907	50.5	56.7	119	7	US-11-199-739-638	Sequence 638, App
835	52	58.4	253	7	US-11-054-515-1101	Sequence 1101, Ap	908	50.5	56.7	120	6	US-10-925-366A-5	Sequence 5, Appl
836	52	58.4	253	7	US-11-054-515-11304	Sequence 1304, Ap	909	50.5	56.7	120	6	US-10-925-366A-280	Sequence 280, App
837	52	58.4	253	7	US-11-054-515-11379	Sequence 1379, Ap	910	50.5	56.7	120	7	US-11-049-536-586	Sequence 586, App
838	52	58.4	253	7	US-11-266-444-854	Sequence 854, App	911	50.5	56.7	120	7	US-11-199-739-586	Sequence 586, App
839	52	58.4	253	7	US-11-266-444-880	Sequence 880, App	912	50.5	56.7	120	7	US-11-102-512-5	Sequence 5, Appl
840	52	58.4	253	7	US-11-266-444-885	Sequence 885, App	913	50.5	56.7	120	7	US-11-217-919-85	Sequence 85, Appl
841	52	58.4	253	7	US-11-266-444-1044	Sequence 1044, Ap	914	50.5	56.7	125	7	US-11-049-536-242	Sequence 242, App
842	52	58.4	253	7	US-11-266-444-1089	Sequence 1089, Ap	915	50.5	56.7	125	7	US-11-049-536-286	Sequence 286, App
843	52	58.4	253	7	US-11-266-444-1091	Sequence 1091, Ap	916	50.5	56.7	125	7	US-11-199-739-242	Sequence 242, App
844	52	58.4	253	7	US-11-266-444-1093	Sequence 1093, Ap	917	50.5	56.7	125	7	US-11-199-739-286	Sequence 286, App
845	52	58.4	253	7	US-11-266-444-1094	Sequence 1094, Ap	918	50.5	56.7	126	7	US-11-049-536-374	Sequence 374, App
846	52	58.4	253	7	US-11-266-444-1096	Sequence 1096, Ap	919	50.5	56.7	126	7	US-11-049-536-430	Sequence 430, App
847	52	58.4	253	7	US-11-266-444-1097	Sequence 1097, Ap	920	50.5	56.7	126	7	US-11-199-739-374	Sequence 374, App
848	52	58.4	253	7	US-11-266-444-1098	Sequence 1098, Ap	921	50.5	56.7	126	7	US-11-199-739-430	Sequence 430, App
849	52	58.4	253	7	US-11-266-444-1100	Sequence 1100, Ap	922	50.5	56.7	127	7	US-11-049-536-446	Sequence 446, App
850	52	58.4	253	7	US-11-266-444-1101	Sequence 1101, Ap	923	50.5	56.7	127	7	US-11-199-739-446	Sequence 446, App
851	52	58.4	253	7	US-11-266-444-1304	Sequence 1304, Ap	924	50.5	56.7	128	7	US-11-049-536-102	Sequence 102, App
852	52	58.4	253	7	US-11-266-444-1379	Sequence 1379, Ap	925	50.5	56.7	128	7	US-11-199-739-102	Sequence 102, App
853	52	58.4	256	7	US-11-054-515-1318	Sequence 1318, Ap	926	50.5	56.7	147	7	US-11-049-536-52	Sequence 52, Appl
854	52	58.4	256	7	US-11-266-444-1318	Sequence 1318, Ap	927	50.5	56.7	147	7	US-11-199-739-52	Sequence 52, Appl
855	52	58.4	262	7	US-11-054-515-2081	Sequence 2081, Ap	928	50.5	56.7	250	7	US-11-054-515-883	Sequence 883, App
856	52	58.4	262	7	US-11-266-444-2081	Sequence 2081, Ap	929	50.5	56.7	250	7	US-11-266-444-883	Sequence 883, App
857	51.5	57.9	219	7	US-11-128-440-12	Sequence 12, Appl	930	50	56.2	17	US-11-193-512-35	Sequence 35, Appl	
858	51.5	57.9	253	7	US-11-054-515-858	Sequence 858, App	931	50	56.2	115	6	US-10-925-366A-334	Sequence 334, App
859	51.5	57.9	253	7	US-11-266-444-858	Sequence 858, App	932	50	56.2	115	7	US-11-127-903-26	Sequence 26, Appl
860	51	57.3	102	6	US-10-997-201A-6	Sequence 6, Appl	933	50	56.2	115	7	US-11-127-903-35	Sequence 35, Appl
861	51	57.3	116	6	US-10-925-366A-231	Sequence 231, App	934	50	56.2	115	7	US-11-217-919-137	Sequence 137, App
862	51	57.3	117	7	US-11-102-512-12	Sequence 12, Appl	935	50	56.2	116	6	US-10-925-366A-230	Sequence 230, App
863	51	57.3	120	7	US-11-102-512-23	Sequence 23, Appl	936	50	56.2	116	6	US-10-925-366A-282	Sequence 282, App
864	51	57.3	122	7	US-11-102-512-48	Sequence 48, Appl	937	50	56.2	116	7	US-11-217-919-87	Sequence 87, Appl
865	51	57.3	123	7	US-11-102-512-79	Sequence 79, Appl	938	50	56.2	117	6	US-10-771-257-60	Sequence 60, Appl
866	51	57.3	124	6	US-10-925-366A-211	Sequence 211, App	939	50	56.2	117	6	US-10-956-008-18	Sequence 18, Appl
867	51	57.3	124	7	US-11-102-512-74	Sequence 74, Appl	940	50	56.2	117	7	US-11-127-677-58	Sequence 58, Appl
868	51	57.3	128	6	US-10-993-543-72	Sequence 72, Appl	941	50	56.2	117	7	US-11-049-536-458	Sequence 458, App
869	51	57.3	146	7	US-11-128-900-11	Sequence 11, Appl	942	50	56.2	117	7	US-11-049-536-610	Sequence 610, App
870	51	57.3	146	7	US-11-128-900-82	Sequence 82, Appl	943	50	56.2	117	7	US-11-199-739-458	Sequence 458, App
871	51	57.3	146	7	US-11-049-536-16	Sequence 16, Appl	944	50	56.2	117	7	US-11-199-739-610	Sequence 610, App
872	51	57.3	146	7	US-11-199-739-16	Sequence 16, Appl	945	50	56.2	118	6	US-10-850-635-8	Sequence 8, Appl
873	51	57.3	208	7	US-11-128-440-4	Sequence 4, Appl	946	50	56.2	119	7	US-11-127-903-31	Sequence 31, Appl
874	51	57.3	245	7	US-11-054-515-1826	Sequence 1826, Ap	947	50	56.2	119	7	US-11-127-903-41	Sequence 41, Appl
875	51	57.3	245	7	US-11-266-444-1826	Sequence 1826, Ap	948	50	56.2	119	7	US-11-049-536-394	Sequence 394, App
876	51	57.3	249	7	US-11-054-515-1109	Sequence 1109, Ap	949	50	56.2	119	7	US-11-049-536-418	Sequence 418, App
877	51	57.3	249	7	US-11-266-444-1109	Sequence 1109, Ap	950	50	56.2	119	7	US-11-199-739-394	Sequence 394, App
878	51	57.3	252	7	US-11-054-515-1690	Sequence 1690, Ap	951	50	56.2	119	7	US-11-199-739-418	Sequence 418, App
879	51	57.3	252	7	US-11-266-444-1690	Sequence 1690, Ap	952	50	56.2	120	7	US-11-102-512-17	Sequence 17, Appl
880	51	57.3	254	7	US-11-054-515-1428	Sequence 1428, Ap	953	50	56.2	121	7	US-11-049-536-622	Sequence 622, App
881	51	57.3	254	7	US-11-266-444-1428	Sequence 1428, Ap	954	50	56.2	121	7	US-11-199-739-622	Sequence 622, App
882	51	57.3	255	7	US-11-054-515-1233	Sequence 1233, Ap	955	50	56.2	122	7	US-11-049-536-186	Sequence 186, App
883	51	57.3	255	7	US-11-266-444-1233	Sequence 1233, Ap	956	50	56.2	122	7	US-11-049-536-278	Sequence 278, App
884	51	57.3	256	7	US-11-054-515-907	Sequence 907, App	957	50	56.2	122	7	US-11-199-739-186	Sequence 186, App
885	51	57.3	256	7	US-11-054-515-1015	Sequence 1015, Ap	958	50	56.2	122	7	US-11-199-739-278	Sequence 278, App
886	51	57.3	256	7	US-11-266-444-907	Sequence 907, App	959	50	56.2	123	7	US-11-049-536-238	Sequence 238, App
887	51	57.3	256	7	US-11-266-444-1015	Sequence 1015, Ap	960	50	56.2	123	7	US-11-049-536-378	Sequence 378, App
888	50.5	56.7	116	7	US-11-049-536-614	Sequence 614, App	961	50	56.2	124	7	US-11-049-536-398	Sequence 398, App
889	50.5	56.7	116	7	US-11-199-739-614	Sequence 614, App	962	50	56.2	123	7	US-11-199-739-238	Sequence 238, App
890	50.5	56.7	117	7	US-11-049-536-190	Sequence 190, App	963	50	56.2	123	7	US-11-199-739-378	Sequence 378, App
891	50.5	56.7	117	7	US-11-049-536-462	Sequence 462, App	964	50	56.2	123	7	US-11-199-739-398	Sequence 398, App
892	50.5	56.7	117	7	US-11-049-536-530	Sequence 530, App	965	50	56.2	124	7	US-11-049-536-298	Sequence 298, App
893	50.5	56.7	117	7	US-11-199-739-190	Sequence 190, App	966	50	56.2	124	7	US-11-199-739-298	Sequence 298, App
894	50.5	56.7	117	7	US-11-199-739-462	Sequence 462, App	967	50	56.2	124	7	US-11-102-512-71	Sequence 71, Appl
895	50.5	56.7	117	7	US-11-199-739-530	Sequence 530, App	968	50	56.2	126	7	US-11-155-775-18	Sequence 18, Appl
896	50.5	56.7	118	7	US-11-049-536-546	Sequence 546, App	969	50	56.2	126	7	US-11-064-174-16	Sequence 16, Appl
897	50.5	56.7	118	7	US-11-199-739-546	Sequence 546, App	970	50	56.2	126	7	US-11-064-174-152	Sequence 152, App
898	50.5	56.7	119	7	US-11-049-536-330	Sequence 330, App	971	50	56.2	127	7	US-11-064-174-139	Sequence 139, App
899	50.5	56.7	119	7	US-11-049-536-402	Sequence 402, App	972	50	56.2	127	7	US-11-073-942-19	Sequence 19, Appl
900	50.5	56.7	119	7	US-11-049-536-538	Sequence 538, App	973	50	56.2	129	6	US-10-993-543-180	Sequence 180, App
901	50.5	56.7	119	7	US-11-049-536-582	Sequence 582, App	974	50	56.2	132	6	US-10-993-543-12	Sequence 12, Appl

975 50 56.2 133 6 US-10-993-543-124 Sequence 124, Ap  
976 50 56.2 137 7 US-11-049-536-68 Sequence 68, Appl  
977 50 56.2 137 7 US-11-049-536-80 Sequence 80, Appl  
978 50 56.2 137 7 US-11-199-739-68 Sequence 68, Appl  
979 50 56.2 137 7 US-11-199-739-80 Sequence 80, Appl  
980 50 56.2 140 7 US-11-193-512-23 Sequence 23, Appl  
981 50 56.2 238 7 US-11-054-515-2053 Sequence 2053, Ap  
982 50 56.2 238 7 US-11-266-444-2053 Sequence 2053, Ap  
983 50 56.2 240 7 US-11-054-515-1998 Sequence 1898, Ap  
984 50 56.2 240 7 US-11-054-515-1912 Sequence 1912, Ap  
985 50 56.2 240 7 US-11-054-515-1918 Sequence 1918, Ap  
986 50 56.2 240 7 US-11-266-444-1898 Sequence 1898, Ap  
987 50 56.2 240 7 US-11-266-444-1912 Sequence 1912, Ap  
988 50 56.2 240 7 US-11-266-444-1918 Sequence 1918, Ap  
989 50 56.2 243 7 US-11-054-515-1935 Sequence 1935, Ap  
990 50 56.2 243 7 US-11-266-444-1935 Sequence 1935, Ap  
991 50 56.2 244 7 US-11-054-515-1933 Sequence 1933, Ap  
992 50 56.2 244 7 US-11-266-444-1933 Sequence 1933, Ap  
993 50 56.2 247 7 US-11-054-515-1939 Sequence 1939, Ap  
994 50 56.2 247 7 US-11-266-444-1939 Sequence 1939, Ap  
995 50 56.2 248 7 US-11-054-515-1890 Sequence 1890, Ap  
996 50 56.2 248 7 US-11-266-444-1890 Sequence 1890, Ap  
997 50 56.2 250 7 US-11-054-515-1461 Sequence 1461, Ap  
998 50 56.2 250 7 US-11-266-444-1461 Sequence 1461, Ap  
999 50 56.2 254 7 US-11-054-515-1302 Sequence 1302, Ap  
1000 50 56.2 254 7 US-11-266-444-1302 Sequence 1302, Ap

ALIGNMENTS

RESULT 1  
US-10-473-037-4  
; Sequence 4, Application US/10473037  
; Publication No. US20050260206A1  
; GENERAL INFORMATION:  
; APPLICANT: KYOWA HAKKO KOGYO CO., LTD.  
; TITLE OF INVENTION: Agents for treatment of cancer using recombinant anti-GD3 antibod  
; TITLE OF INVENTION: the antibody fragments  
; FILE REFERENCE: 11374W01  
; CURRENT APPLICATION NUMBER: US/10/473,037  
; CURRENT FILING DATE: 2003-09-26  
; PRIOR APPLICATION NUMBER: JP2001-097483  
; PRIOR FILING DATE: 2001-03-29  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 4  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-473-037-4

Query Match 100.0%; Score 89; DB 6; Length 17;  
Best Local Similarity 100.0%; Pred. No. 4.8e-07;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 YISGGSGTYSDSVKG 17  
| | | | | | | | | | | | | | | | | |  
Db 1 YISGGSGTYSDSVKG 17  
  
RESULT 2  
US-10-473-037-9  
; Sequence 9, Application US/10473037  
; Publication No. US20050260206A1  
; GENERAL INFORMATION:  
; APPLICANT: KYOWA HAKKO KOGYO CO., LTD.  
; TITLE OF INVENTION: Agents for treatment of cancer using recombinant anti-GD3 antibod  
; TITLE OF INVENTION: the antibody fragments  
; FILE REFERENCE: 11374W01  
; CURRENT APPLICATION NUMBER: US/10/473,037  
; CURRENT FILING DATE: 2003-09-26  
; PRIOR APPLICATION NUMBER: JP2001-097483

; PRIOR FILING DATE: 2001-03-29  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 9  
; LENGTH: 119  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:synthetic protein  
US-10-473-037-9  
  
Query Match 100.0%; Score 89; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.2e-06;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 YISGGSGTYSDSVKG 17  
| | | | | | | | | | | | | | | | | |  
Db 50 YISGGSGTYSDSVKG 66  
  
RESULT 3  
US-10-473-037-49  
; Sequence 49, Application US/10473037  
; Publication No. US20050260206A1  
; GENERAL INFORMATION:  
; APPLICANT: KYOWA HAKKO KOGYO CO., LTD.  
; TITLE OF INVENTION: Agents for treatment of cancer using recombinant anti-GD3 antibod  
; TITLE OF INVENTION: the antibody fragments  
; FILE REFERENCE: 11374W01  
; CURRENT APPLICATION NUMBER: US/10/473,037  
; CURRENT FILING DATE: 2003-09-26  
; PRIOR APPLICATION NUMBER: JP2001-097483  
; PRIOR FILING DATE: 2001-03-29  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 49  
; LENGTH: 119  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-473-037-49

Query Match 100.0%; Score 89; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.2e-06;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 YISGGSGTYSDSVKG 17  
| | | | | | | | | | | | | | | | | |  
Db 50 YISGGSGTYSDSVKG 66  
  
RESULT 4  
US-11-228-293-18  
; Sequence 18, Application US/11228293  
; Publication No. US20060057139A1  
; GENERAL INFORMATION:  
; APPLICANT: SHITARA, KENYA  
; APPLICANT: HANAI, NOBUO  
; APPLICANT: HASEGAWA, MAMORU  
; APPLICANT: MIYAJI, HIROMASA  
; APPLICANT: KUWANA, YOSHIHISA  
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY  
; FILE REFERENCE: 249-101  
; CURRENT APPLICATION NUMBER: US/11/228,293  
; CURRENT FILING DATE: 2005-09-19  
; PRIOR APPLICATION NUMBER: US/09/225,322  
; PRIOR FILING DATE: 1999-01-05  
; PRIOR APPLICATION NUMBER: US 08/454,680  
; PRIOR FILING DATE: 1995-05-31  
; PRIOR APPLICATION NUMBER: US 08/408,133  
; PRIOR FILING DATE: 1995-03-21  
; PRIOR APPLICATION NUMBER: US 08/292,178  
; PRIOR FILING DATE: 1994-08-17  
; PRIOR APPLICATION NUMBER: US07/947,674

; PRIOR FILING DATE: 1992-09-17
; PRIOR APPLICATION NUMBER: JP 3-238375
; PRIOR FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:cDNA KM-641
US-11-228-293-18

Query Match 100.0%; Score 89; DB 7; Length 130;
Best Local Similarity 100.0%; Pred. No. 3.5e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YISSGGSGTYSDSVKG 17
|||||
DB 60 YISSGGSGTYSDSVKG 76

RESULT 5
US-11-228-319-18
; Sequence 18, Application US/11228319
; Publication No. US20060058512A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUMANA, YOSHIIISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/11/228,319
; CURRENT FILING DATE: 2005-09-19
; PRIOR APPLICATION NUMBER: US/09/225,322
; PRIOR FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: US 08/454,680
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
; PRIOR APPLICATION NUMBER: US07/947,674
; PRIOR FILING DATE: 1992-09-17
; PRIOR APPLICATION NUMBER: JP 3-238375
; PRIOR FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:cDNA KM-641
US-11-228-319-18

Query Match 100.0%; Score 89; DB 7; Length 130;
Best Local Similarity 100.0%; Pred. No. 3.5e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YISSGGSGTYSDSVKG 17
|||||
DB 60 YISSGGSGTYSDSVKG 76

RESULT 6
US-10-473-037-1
; Sequence 1, Application US/10473037
; Publication No. US20050260206A1
; GENERAL INFORMATION:
; APPLICANT: KYOWA HAKKO KOGYO CO., LTD.

; TITLE OF INVENTION: Agents for treatment of cancer using recombinant anti-GD3 antibod
; FILE REFERENCE: 11374WQ1
; CURRENT APPLICATION NUMBER: US/10/473,037
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: JP2001-097483
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 138
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-473-037-1

Query Match 100.0%; Score 89; DB 6; Length 138;
Best Local Similarity 100.0%; Pred. No. 3.7e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YISSGGSGTYSDSVKG 17
|||||
DB 69 YISSGGSGTYSDSVKG 85

RESULT 7
US-10-925-366A-208
; Sequence 208, Application US/10925366A
; Publication No. US20050271663A1
; GENERAL INFORMATION:
; APPLICANT: Ignatovich, Olga
; APPLICANT: Demilt, Rudolph M.T.
; APPLICANT: Benjamin, Woolven
; APPLICANT: Grant, Steven
; APPLICANT: Jones, Philip
; APPLICANT: Basran, Amrik
; APPLICANT: Brewis, Neil
; TITLE OF INVENTION: Compositions and Methods for Treating Inflammatory Disorders
; FILE REFERENCE: 8039/2105
; CURRENT APPLICATION NUMBER: US/10/925,366A
; CURRENT FILING DATE: 2004-08-24
; PRIOR APPLICATION NUMBER: US 10/744,774
; PRIOR FILING DATE: 2003-12-23
; PRIOR APPLICATION NUMBER: PCT/GB2003/002804
; PRIOR FILING DATE: 2003-06-30
; PRIOR APPLICATION NUMBER: PCT/GB2002/03014
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: GB 0230202.4
; PRIOR FILING DATE: 2002-12-27
; PRIOR APPLICATION NUMBER: GB 115841.9
; PRIOR FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: PCT/GB2004/002829
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: US 60/535,076
; PRIOR FILING DATE: 2004-01-08
; PRIOR APPLICATION NUMBER: PCT/GB2003/005646
; PRIOR FILING DATE: 2003-12-24
; PRIOR APPLICATION NUMBER: GB 0327706.8
; PRIOR FILING DATE: 2003-11-28
; PRIOR APPLICATION NUMBER: US 60/509,613
; PRIOR FILING DATE: 2003-10-08
; NUMBER OF SEQ ID NOS: 368
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 208
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Antibody Domain
US-10-925-366A-208

Query Match 96.6%; Score 86; DB 6; Length 118;
Best Local Similarity 94.1%; Pred. No. 8.7e-06;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 1 YISGGSGTYSDSVK 17
    |||||
Db 50 YISGGSGTYADSVK 66

RESULT 8
US-11-228-293-8
; Sequence 8, Application US/11228293
; Publication No. US20060057139A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUMANA, YOSHIIISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/11/228,293
; PRIOR FILING DATE: 2005-09-19
; PRIOR APPLICATION NUMBER: US/09/225,322
; PRIOR FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: US 08/454,680
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
; PRIOR APPLICATION NUMBER: US07/947,674
; PRIOR FILING DATE: 1992-09-17
; PRIOR APPLICATION NUMBER: JP 3-238375
; PRIOR FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 8
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: cDNA KM-641
US-11-228-293-8

Query Match 92.1%; Score 82; DB 7; Length 130;
Best Local Similarity 100.0%; Pred. No. 3.6e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ISSGGSGTYSDSVK 17
    |||||
Db 61 ISSGGSGTYSDSVK 76

RESULT 10
US-11-102-512-24
; Sequence 24, Application US/11102512
; Publication No. US20060062784A1
; GENERAL INFORMATION:
; APPLICANT: Grant et al., S.
; TITLE OF INVENTION: Compositions monovalent for CD40L binding and methods of use
; FILE REFERENCE: 8039/21328
; CURRENT APPLICATION NUMBER: US/11/102,512
; CURRENT FILING DATE: 2005-04-08
; PRIOR APPLICATION NUMBER: 60/610,819
; PRIOR FILING DATE: 2004-09-17
; NUMBER OF SEQ ID NOS: 247
; SOFTWARE: Patent In version 3.3
; SEQ ID NO 24
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-102-512-24

Query Match 82.0%; Score 73; DB 7; Length 116;
Best Local Similarity 87.5%; Pred. No. 0.00066;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 ISSGGSGTYSDSVK 17
    |||||
Db 51 ISSGGSGTYADSVK 66

RESULT 11
US-11-054-515-1906
; Sequence 1906, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748

QY 1 YISGGSGTYSDSVK 17
    |||||
Db 50 YISGGSGTYADSVK 66

RESULT 8
US-11-228-293-8
; Sequence 8, Application US/11228293
; Publication No. US20060057139A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUMANA, YOSHIIISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/11/228,319
; PRIOR FILING DATE: 2005-09-19
; PRIOR APPLICATION NUMBER: US/09/225,322
; PRIOR FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: US 08/454,680
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
```

```
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1906
; LENGTH: 237
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-2039

Query Match      80.9%; Score 72; DB 7; Length 237;
Best Local Similarity 82.4%; Pred. No. 0.0018;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
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Qy 1 YISSGGSGTYSDSVKG 17
|||||:|||||
Db 50 YISSGGSTYYADSVKG 66
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RESULT 12
US-11-054-515-2039
; Sequence 2039, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2039
; LENGTH: 237
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-2039
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Query Match      80.9%; Score 72; DB 7; Length 237;
Best Local Similarity 82.4%; Pred. No. 0.0018;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
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Qy 1 YISSGGSGTYSDSVKG 17
|||||:|||||
Db 50 YISSGGSTYYADSVKG 66
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RESULT 13
US-11-266-444-1906
; Sequence 1906, Application US/11266444
; Publication No. US20060062789A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to B Lymphocyte Stimulators
; FILE REFERENCE: PF523P1D1
; CURRENT APPLICATION NUMBER: US/11/266,444
; CURRENT FILING DATE: 2005-11-04
; PRIOR APPLICATION NUMBER: 09/880,746
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1906
; LENGTH: 237
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-266-444-1906
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Query Match      80.9%; Score 72; DB 7; Length 237;
Best Local Similarity 82.4%; Pred. No. 0.0018;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
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```
Qy 1 YISSGGSGTYSDSVKG 17
|||||:|||||
Db 50 YISSGGSTYYADSVKG 66
```

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RESULT 14
US-11-266-444-2039
; Sequence 2039, Application US/11266444
; Publication No. US20060062789A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to B Lymphocyte Stimulators
; FILE REFERENCE: PF523P1D1
; CURRENT APPLICATION NUMBER: US/11/266,444
; CURRENT FILING DATE: 2005-11-04
; PRIOR APPLICATION NUMBER: 09/880,746
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2039
; LENGTH: 237
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-266-444-2039
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```
Query Match      80.9%; Score 72; DB 7; Length 237;
Best Local Similarity 82.4%; Pred. No. 0.0018;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
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Qy 1 YISSGSGTYYSDSVKG 17  
 ||||| |||||:|||||  
 Db 50 YISSGSGTYYADSVKG 66

RESULT 15

US-11-054-515-1905  
 ; Sequence 1905, Application US/11054515  
 ; Publication No. US2005025532A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ruben et al.  
 ; TITLE OF INVENTION: Antibodies that Immunosepecifically Bind Blys  
 ; FILE REFERENCE: PF523P3  
 ; CURRENT APPLICATION NUMBER: US/11/054,515  
 ; CURRENT FILING DATE: 2005-02-10  
 ; PRIOR APPLICATION NUMBER: 60/543,296  
 ; PRIOR FILING DATE: 2004-02-11  
 ; PRIOR APPLICATION NUMBER: 60/580,347  
 ; PRIOR FILING DATE: 2004-06-18  
 ; PRIOR APPLICATION NUMBER: 10/293,418  
 ; PRIOR FILING DATE: 2002-11-14  
 ; PRIOR APPLICATION NUMBER: 60/331,469  
 ; PRIOR FILING DATE: 2001-11-16  
 ; PRIOR APPLICATION NUMBER: 60/340,817  
 ; PRIOR FILING DATE: 2001-12-19  
 ; PRIOR APPLICATION NUMBER: 09/880,748  
 ; PRIOR FILING DATE: 2001-06-15  
 ; PRIOR APPLICATION NUMBER: 60/293,499  
 ; PRIOR FILING DATE: 2001-05-25  
 ; PRIOR APPLICATION NUMBER: 60/277,379  
 ; PRIOR FILING DATE: 2001-03-21  
 ; PRIOR APPLICATION NUMBER: 60/276,248  
 ; PRIOR FILING DATE: 2001-03-16  
 ; PRIOR APPLICATION NUMBER: 60/240,816  
 ; PRIOR FILING DATE: 2000-10-17  
 ; Remaining Prior Application data removed - See File Wrapper or PALM.  
 ; NUMBER OF SEQ ID NOS: 3247  
 ; SEQ ID NO 1905  
 ; LENGTH: 240  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-11-054-515-1905

Query Match 80.9%; Score 72; DB 7; Length 240;  
 Best Local Similarity 82.4%; Pred. No. 0.0019; 2; Mismatches 0; Gaps 0;  
 Matches 14; Conservative 1; Indels 0;

Qy 1 YISSGSGTYYSDSVKG 17  
 ||||| |||||:|||||  
 Db 50 YISSGSGTYYADSVKG 66

RESULT 16

US-11-266-444-1905  
 ; Sequence 1905, Application US/11266444  
 ; Publication No. US20060062789A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ruben et al.  
 ; TITLE OF INVENTION: Antibodies that Immunosepecifically Bind to B Lymphocyte Stimulat  
 ; FILE REFERENCE: PF523P1D1  
 ; CURRENT APPLICATION NUMBER: US/11/266,444  
 ; CURRENT FILING DATE: 2005-11-04  
 ; PRIOR APPLICATION NUMBER: 09/880,746  
 ; PRIOR FILING DATE: 2001-06-15  
 ; PRIOR APPLICATION NUMBER: 60/212,210  
 ; PRIOR FILING DATE: 2000-06-16  
 ; PRIOR APPLICATION NUMBER: 60/240,816  
 ; PRIOR FILING DATE: 2000-10-17  
 ; PRIOR APPLICATION NUMBER: 60/276,248  
 ; PRIOR FILING DATE: 2001-03-16  
 ; PRIOR APPLICATION NUMBER: 60/277,379  
 ; PRIOR FILING DATE: 2001-03-21  
 ; PRIOR APPLICATION NUMBER: 60/293,499

; PRIOR FILING DATE: 2001-05-25  
 ; NUMBER OF SEQ ID NOS: 3239  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 1905  
 ; LENGTH: 240  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-11-266-444-1905

Query Match 80.9%; Score 72; DB 7; Length 240;  
 Best Local Similarity 82.4%; Pred. No. 0.0019;  
 Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YISSGSGTYYSDSVKG 17  
 ||||| |||||:|||||  
 Db 50 YISSGSGTYYADSVKG 66

RESULT 17

US-11-102-512-56  
 ; Sequence 56, Application US/11102512  
 ; Publication No. US20060062784A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Grant et al., S.  
 ; TITLE OF INVENTION: Compositions monovalent for CD40L binding and methods of use  
 ; FILE REFERENCE: 8039/2132B  
 ; CURRENT APPLICATION NUMBER: US/11/102,512  
 ; CURRENT FILING DATE: 2005-04-08  
 ; PRIOR APPLICATION NUMBER: 60/610,819  
 ; PRIOR FILING DATE: 2004-09-17  
 ; NUMBER OF SEQ ID NOS: 247  
 ; SOFTWARE: PatentIn version 3.3  
 ; SEQ ID NO 56  
 ; LENGTH: 123  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-11-102-512-56

Query Match 78.7%; Score 70; DB 7; Length 123;  
 Best Local Similarity 76.5%; Pred. No. 0.0019;  
 Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YISSGSGTYYSDSVKG 17  
 :|| |||||:|||||  
 Db 50 WISPSGSGTYYADSVKG 66

RESULT 18

US-10-923-112A-40  
 ; Sequence 40, Application US/10923112A  
 ; Publication No. US20060040879A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Kosak, Kenneth M.  
 ; TITLE OF INVENTION: Chloroquine Coupled Nucleic Acids and Methods for Their Synthesis  
 ; FILE REFERENCE: Confirmation No. 3293  
 ; CURRENT APPLICATION NUMBER: US/10/923,112A  
 ; CURRENT FILING DATE: 2004-08-21  
 ; NUMBER OF SEQ ID NOS: 54  
 ; SOFTWARE: PatentIn version 3.3  
 ; SEQ ID NO 40  
 ; LENGTH: 30  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Table I Transduction Peptide  
 US-10-923-112A-40

Query Match 77.5%; Score 69; DB 6; Length 30;  
 Best Local Similarity 76.5%; Pred. No. 0.00067;  
 Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 YISSGSGTYYSDSVKG 17  
 ||||| |||||:|||||



US-11-102-512-77  
; Sequence 77, Application US/11102512  
; Publication No. US20060062784A1  
; GENERAL INFORMATION:  
; APPLICANT: Grant et al., S.  
; TITLE OF INVENTION: Compositions monovalent for CD40L binding and methods of use  
; FILE REFERENCE: 8039/2132B  
; CURRENT APPLICATION NUMBER: US/11/102,512  
; CURRENT FILING DATE: 2005-04-08  
; PRIOR APPLICATION NUMBER: 60/610,819  
; PRIOR FILING DATE: 2004-09-17  
; NUMBER OF SEQ ID NOS: 247  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 77  
; LENGTH: 116  
; TYPE: PRT  
; ORGANISM: Homo sapiens

US-11-102-512-77  
Query Match 76.4%; Score 68; DB 7; Length 116;  
Best Local Similarity 81.2%; Pred. No. 0.0035; 2; Indels 0; Gaps 0;  
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 2 ISSGGSGTYSDSVKG 17  
Db 51 ISSDGGTYADSVKG 66

RESULT 24  
US-11-037-199-28  
; Sequence 28, Application US/11037199  
; Publication No. US20060030015A1  
; GENERAL INFORMATION:  
; APPLICANT: Japan Science and Technology Corporation  
; TITLE OF INVENTION: Novel methods of producing antibody-enzyme, the antibody-enzymes,  
; FILE REFERENCE: A251-01/PCT  
; CURRENT FILING DATE: 2005-01-19  
; PRIOR APPLICATION NUMBER: US/11/037,199  
; PRIOR FILING DATE: 2002-01-19  
; PRIOR APPLICATION NUMBER: JP 2002-211756  
; PRIOR FILING DATE: 2002-7-19  
; PRIOR APPLICATION NUMBER: JP 2002-211768  
; PRIOR FILING DATE: 2003-051943  
; PRIOR APPLICATION NUMBER: JP 2003-051943  
; PRIOR FILING DATE: 2003-2-27  
; PRIOR APPLICATION NUMBER: JP 2003-198270  
; PRIOR FILING DATE: 2003-7-17  
; PRIOR APPLICATION NUMBER: JP 2003-198281  
; PRIOR FILING DATE: 2003-7-17  
; NUMBER OF SEQ ID NOS: 49  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 28  
; LENGTH: 117  
; TYPE: PRT  
; ORGANISM: Homo sapiens

US-11-037-199-28  
Query Match 76.4%; Score 68; DB 7; Length 116;  
Best Local Similarity 81.2%; Pred. No. 0.0035; 2; Indels 0; Gaps 0;  
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 2 ISSGGSGTYSDSVKG 17  
Db 51 ISSDGGTYADSVKG 66

RESULT 25  
US-11-037-199-36  
; Sequence 36, Application US/11037199  
; Publication No. US20060030015A1  
; GENERAL INFORMATION:  
; APPLICANT: Japan Science and Technology Corporation  
; TITLE OF INVENTION: Novel methods of producing antibody-enzyme, the antibody-enzymes,  
; FILE REFERENCE: A251-01/PCT  
; CURRENT FILING DATE: 2005-01-19  
; PRIOR APPLICATION NUMBER: US/11/037,199  
; PRIOR FILING DATE: 2002-01-19  
; PRIOR APPLICATION NUMBER: JP 2002-211756  
; PRIOR FILING DATE: 2002-7-19  
; PRIOR APPLICATION NUMBER: JP 2002-211768  
; PRIOR FILING DATE: 2003-051943  
; PRIOR APPLICATION NUMBER: JP 2003-051943  
; PRIOR FILING DATE: 2003-2-27  
; PRIOR APPLICATION NUMBER: JP 2003-198270  
; PRIOR FILING DATE: 2003-7-17  
; PRIOR APPLICATION NUMBER: JP 2003-198281  
; PRIOR FILING DATE: 2003-7-17  
; PRIOR APPLICATION NUMBER: JP 2003-198292  
; PRIOR FILING DATE: 2003-7-17  
; NUMBER OF SEQ ID NOS: 49  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 28  
; LENGTH: 117  
; TYPE: PRT  
; ORGANISM: Homo sapiens

US-11-037-199-28  
Query Match 76.4%; Score 68; DB 7; Length 117;  
Best Local Similarity 87.5%; Pred. No. 0.0035; 2; Indels 0; Gaps 0;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 2 ISSGGSGTYSDSVKG 17  
Db 51 ISSGGSGTYSDSVKG 66

RESULT 26  
US-11-037-301A-9  
; Sequence 9, Application US/11037301A  
; Publication No. US20050255101A1  
; GENERAL INFORMATION:  
; APPLICANT: Denkeberg, Galit  
; TITLE OF INVENTION: ANTIBODY HAVING A T-CELL RECEPTOR-LIKE SPECIFICITY, YET HIGHER AFFINITY  
; FILE REFERENCE: 01/23094  
; CURRENT APPLICATION NUMBER: US/10/073,301A  
; CURRENT FILING DATE: 2002-07-02  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 9  
; LENGTH: 237  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: G1 single chain Fv- recombinant antibody protein sequence

US-10-073-301A-9  
Query Match 76.4%; Score 68; DB 6; Length 237;  
Best Local Similarity 87.5%; Pred. No. 0.007; 2; Indels 0; Gaps 0;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 2 ISSGGSGTYSDSVKG 17  
Db 51 ISSGGSGTYSDSVKG 66

RESULT 27  
US-11-203-137-9  
; Sequence 9, Application US/11203137  
; Publication No. US20050287141A1  
; GENERAL INFORMATION:  
; APPLICANT: Reiter, Yoram

; APPLICANT: Japan Science and Technology Corporation  
; TITLE OF INVENTION: Novel methods of producing antibody-enzyme, the antibody-enzymes,  
; FILE REFERENCE: A251-01/PCT  
; CURRENT APPLICATION NUMBER: US/11/037,199  
; CURRENT FILING DATE: 2005-01-19  
; PRIOR APPLICATION NUMBER: JP 2002-211756  
; PRIOR FILING DATE: 2002-7-19  
; PRIOR APPLICATION NUMBER: JP 2002-211768  
; PRIOR FILING DATE: 2002-7-19  
; PRIOR APPLICATION NUMBER: JP 2003-051943  
; PRIOR FILING DATE: 2003-2-27  
; PRIOR APPLICATION NUMBER: JP 2003-198270  
; PRIOR FILING DATE: 2003-7-17  
; PRIOR APPLICATION NUMBER: JP 2003-198281  
; PRIOR FILING DATE: 2003-7-17  
; PRIOR APPLICATION NUMBER: JP 2003-198292  
; PRIOR FILING DATE: 2003-7-17  
; NUMBER OF SEQ ID NOS: 49  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 36  
; LENGTH: 117  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-037-199-36

Query Match 76.4%; Score 68; DB 7; Length 117;  
Best Local Similarity 87.5%; Pred. No. 0.0035; 2; Indels 0; Gaps 0;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 2 ISSGGSGTYSDSVKG 17  
Db 53 ISSGGSGTYSDSVKG 68

RESULT 26  
US-10-073-301A-9  
; Sequence 9, Application US/10073301A  
; Publication No. US20050255101A1  
; GENERAL INFORMATION:  
; APPLICANT: Reiter, Yoram  
; APPLICANT: Denkeberg, Galit  
; TITLE OF INVENTION: ANTIBODY HAVING A T-CELL RECEPTOR-LIKE SPECIFICITY, YET HIGHER AFFINITY  
; FILE REFERENCE: 01/23094  
; CURRENT APPLICATION NUMBER: US/10/073,301A  
; CURRENT FILING DATE: 2002-07-02  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 9  
; LENGTH: 237  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: G1 single chain Fv- recombinant antibody protein sequence

US-10-073-301A-9  
Query Match 76.4%; Score 68; DB 6; Length 237;  
Best Local Similarity 87.5%; Pred. No. 0.007; 2; Indels 0; Gaps 0;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 2 ISSGGSGTYSDSVKG 17  
Db 51 ISSGGSGTYSDSVKG 66

RESULT 27  
US-11-203-137-9  
; Sequence 9, Application US/11203137  
; Publication No. US20050287141A1  
; GENERAL INFORMATION:  
; APPLICANT: Reiter, Yoram



```
; APPLICANT: Denberg, Galit
; TITLE OF INVENTION: ANTIBODY HAVING A T-CELL RECEPTOR-LIKE SPECIFICITY, YET HIGHER AFFINITY
; TITLE OF INVENTION: AND THE USE OF SAME IN THE DETECTION AND TREATMENT OF CANCER, VIRAL DISEASES
; TITLE OF INVENTION: AND AUTOIMMUNE DISEASE
; FILE REFERENCE: 30177
; CURRENT APPLICATION NUMBER: US/11/203,137
; CURRENT FILING DATE: 2005-08-15
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 237
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: G1 single chain Fv- recombinant antibody protein sequence
US-11-203-137-9

Query Match          76.4%; Score 68; DB 7; Length 237;
Best Local Similarity 87.5%; Pred. No. 0.007;
Matches 14; Conservative 0; Mismatches 0; Gaps 0;

QY  2 ISSGGSGTYSDSVK 17
    ||||| |||||
Db   51 ISSGGSGTYSDSVK 66

RESULT 28
US-11-102-512-20
; Sequence 20, Application US/11102512
; Publication No. US20060062784A1
; GENERAL INFORMATION:
; APPLICANT: Grant et al., S.
; TITLE OF INVENTION: Compositions monovalent for CD40L binding and methods of use
; FILE REFERENCE: 8039/2132B
; CURRENT APPLICATION NUMBER: US/11/102,512
; CURRENT FILING DATE: 2005-04-08
; PRIOR APPLICATION NUMBER: 60/610,819
; PRIOR FILING DATE: 2004-09-17
; NUMBER OF SEQ ID NOS: 247
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 20
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-102-512-20

Query Match          75.3%; Score 67; DB 7; Length 119;
Best Local Similarity 76.5%; Pred. No. 0.005;
Matches 13; Conservative 1; Mismatches 0; Gaps 0;

QY  1 YISSGGSGTYSDSVK 17
    ||||| |||||
Db   50 YISSDGYSTYADSVK 66

RESULT 29
US-11-054-515-1314
; Sequence 1314, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
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; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1314
; LENGTH: 246
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1314

Query Match          75.3%; Score 67; DB 7; Length 246;
Best Local Similarity 75.0%; Pred. No. 0.01;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY  2 ISSGGSGTYSDSVK 17
    :||||| |||||
Db   51 LSSGGSGTYADSVK 66

RESULT 30
US-11-266-444-1314
; Sequence 1314, Application US/11266444
; Publication No. US20060062789A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to B Lymphocyte Stimulator
; FILE REFERENCE: PF523P1D1
; CURRENT APPLICATION NUMBER: US/11/266,444
; CURRENT FILING DATE: 2005-11-04
; PRIOR APPLICATION NUMBER: 09/880,746
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1314
; LENGTH: 246
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-266-444-1314

Query Match          75.3%; Score 67; DB 7; Length 246;
Best Local Similarity 75.0%; Pred. No. 0.01;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY  2 ISSGGSGTYSDSVK 17
    :||||| |||||
Db   51 LSSGGSGTYADSVK 66

RESULT 31
US-10-982-440-111
; Sequence 111, Application US/10982440
; Publication No. US20060018909A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Oliner, John
; APPLICANT: Graham, Kevin
; TITLE OF INVENTION: Angiopoietin-2 Specific Binding Agents
; FILE REFERENCE: 04-881-A
; CURRENT APPLICATION NUMBER: US/10/982,440
; CURRENT FILING DATE: 2004-11-04
; PRIOR APPLICATION NUMBER: 60/620,161
; PRIOR FILING DATE: 2004-10-19
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 111
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-982-440-111

Query Match      74.2%; Score 66; DB 6; Length 17;
Best Local Similarity 76.5%; Pred. No. 0.001;
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 YISSGGSTYYSDSVKG 17
   ||||| ||| |||:|||||
Db 1 YISSGGSTYYADSVKG 17

RESULT 32
US-11-149-943-16
; Sequence 16, Application US/11/149943
; Publication No. US20060003412A1
; GENERAL INFORMATION:
; APPLICANT: Chamberlain, Aaron Keith
; APPLICANT: Desjarlais, John R.
; TITLE OF INVENTION: PROTEIN ENGINEERING WITH ANALOGOUS CONTACT ENVIRONMENTS
; FILE REFERENCE: 185833/US/3
; CURRENT APPLICATION NUMBER: US/11/149,943
; CURRENT FILING DATE: 2005-06-09
; PRIOR APPLICATION NUMBER: US 60/602,566
; PRIOR FILING DATE: 2004-08-17
; PRIOR APPLICATION NUMBER: US 11/008,647
; PRIOR FILING DATE: 2004-12-08
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 16
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-149-943-16

Query Match      74.2%; Score 66; DB 7; Length 22;
Best Local Similarity 76.5%; Pred. No. 0.0013;
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 YISSGGSTYYSDSVKG 17
   ||||| ||| |||:|||||
Db 1 YISSGGSTYYADSVKG 17

RESULT 33
US-11-144-248-30
; Sequence 30, Application US/11/144248
; Publication No. US20050244408A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Bruce D.
; APPLICANT: Beebe, Jean
; APPLICANT: Miller, Penelope E.
; APPLICANT: Moyer, James D.
; APPLICANT: Corvalan, Jose R.
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
; FILE REFERENCE: ABX-PF2
; CURRENT APPLICATION NUMBER: US/11/144,248
; CURRENT FILING DATE: 2005-06-02
; PRIOR APPLICATION NUMBER: US/10/038,591
```

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; PRIOR FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: 60/259,927
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 30
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-144-248-30

Query Match      74.2%; Score 66; DB 7; Length 98;
Best Local Similarity 76.5%; Pred. No. 0.0058;
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 YISSGGSTYYSDSVKG 17
   ||||| ||| |||:|||||
Db 50 YISSGGSTYYADSVKG 66

RESULT 34
US-11-054-669-17
; Sequence 17, Application US/11/054669
; Publication No. US20050261480A1
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: SUPER HUMANIZED ANTIBODIES
; FILE REFERENCE: 30219/US/3
; CURRENT APPLICATION NUMBER: US/11/054,669
; CURRENT FILING DATE: 2005-02-08
; PRIOR APPLICATION NUMBER: US 10/194,975
; PRIOR FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 17
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-669-17

Query Match      74.2%; Score 66; DB 7; Length 98;
Best Local Similarity 76.5%; Pred. No. 0.0058;
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 YISSGGSTYYSDSVKG 17
   ||||| ||| |||:|||||
Db 50 YISSGGSTYYADSVKG 66

RESULT 35
US-11-084-554-27
; Sequence 27, Application US/11/084554
; Publication No. US20050260679A1
; GENERAL INFORMATION:
; APPLICANT: Kellermann, Sirid-Ai
; APPLICANT: Green, Larry L.
; APPLICANT: Korver, Wouter
; TITLE OF INVENTION: REDUCING THE RISK OF HUMAN ANTI-HUMAN
; TITLE OF INVENTION: ANTIBODIES THROUGH V GENE MANIPULATION
; FILE REFERENCE: ABGENIX.100A
; CURRENT APPLICATION NUMBER: US/11/084,554
; CURRENT FILING DATE: 2005-03-17
; PRIOR APPLICATION NUMBER: 60/554,372
; PRIOR FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: 60/574,661
; PRIOR FILING DATE: 2004-05-24
; NUMBER OF SEQ ID NOS: 266
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 98
; TYPE: PRT
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; ORGANISM: Homo sapiens
US-11-084-554-27

Query Match          74.2%; Score 66; DB 7; Length 98;
Best Local Similarity 76.5%; Pred. No. 0.0058;
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 YISSGGSGTYYSDSVKG 17
    ||||| ||| :|||
Db 50 YISSGGSTIYYADSVKG 66

RESULT 36
US-11-144-222-30.
; Sequence 30, Application US/11144222
; Publication No. US20050281812A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Bruce D.
; APPLICANT: Beebe, Jean
; APPLICANT: Miller, Penelope E.
; APPLICANT: Moyer, James D.
; APPLICANT: Corvalan, Jose R.
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
; FILE REFERENCE: ABX-PF2
; CURRENT APPLICATION NUMBER: US/11/144,222
; CURRENT FILING DATE: 2005-06-02
; PRIOR APPLICATION NUMBER: US/10/038,591
; PRIOR FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: 60/259,927
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-144-222-30

Query Match          74.2%; Score 66; DB 7; Length 98;
Best Local Similarity 76.5%; Pred. No. 0.0058;
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 YISSGGSGTYYSDSVKG 17
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Db 50 YISSGGSTIYYADSVKG 66

RESULT 37
US-11-004-590-16
; Sequence 16, Application US/11004590
; Publication No. US2006000883A1
; GENERAL INFORMATION:
; APPLICANT: Lazar, Gregory Alan
; APPLICANT: Desjarlais, John R.
; APPLICANT: Hammond, Phillip W.
; TITLE OF INVENTION: METHODS OF GENERATING VARIANT PROTEINS WITH INCREASED HOST STRING
; FILE REFERENCE: 185832/US/5
; CURRENT APPLICATION NUMBER: US/11/004,590
; CURRENT FILING DATE: 2004-12-03
; PRIOR APPLICATION NUMBER: US 60/527,167
; PRIOR FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: US 60/581,613
; PRIOR FILING DATE: 2004-06-21
; PRIOR APPLICATION NUMBER: US 60/601,665
; PRIOR FILING DATE: 2004-08-13
; PRIOR APPLICATION NUMBER: US 60/619,483
; PRIOR FILING DATE: 2004-10-14
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 16
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-182-343-30

Query Match          74.2%; Score 66; DB 7; Length 98;
Best Local Similarity 76.5%; Pred. No. 0.0058;
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 YISSGGSGTYYSDSVKG 17
    ||||| ||| :|||
Db 50 YISSGGSTIYYADSVKG 66

RESULT 39
US-11-182-343-30
; Sequence 30, Application US/11182343
; Publication No. US20060018910A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Bruce
; APPLICANT: Gualberto, Antonio
; APPLICANT: Melvin, Carrie
; APPLICANT: Roberts, Luisa M.
; TITLE OF INVENTION: COMBINATION TREATMENT FOR BREAST CANCER
; FILE REFERENCE: PC32226A
; CURRENT APPLICATION NUMBER: US/11/182,343
; CURRENT FILING DATE: 2005-07-15
; PRIOR APPLICATION NUMBER: 60/588,721
; PRIOR FILING DATE: 2004-07-16
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 30
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-182-343-30
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; ORGANISM: Homo sapiens
US-10-982-440-53

Query Match      74.2%; Score 66; DB 6; Length 122;
Best Local Similarity 76.5%; Pred. No. 0.0072; 3; Indels 0; Gaps 0;
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 YISSGSGTYYSDSVKG 17
    ||||| ||| |||:|||||
Db 50 YISSGSGTYYADSVKG 66

RESULT 45
US-11-054-515-2010
; Sequence 2010, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2010
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-2010

Query Match      74.2%; Score 66; DB 7; Length 236;
Best Local Similarity 76.5%; Pred. No. 0.014; 3; Indels 0; Gaps 0;
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 YISSGSGTYYSDSVKG 17
    ||||| ||| |||:|||||
Db 50 YISSGSGTYYADSVKG 66

RESULT 46
US-11-266-444-2010
; Sequence 2010, Application US/11266444
; Publication No. US2006062789A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to B Lymphocyte Stimulat
; FILE REFERENCE: PF523P1D1
; CURRENT APPLICATION NUMBER: US/11/266,444
; CURRENT FILING DATE: 2005-11-04
; PRIOR APPLICATION NUMBER: 09/880,746
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
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; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2010
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-266-444-2010

Query Match      74.2%; Score 66; DB 7; Length 236;
Best Local Similarity 76.5%; Pred. No. 0.014; 3; Indels 0; Gaps 0;
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 YISSGSGTYYSDSVKG 17
    ||||| ||| |||:|||||
Db 50 YISSGSGTYYADSVKG 66

RESULT 47
US-11-054-515-2003
; Sequence 2003, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2003
; LENGTH: 237
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-2003

Query Match      74.2%; Score 66; DB 7; Length 237;
Best Local Similarity 76.5%; Pred. No. 0.014; 3; Indels 0; Gaps 0;
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 YISSGSGTYYSDSVKG 17
    ||||| ||| |||:|||||
Db 50 YISSGSGTYYADSVKG 66

RESULT 48
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GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: April 6, 2006, 08:54:46 ; Search time 74.2373 Seconds  
(without alignments)  
59.186 Million cell updates/sec

Title: US-10-089-500-5  
Perfect score: 54  
Sequence: 1 VKLGRYYFDS 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

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2: Geneseqp1990s.\*  
3: Geneseqp2000s.\*  
4: Geneseqp2001s.\*  
5: Geneseqp2002s.\*  
6: Geneseqp2003as.\*  
7: Geneseqp2003bs.\*  
8: Geneseqp2004s.\*  
9: Geneseqp2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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1	54	100.0	10	4	Aa881981
2	54	100.0	10	6	Abu11006
3	54	100.0	10	9	Adz57812
4	54	100.0	119	4	Aa881985
5	54	100.0	119	4	Aa881989
6	54	100.0	119	6	Abu11012
7	54	100.0	119	6	Abu11010
8	54	100.0	119	9	Adz57816
9	54	100.0	119	9	Adz57818
10	54	100.0	130	2	Aa881977
11	54	100.0	130	2	Aa881987
12	54	100.0	130	2	Aa881991
13	54	100.0	130	2	Aa881991
14	54	100.0	130	3	Aa881977
15	54	100.0	138	6	Abu11002
16	54	100.0	138	6	Abu11002
17	54	100.0	582	4	Aa881987
18	54	100.0	582	4	Aa881987
19	42	77.8	120	2	Aa881991
20	41	75.9	368	8	Adz57816
21	40	74.1	446	8	Adz57818
22	40	74.1	4130	8	Adz57816
23	39	72.2	427	8	Adz57816
24	39	72.2	434	7	Abm88891

25	38	70.4	1781	5	AAU74519
26	37	68.5	94	7	ADU06503
27	37	68.5	137	7	ADC96455
28	37	68.5	179	8	ABO00524
29	37	68.5	222	8	ADN46177
30	37	68.5	380	4	AAE03835
31	37	68.5	380	5	ABG64570
32	37	68.5	380	8	ADL77837
33	37	68.5	380	8	ADU10470
34	37	68.5	388	5	ABP40106
35	37	68.5	388	8	ADS05035
36	37	68.5	393	4	AA888481
37	37	68.5	393	9	ADY63323
38	37	68.5	685	7	ABO64573
39	37	68.5	2022	6	ABR63232
40	36	66.7	160	5	ABP30519
41	36	66.7	163	5	ABP26309
42	36	66.7	257	3	AAQ09510
43	36	66.7	257	3	AAQ48547
44	36	66.7	258	8	ADN46472
45	36	66.7	260	3	AAQ48546
46	36	66.7	260	3	AAQ09509
47	36	66.7	354	3	AAQ48543
48	36	66.7	361	4	ABB67540
49	36	66.7	361	4	ABW75213
50	36	66.7	361	5	AAE30515
51	36	66.7	387	7	ADB70112
52	36	66.7	389	3	AAQ48542
53	36	66.7	409	3	AAQ48541
54	36	66.7	433	8	ADS22042
55	36	66.7	675	8	ABR889436
56	35	64.8	23	5	ABP46121
57	35	64.8	23	5	ABP47065
58	35	64.8	23	7	ADG97892
59	35	64.8	23	7	ADG96948
60	35	64.8	123	9	ADX15470
61	35	64.8	123	9	ADX15486
62	35	64.8	123	9	ADX15478
63	35	64.8	123	9	ADX15482
64	35	64.8	226	4	AAQ82419
65	35	64.8	255	5	ABP45043
66	35	64.8	255	5	ABP45775
67	35	64.8	255	5	ABP45045
68	35	64.8	255	5	ABP43993
69	35	64.8	255	5	ABP45054
70	35	64.8	255	7	ADG95872
71	35	64.8	255	7	ADG94820
72	35	64.8	255	7	ADG95881
73	35	64.8	255	7	ADG96602
74	35	64.8	255	7	ADG95870
75	35	64.8	258	5	ABP45762
76	35	64.8	258	7	ADG96589
77	35	64.8	264	9	ADW11894
78	35	64.8	287	6	ABU43004
79	35	64.8	288	5	ABP40118
80	35	64.8	288	8	ADS05078
81	35	64.8	294	6	ABU43634
82	35	64.8	310	9	ADW96433
83	35	64.8	310	9	ADW96435
84	35	64.8	319	9	ADW96415
85	35	64.8	349	3	AA202948
86	35	64.8	358	9	ADW96457
87	35	64.8	358	9	ADW96431
88	35	64.8	372	5	ABW3589
89	35	64.8	376	4	ABW3403
90	35	64.8	459	6	ABW07190
91	35	64.8	475	8	ADK16599
92	35	64.8	661	6	ABU20548
93	35	64.8	686	8	ADS23830
94	35	64.8	696	8	ADN23543
95	35	64.8	819	9	ABW64944
96	35	64.8	1110	9	ABW92836
97	34	63.0	56	5	ABP43111

Aau74519	Lactobacil
Adf06503	Bacterial
Adc96455	E. faecali
Abn00524	Novel hum
Adn46177	Thermoco
Aag03835	Human gan
Abg64570	Human alb
Adl77837	Albumin f
Adi10470	Human the
Abp40106	Staphyloc
Adi05035	Staphyloc
Abb88481	Human mem
Ady63323	Human cilo
Abg64573	Klebsiell
Abf63232	Glucanase
Abp26309	Streptoco
Aag09510	Arabidops
Aag48547	Arabidops
Adn46472	Thermoco
Aag48546	Arabidops
Aag09509	Arabidops
Aag48543	Arabidops
Abb67540	Drosophil
Aab75213	Drosophil
Aae30515	Fruit fly
Adb70112	C. neofor
Aag48542	Arabidops
Aag48541	Arabidops
Adi22042	Bacterial
Adi89436	Cry25Aa.
Abp46121	Human Bly
Adg97892	Human Bly
Adg97892	scfV VHCD
Adg96948	scfV VHCD
Adx15470	Human ant
Adx15486	Human ant
Adx15478	Human ant
Adx15482	Human ant
Aag82419	S. epidid
Abp45043	Human Bly
Abp45775	Human Bly
Abp45045	Human Bly
Abp43993	Human Bly
Abp45054	Human Bly
Adg95872	Single ch
Adg94820	Single ch
Adg95881	Single ch
Adg96602	Single ch
Adg95870	Single ch
Abp45762	Human Bly
Adg96589	Single ch
Adw11894	Thalassio
Abu43004	Protein e
Abp40118	Staphyloc
Adi05078	Staphyloc
Abu43634	Protein e
Adw96433	Thalassio
Adw96435	Thalassio
Adw96415	Thalassio
Adi02948	Drosophil
Adw96457	Thalassio
Adw96431	Thalassio
Abw3589	Lactococo
Abw3403	Drosophil
Abw07190	Alloiooco
Adk16599	Protein e
Abu20548	Nanoarcha
Adn23543	Bacterial
Adn23830	Bacterial
Abw64944	M. xanthu
Abw92836	Human ova
Abp43111	Human ova

98	34	63.0	115	2	AAR52051	Aar52051	Heavy cha	171	33	61.1	101	4	ABB37915	Abb37915	Peptide #
99	34	63.0	123	8	ADO32167	Ado32167	Mouse ant	172	33	61.1	101	4	AAM31325	Aam31325	Peptide #
100	34	63.0	124	8	ADW86141	Adw86141	Novel cyt	173	33	61.1	101	4	ABB23170	Abb23170	Protein #
101	34	63.0	128	6	AAO29546	Aao29546	Human 7.3	174	33	61.1	101	4	AAM71048	Aam71048	Human bon
102	34	63.0	128	6	ABG71908	Abg71908	Human ant	175	33	61.1	101	4	AAM58547	Aam58547	Human bra
103	34	63.0	219	6	ABW90012	Abw90012	Expressed	176	33	61.1	101	4	ABG52763	Abg52763	Human liv
104	34	63.0	230	6	ABU15039	Abu15039	Protein e	177	33	61.1	101	5	ABG40841	Abg40841	Human pep
105	34	63.0	245	4	ABG16544	Abg16544	Novel hum	178	33	61.1	105	2	AAW41018	Aaw41018	Anti-glut
106	34	63.0	268	2	AAR44226	Aar44226	Chimeric	179	33	61.1	105	4	AAM19241	Aam19241	Peptide #
107	34	63.0	271	7	ADH86994	Adh86994	Enterococ	180	33	61.1	105	4	ABB38479	Abb38479	Peptide #
108	34	63.0	277	2	AAM55516	Aam55516	H. pylori	181	33	61.1	105	4	AAM31921	Aam31921	Peptide #
109	34	63.0	277	2	AAV17199	Aav17199	H. pylori	182	33	61.1	105	4	ABB23635	Abb23635	Protein #
110	34	63.0	279	5	ABU50985	Abu50985	Helicobac	183	33	61.1	105	4	AAM71626	Aam71626	Human bon
111	34	63.0	284	2	AAW55375	Aaw55375	H. pylori	184	33	61.1	105	4	AAM59091	Aam59091	Human bra
112	34	63.0	285	2	AAW98454	Aaw98454	H. pylori	185	33	61.1	105	4	ABG53310	Abg53310	Human liv
113	34	63.0	319	7	ADC96783	Adc96783	E. faeciu	186	33	61.1	105	5	ABG41440	Abg41440	Human pep
114	34	63.0	328	5	ABU51082	Abu51082	Helicobac	187	33	61.1	105	9	ADY93867	Ady93867	Anti-SARS
115	34	63.0	329	3	ABU52512	Abu52512	Helicobac	188	33	61.1	115	7	ADF11397	Adf11397	2E11 anti
116	34	63.0	357	3	AAG13328	Aag13328	Arabidops	189	33	61.1	115	8	ADP22214	Adp22214	Human ant
117	34	63.0	357	5	ABG92767	Abg92767	Herbicida	190	33	61.1	116	4	AAU02631	Aau02631	Anti-adip
118	34	63.0	361	3	AGI13327	Agi13327	Arabidops	191	33	61.1	116	7	ADF11393	Adf11393	22B3 anti
119	34	63.0	361	8	ADR88998	Adr88998	A. thalia	192	33	61.1	116	7	ADF11413	Adf11413	9H7 anti-
120	34	63.0	365	7	ADH87046	Adh87046	Enterococ	193	33	61.1	116	7	ADF11409	Adf11409	16E1 anti
121	34	63.0	436	5	ABU50710	Abu50710	Helicobac	194	33	61.1	116	7	ADF11401	Adf11401	2D8 anti-
122	34	63.0	492	9	ABE49916	Abe49916	E. coli p	195	33	61.1	116	8	ADS88105	Ads88105	Human CD2
123	34	63.0	498	4	ABG23519	Abg23519	Novel hum	196	33	61.1	116	9	ADY93863	Ady93863	Anti-SARS
124	34	63.0	510	4	AAU34564	Aau34564	E. coli c	197	33	61.1	117	9	ABE46919	Abe46919	Human var
125	34	63.0	510	6	ABU15038	Abu15038	Protein e	198	33	61.1	117	9	ABE46921	Abe46921	Human var
126	34	63.0	524	3	ABU18304	Abu18304	Plasmodiu	199	33	61.1	118	9	AEA79525	Aea79525	Integrin
127	34	63.0	532	4	ABU12372	Abu12372	Human bon	200	33	61.1	118	9	AEA79527	Aea79527	Integrin
128	34	63.0	537	6	ABM67274	Abm67274	Photorhab	201	33	61.1	118	9	AEA79526	Aea79526	Integrin
129	34	63.0	568	5	ABU51967	Abu51967	Helicobac	202	33	61.1	118	9	AEA79531	Aea79531	Integrin
130	34	63.0	581	4	ABU12455	Abu12455	Human bon	203	33	61.1	118	9	AEA79530	Aea79530	Integrin
131	34	63.0	604	5	AAU74657	Aau74657	Yeast cyc	204	33	61.1	118	9	AEA79528	Aea79528	Integrin
132	34	63.0	639	5	ABU50995	Abu50995	Helicobac	205	33	61.1	118	9	AEA79529	Aea79529	Integrin
133	34	63.0	659	5	ABU51075	Abu51075	Helicobac	206	33	61.1	119	8	ADT88872	Adt88872	Human IGF
134	34	63.0	705	8	ADN19211	Adn19211	Bacterial	207	33	61.1	119	8	ADT88864	Adt88864	Human IGF
135	34	63.0	731	5	ABU52070	Abu52070	Helicobac	208	33	61.1	119	8	ADT88866	Adt88866	Human IGF
136	34	63.0	790	7	ADF06175	Adf06175	Bacterial	209	33	61.1	119	8	ADT88862	Adt88862	Human IGF
137	34	63.0	1943	6	ABU30826	Abu30826	Protein e	210	33	61.1	119	8	ADT88873	Adt88873	Human IGF
138	34	63.0	1974	2	AAW98391	Aaw98391	H. pylori	211	33	61.1	121	7	ADP03960	Adp03960	Murine-ex
139	34	63.0	2147	6	ABR63231	AbR63231	Glucanusc	212	33	61.1	121	8	ADS92886	Ads92886	Human Myo
140	33	61.1	9	8	ADN12058	Adn12058	Humanised	213	33	61.1	121	8	ADS92874	Ads92874	Human Myo
141	33	61.1	12	8	ADN92903	Adn92903	Human Myo	214	33	61.1	123	5	ABB07236	Abb07236	Anti-IL-4
142	33	61.1	15	9	ADY93858	Ady93858	Anti-SARS	215	33	61.1	123	9	AEA08941	Aea08941	Antibody
143	33	61.1	17	4	AAH81980	Aah81980	Gangliosid	216	33	61.1	124	2	AAV15410	Aav15410	Anti-lact
144	33	61.1	17	5	ABG70445	Abg70445	CDR2 regi	217	33	61.1	125	8	ADO25821	Ado25821	Camelidae
145	33	61.1	17	5	AAU82481	Aau82481	Llama CDR	218	33	61.1	125	8	ADO25822	Ado25822	Camelidae
146	33	61.1	17	5	AAU82546	Aau82546	Llama CDR	219	33	61.1	132	3	AAAG24252	Aag24252	ArabiDops
147	33	61.1	17	6	ABU11005	Abu11005	Modified	220	33	61.1	151	2	AAW40495	Aaw40495	Human hea
148	33	61.1	17	9	AD257811	Ad257811	Gangliosid	221	33	61.1	158	5	ABP07106	Abp07106	Human ORF
149	33	61.1	17	9	AEA45760	Aea45760	Apolipopr	222	33	61.1	164	6	ABM72205	Abm72205	Staphyloc
150	33	61.1	40	3	ABU34011	Abu34011	Human sec	223	33	61.1	196	7	ADC96182	Adc96182	E. faeciu
151	33	61.1	40	6	ABU25307	Abu25307	SAC isola	224	33	61.1	202	4	AAU19183	Aau19183	Human G p
152	33	61.1	51	3	AAV64879	Aav64879	Human 5'	225	33	61.1	208	2	AAV41168	Aav41168	Llama Vhh
153	33	61.1	51	8	ADU72443	Adu72443	Signal pe	226	33	61.1	210	8	ADN46769	Adn46769	Thermococ
154	33	61.1	51	9	AD273434	Ad273434	Human inc	227	33	61.1	219	8	ADN46336	Adn46336	Thermococ
155	33	61.1	52	4	ABU03994	Abu03994	Human mus	228	33	61.1	219	8	ADN46336	Adn46336	Thermococ
156	33	61.1	52	6	ADJ29314	Adj29314	Human mus	229	33	61.1	236	5	AAU90905	Aau90905	Insulin/i
157	33	61.1	52	8	AAU29314	Aau29314	Peptide #	230	33	61.1	239	9	ABE46937	Abe46937	Human CD1
158	33	61.1	95	4	AAM33349	Aam33349	Human bon	231	33	61.1	240	9	ABE46939	Abe46939	Human CD1
159	33	61.1	95	4	AAW73134	Aaw73134	Human liv	232	33	61.1	247	5	AAU90904	Aau90904	Insulin/i
160	33	61.1	95	4	ABG54850	Abg54850	Human pep	233	33	61.1	247	8	ADH34575	Adh34575	scFv SC02
161	33	61.1	95	5	ABG42982	Abg42982	Human pep	234	33	61.1	247	8	ADH34573	Adh34573	scFv SC02
162	33	61.1	97	3	AAH40091	Aah40091	Anti-hiLi	235	33	61.1	247	9	ABE27279	Abe27279	Pinus rad
163	33	61.1	97	3	AAH40092	Aah40092	Anti-hiLi	236	33	61.1	251	8	ADO04876	Ado04876	Anti-mous
164	33	61.1	97	5	ABG78195	Abg78195	Human Fv	237	33	61.1	252	8	ADO04874	Ado04874	Anti-mous
165	33	61.1	97	5	ABG78196	Abg78196	Human Fv	238	33	61.1	252	8	ADO04875	Ado04875	Anti-mous
166	33	61.1	97	5	ABG91886	Abg91886	Human ant	239	33	61.1	258	8	ADN92872	Adn92872	Human Myo
167	33	61.1	97	5	ABG91887	Abg91887	Human ant	240	33	61.1	258	8	ADN92884	Adn92884	Human Myo
168	33	61.1	97	6	ABO27115	AbO27115	Human ger	241	33	61.1	262	4	ABH62650	Abh62650	Drosophil
169	33	61.1	97	9	ADY93868	Ady93868	Anti-SARS	242	33	61.1	268	5	ABG95109	Abg95109	Human tra
170	33	61.1	101	4	AAH18809	Aah18809	Peptide #	243	33	61.1	271	6	AAE36354	Aae36354	Human hom



244	33	61.1	271	8	ADS85012	Adas5012 Human ato	317	32	59.3	119	8	ADS12501	Adal12501 Human IGF
245	33	61.1	302	6	ABM68633	Abm68633 Phototrab	318	32	59.3	121	8	ADO25841	Ado25841 Camelidae
246	33	61.1	303	4	ABM63182	Abm63182 Drosophila	319	32	59.3	123	9	ABE11686	Abe11686 Ant1-Pseu
247	33	61.1	318	5	ABP73520	Abp73520 Candida a	320	32	59.3	126	5	ABB89213	Abb89213 Human pol
248	33	61.1	342	8	ADV86525	Adv86525 HSP70 pro	321	32	59.3	136	9	ADZ57715	Adz57715 Germline
249	33	61.1	349	4	ABG61624	Abg61624 Abscisic	322	32	59.3	142	2	AAV85892	Aav85892 S. pneumo
250	33	61.1	359	5	ABG91557	Abg91557 Purine/py	323	32	59.3	149	8	ABO58376	Abos58376 Human gen
251	33	61.1	359	8	ADS29249	AdS29249 Bacterial	324	32	59.3	155	8	ADK88947	Adk88947 Plant ful
252	33	61.1	360	6	ABU50268	Abu50268 Protein e	325	32	59.3	170	2	AAW89913	Aaw89913 Antigen f
253	33	61.1	368	7	ABO61266	AbO61266 Klebsiell	326	32	59.3	235	8	ADY11418	Ady11418 Plant ful
254	33	61.1	400	5	ABB48573	Abb48573 Listeria	327	32	59.3	235	8	ADK88034	Adk88034 Human IGF
255	33	61.1	426	4	AAU43350	Aau43350 Propionib	328	32	59.3	247	8	ADS12383	Ads12383 Human IGF
256	33	61.1	426	6	ABM39869	Abm39869 Propionib	329	32	59.3	256	5	ABP45956	Abp45956 Human Bly
257	33	61.1	436	8	ADT60120	Adt60120 Plant pol	330	32	59.3	256	7	ADG96783	Adg96783 Single ch
258	33	61.1	443	8	ADX80567	Adx80567 Plant ful	331	32	59.3	264	7	ADC95407	Adc95407 E. faeciu
259	33	61.1	445	7	ADF11421	Adf11421 2E11 anti	332	32	59.3	272	6	ADO9584	Ado9584 Allololoc
260	33	61.1	446	7	ADF11425	Adf11425 2D8 anti-	333	32	59.3	273	6	ADA34880	Ada34880 Acinetoba
261	33	61.1	446	7	ADF11437	Adf11437 9H7 anti-	334	32	59.3	275	2	AAV35686	Aav35686 Amino aci
262	33	61.1	446	7	ADF11433	Adf11433 16E1 anti	335	32	59.3	318	6	ADO9586	Ado9586 Allololoc
263	33	61.1	446	7	ADF11417	Adf11417 22B3 anti	336	32	59.3	329	8	ADN22403	Adn22403 Bacterial
264	33	61.1	447	9	ABE46964	Abe46964 CD1a spec	337	32	59.3	330	9	ABE91518	Abe91518 Microbial
265	33	61.1	447	9	ABE46962	Abe46962 CD1a spec	338	32	59.3	338	8	ADM92086	Adm92086 S. pneumon
266	33	61.1	450	8	ADH34587	Adh34587 023 heavy	339	32	59.3	340	8	ADT50085	Adt50085 S. pneumon
267	33	61.1	454	5	ABR76124	AbR76124 Recombina	340	32	59.3	349	8	ADM46159	Adm46159 Acinetoba
268	33	61.1	455	2	AAR06257	Aar06257 Chicken a	341	32	59.3	370	6	ABU00728	Abu00728 S. pneumo
269	33	61.1	456	2	AAR06254	Aar06254 Human ace	342	32	59.3	370	8	ADK47450	Adk47450 Streptoco
270	33	61.1	456	2	AAR06256	Aar06256 Calf acet	343	32	59.3	374	5	ABB48510	Abb48510 Listeria
271	33	61.1	462	5	ABR76126	AbR76126 Recombina	344	32	59.3	374	6	ABU32525	Abu32525 Protein e
272	33	61.1	468	5	ADB12545	AdB12545 Allololoc	345	32	59.3	380	2	AAW89183	Aaw89183 S. pneumo
273	33	61.1	537	6	ABM67373	Abm67373 Phototrab	346	32	59.3	385	9	ADH88423	Adh88423 Enterocec
274	33	61.1	537	6	ABU07374	Abu07374 Human pro	347	32	59.3	388	9	ADM11170	Adm11170 Helicobac
275	33	61.1	537	7	ADG39780	Adg39780 Human nov	348	32	59.3	392	6	ABU32115	Abu32115 Protein e
276	33	61.1	538	6	ADB12543	AdB12543 Allololoc	349	32	59.3	393	8	ADT60626	Adt60626 Plant pol
277	33	61.1	541	6	ABM69122	Abm69122 Phototrab	350	32	59.3	396	6	ABU18660	Abu18660 Protein e
278	33	61.1	549	7	ADP04435	Adp04435 Streptoco	351	32	59.3	401	8	ADN47685	Adn47685 Thermoco
279	33	61.1	575	5	ADI28016	Adi28016 BCMCAD pr	352	32	59.3	404	2	AAV18097	Aav18097 Human sel
280	33	61.1	575	7	ADG39828	Adg39828 Protein s	353	32	59.3	422	7	ABO66198	AbO66198 Klebsiell
281	33	61.1	575	7	ADJ70095	Adj70095 Human hea	354	32	59.3	424	8	ADN19447	Adn19447 Bacterial
282	33	61.1	575	8	ABM81819	Abm81819 Tumour-as	355	32	59.3	441	8	ADT49212	Adt49212 Microbulb
283	33	61.1	612	5	ABP30503	Abp30503 Streptoco	356	32	59.3	441	8	ADT49215	Adt49215 Microbulb
284	33	61.1	617	5	ABP26564	Abp26564 Streptoco	357	32	59.3	444	4	ABB64517	Abb64517 Drosophill
285	33	61.1	617	8	ADV88083	Adv88083 Streptoco	358	32	59.3	446	4	ABB64370	Abb64370 Drosophill
286	33	61.1	617	8	ADV81514	Adv81514 Streptoco	359	32	59.3	458	5	ABB55232	Abb55232 Lactococ
287	33	61.1	617	8	ADV79336	Adv79336 Streptoco	360	32	59.3	459	2	AAW83182	Aaw83182 S. pneumo
288	33	61.1	618	5	ABP26565	Abp26565 Streptoco	361	32	59.3	459	5	ABP26548	Abp26548 Streptoco
289	33	61.1	618	6	ABU46844	Abu46844 Protein e	362	32	59.3	459	7	ADJ11438	Adj11438 Rice prot
290	33	61.1	620	7	ADJ70006	Adj70006 Human hea	363	32	59.3	459	8	ADK48694	Adk48694 Streptoco
291	33	61.1	676	5	ABP29594	Abp29594 Streptoco	364	32	59.3	459	8	ADV89396	Adv89396 Streptoco
292	33	61.1	676	6	ABU46865	Abu46865 Protein e	365	32	59.3	459	8	ADV80649	Adv80649 Streptoco
293	33	61.1	690	3	AG223045	Ag223045 Arabidops	366	32	59.3	459	8	ADV82818	Adv82818 Streptoco
294	33	61.1	691	3	AG223044	Ag223044 Arabidops	367	32	59.3	460	5	ABP26549	Abp26549 Streptoco
295	33	61.1	714	6	ABM65388	Abm65388 Propionib	368	32	59.3	460	6	ABU46495	Abu46495 Protein e
296	33	61.1	766	6	ADA36943	Ada36943 Acinetoba	369	32	59.3	460	7	ABJ72186	Abj72186 Streptoco
297	33	61.1	826	6	ABU50421	Abu50421 Protein e	370	32	59.3	466	6	ABU44496	Abu44496 Protein e
298	33	61.1	850	4	ABG04634	Abg04634 Novel hum	371	32	59.3	470	5	AAU74296	Aau74296 Anti-huma
299	33	61.1	869	4	ABG19658	Abg19658 Novel hum	372	32	59.3	472	4	AAU37949	Aau37949 Streptoco
300	33	61.1	911	2	AAV55957	Aav55957 Mouse str	373	32	59.3	474	4	ABB59179	Abb59179 Drosophill
301	33	61.1	2000	7	ADK62360	Adk62360 Disease t	374	32	59.3	479	6	AAU37714	Aau37714 Streptoco
302	33	61.1	3194	6	ABE91132	Abe91132 Protein e	375	32	59.3	479	6	ABU01401	Abu01401 S. pneumo
303	33	61.1	3194	9	ABE91130	Abe91130 Microbial	376	32	59.3	479	6	ABU46013	Abu46013 Protein e
304	33	61.1	3871	8	ADN23885	Adn23885 Bacterial	377	32	59.3	484	7	ABO63015	AbO63015 Klebsiell
305	33	61.1	3871	8	ADN23886	Adn23886 Bacterial	378	32	59.3	488	7	ADJ70795	Adj70795 Human hea
306	32	59.3	13	5	AAU74522	Aau74522 Lactobaci	379	32	59.3	496	4	AAU33825	Aau33825 Staphyloc
307	32	59.3	14	9	ADZ41960	Adz41960 Ig V-regi	380	32	59.3	496	8	ADS28627	Ads28627 Bacterial
308	32	59.3	14	9	ADZ41915	Adz41915 Ig V-regi	381	32	59.3	497	8	ADZ28149	Adz28149 Bacterial
309	32	59.3	19	5	ABP47102	Abp47102 Human Bly	382	32	59.3	498	4	AAU36742	Aau36742 Staphyloc
310	32	59.3	19	5	ABP47102	Abp47102 scFV VHCD	383	32	59.3	498	6	ABU16027	Abu16027 Protein e
311	32	59.3	20	7	ADN14211	Adn14211 Tuberculo	384	32	59.3	499	4	AAW82195	Aaw82195 S. epider
312	32	59.3	21	7	ADG03405	Adg03405 GPIIb/III	385	32	59.3	499	6	ABU43435	Abu43435 Protein e
313	32	59.3	55	3	AAV65143	Aav65143 Human 5'	386	32	59.3	499	6	ABU43187	Abu43187 Protein e
314	32	59.3	55	8	ADU72707	Adu72707 Signal pe	387	32	59.3	502	7	ABO65976	AbO65976 Novel hum
315	32	59.3	55	8	ADU72707	Adu72707 Human inc	388	32	59.3	502	7	ABO68578	AbO68578 Pseudomon
316	32	59.3	115	9	AEA08988	Aea08988 Heavy cha	389	32	59.3	504	5	ABP39325	Abp39325 Staphyloc

390	32	59.3	802	7	ADB76391	Human PRO
391	32	59.3	802	7	ADC43817	Human sec
392	32	59.3	802	7	ADC61577	Human sec
393	32	59.3	802	7	ADC63541	Human sec
394	32	59.3	802	7	ADC66641	Human sec
395	32	59.3	802	7	ADC68765	Human sec
396	32	59.3	802	7	ADC62825	Human sec
397	32	59.3	802	7	ADC67890	Human sec
398	32	59.3	802	7	ADC41210	Human sec
399	32	59.3	802	7	ADC67265	Human sec
400	32	59.3	802	7	ADC62201	Human sec
401	32	59.3	802	7	ADC41834	Human sec
402	32	59.3	802	7	ADC49203	Human sec
403	32	59.3	802	7	ADC35257	Human sec
404	32	59.3	802	7	ADC16371	Human sec
405	32	59.3	802	7	ADC72986	Human sec
406	32	59.3	802	7	ADC72344	Human sec
407	32	59.3	802	7	ADC16995	Human sec
408	32	59.3	802	7	ADC47009	Human sec
409	32	59.3	802	7	ADC52766	Human sec
410	32	59.3	802	7	ADC60086	Human sec
411	32	59.3	802	7	ADI60846	Human sec
412	32	59.3	802	7	ADI10377	Human cel
413	32	59.3	802	8	ADE48503	Human sec
414	32	59.3	802	8	ADE89604	Human sec
415	32	59.3	802	8	ADF61244	Human sec
416	32	59.3	802	8	ADF39936	Human sec
417	32	59.3	802	8	ADF45732	Human sec
418	32	59.3	802	8	ADF24128	Human sec
419	32	59.3	802	8	ADF40560	Human sec
420	32	59.3	802	8	ADF23504	Human sec
421	32	59.3	802	8	ADF33487	Human sec
422	32	59.3	802	8	ADF26954	Human sec
423	32	59.3	802	8	ADF27590	Human sec
424	32	59.3	802	8	ADF41184	Human sec
425	32	59.3	802	8	ADF32863	Human sec
426	32	59.3	802	8	ADF25229	Human sec
427	32	59.3	802	8	ADF26330	Human sec
428	32	59.3	802	8	ADF34119	Human sec
429	32	59.3	802	8	ADF46356	Human sec
430	32	59.3	802	8	ADG50342	Human sec
431	32	59.3	802	8	ADG49718	Human sec
432	32	59.3	802	8	ADG49094	Human sec
433	32	59.3	802	8	ADG51590	Human sec
434	32	59.3	802	8	ADG48470	Human sec
435	32	59.3	802	8	ADG50966	Human sec
436	32	59.3	802	8	ADG58910	Human sec
437	32	59.3	802	8	ADG62366	Human sec
438	32	59.3	802	8	ADH25391	Human neu
439	32	59.3	802	8	ADM17168	Human tra
440	32	59.3	802	8	ADM17002	Human sec
441	32	59.3	802	8	ADL07002	Human PRO
442	32	59.3	802	8	ADL91615	Human PRO
443	32	59.3	802	8	ADU50124	PRO18, S
444	32	59.3	802	8	ADW49403	PRO18 pr
445	32	59.3	802	9	ADZ52064	Human sec
446	32	59.3	802	9	ADZ52064	Human sec
447	32	59.3	802	9	ADZ52064	Human sec
448	32	59.3	802	9	ADZ52064	Human sec
449	32	59.3	802	9	ADZ52064	Human sec
450	32	59.3	802	9	ADZ52064	Human sec
451	32	59.3	802	9	ADZ52064	Human sec
452	32	59.3	802	9	ADZ52064	Human sec
453	32	59.3	802	9	ADZ52064	Human sec
454	32	59.3	802	9	ADZ52064	Human sec
455	32	59.3	802	9	ADZ52064	Human sec
456	32	59.3	802	9	ADZ52064	Human sec
457	32	59.3	802	9	ADZ52064	Human sec
458	32	59.3	802	9	ADZ52064	Human sec
459	32	59.3	802	9	ADZ52064	Human sec
460	32	59.3	802	9	ADZ52064	Human sec
461	32	59.3	802	9	ADZ52064	Human sec
462	32	59.3	802	9	ADZ52064	Human sec

536	31.5	58.3	208	4	ABB50217	Abb50217 Human tra	609	31	57.4	111	7	ADD28036	ADD28036 Lymphoma
537	31.5	58.3	208	7	ADJ68912	Adj68912 Human hea	610	31	57.4	114	9	AEA40137	Aea40137 TNF resis
538	31.5	58.3	208	8	ADL12952	Adl12952 Human ste	611	31	57.4	115	5	ABB07232	Abb07232 Anti-IL-4
539	31.5	58.3	208	8	ABM82388	Abm82388 Tumour-as	612	31	57.4	115	9	AEA11019	Aea11019 Human ant
540	31	57.4	8	3	AYY77587	Ayy77587 Anti-huma	613	31	57.4	115	9	AEA08919	Aea08919 Heavy cha
541	31	57.4	8	4	AAB78856	Aab78856 Anti-huma	614	31	57.4	115	9	AEA08891	Aea08891 Heavy cha
542	31	57.4	8	8	ADL11879	Adl11879 CDR-1 hea	615	31	57.4	115	9	AEA08994	Aea08994 Heavy cha
543	31	57.4	8	9	ADZ58521	Adz58521 VEGF rece	616	31	57.4	115	9	AEA08989	Aea08989 Heavy cha
544	31	57.4	8	9	AEA40143	Aea40143 TNF resis	617	31	57.4	115	9	AEA08991	Aea08991 Heavy cha
545	31	57.4	8	9	AEA53829	Aea53829 Novel hum	618	31	57.4	115	9	AEA08992	Aea08992 Heavy cha
546	31	57.4	8	9	AEA53800	Aea53800 Novel hum	619	31	57.4	115	9	AEA08995	Aea08995 Heavy cha
547	31	57.4	8	9	AEA53496	Aea53496 Novel hum	620	31	57.4	115	9	AEA08987	Aea08987 Heavy cha
548	31	57.4	8	9	AEA45972	Aea45972 Apolipopr	621	31	57.4	115	9	AEA08993	Aea08993 Heavy cha
549	31	57.4	8	9	ABE18008	Abe18008 Humanized	622	31	57.4	115	9	AEA08990	Aea08990 Heavy cha
550	31	57.4	10	3	AYY79428	Ayy79428 Tie2 rece	623	31	57.4	115	9	AEA08981	Aea08981 Heavy cha
551	31	57.4	11	2	AAW62194	Aaw62194 Mouse ant	624	31	57.4	115	9	AEA08982	Aea08982 Heavy cha
552	31	57.4	11	2	AAW57590	Aaw57590 Chimeric	625	31	57.4	115	9	AEA08984	Aea08984 Heavy cha
553	31	57.4	11	2	AAW02552	Aaw02552 Artificia	626	31	57.4	116	5	ABB07234	Abb07234 Anti-IL-4
554	31	57.4	11	2	AAW89634	Aaw89634 Mouse hum	627	31	57.4	116	8	ADS84380	Ads84380 Human ant
555	31	57.4	11	3	AYY77520	Ayy77520 Antibody	628	31	57.4	116	8	ADR68522	Adr68522 Anti-EP0-
556	31	57.4	11	4	AAB76934	Aab76934 Human PTH	629	31	57.4	116	9	AEA08939	Aea08939 Antibody
557	31	57.4	11	4	AAB76896	Aab76896 Human PTH	630	31	57.4	117	8	ADL11887	Adl11887 Chimera a
558	31	57.4	11	4	AAG67118	Aag67118 Amino aci	631	31	57.4	117	8	ADL11892	Adl11892 CDR trans
559	31	57.4	11	4	AAG64782	Aag64782 Anti-PTHr	632	31	57.4	117	8	ADL11893	Adl11893 CDR trans
560	31	57.4	11	4	AAG63400	Aag63400 Amino aci	633	31	57.4	117	9	ADZ58539	Adz58539 VEGF rece
561	31	57.4	11	4	AAB76915	Aab76915 Human PTH	634	31	57.4	117	9	ADZ58535	Adz58535 VEGF rece
562	31	57.4	11	5	ABN95194	Abn95194 Human joi	635	31	57.4	117	9	ADZ58531	Adz58531 VEGF rece
563	31	57.4	11	5	ABJ36665	Abj36665 Angiogene	636	31	57.4	119	2	AAW95216	Aaw95216 Human foe
564	31	57.4	11	8	ADO33861	Ado33861 Human par	637	31	57.4	119	3	AAW79424	Aaw79424 Tie2 rece
565	31	57.4	11	9	AEA53512	Aea53512 Novel hum	638	31	57.4	119	5	ABP31467	Abp31467 Human rib
566	31	57.4	11	9	AEA53798	Aea53798 Novel hum	639	31	57.4	119	6	AAO23065	Aao23065 Murine K8
567	31	57.4	11	9	AEA99625	Aea99625 Human CAB	640	31	57.4	120	8	ADK18142	Adk18142 CAB1 heav
568	31	57.4	11	9	AEA99631	Aea99631 Human CAB	641	31	57.4	120	8	ADJ54095	Adj54095 CAB-1 hea
569	31	57.4	11	9	AEA99652	Aea99652 Human CAB	642	31	57.4	120	9	ADZ59990	Adz59990 CAB1 heav
570	31	57.4	12	4	AAU02662	Aau02662 CDR regio	643	31	57.4	120	9	AEA99642	Aea99642 Human CAB
571	31	57.4	12	5	ABP46183	Abp46183 Human Bly	644	31	57.4	121	4	AAU02533	Aau02533 Anti-adip
572	31	57.4	12	8	ADG97010	Adg97010 scFV VHCD	645	31	57.4	123	6	ABR63613	AbR63613 Human gly
573	31	57.4	12	8	ADO05858	Ado05858 MOG-Fab I	646	31	57.4	124	9	ADY96943	Ady96943 Human imm
574	31	57.4	13	8	ADQ17153	Adq17153 Murine an	647	31	57.4	124	9	ADY96951	Ady96951 Human imm
575	31	57.4	13	9	ADM04768	Adm04768 PAPP-A im	648	31	57.4	125	8	ADR40435	Adr40435 Mouse 2c
576	31	57.4	14	6	ABR63617	AbR63617 Human gly	649	31	57.4	125	8	ADR40353	Adr40353 Mouse 2c
577	31	57.4	15	4	ADM78912	Adm78912 Protein G	650	31	57.4	125	8	ADM39241	Adm39241 Pgp-resis
578	31	57.4	16	8	ADM78086	Adm78086 Human SJB	651	31	57.4	127	9	AEA53368	Aea53368 Novel hum
579	31	57.4	18	5	ABP46520	Abp46520 Human Bly	652	31	57.4	130	2	AAW47581	Aaw47581 Human non
580	31	57.4	18	7	ADG97747	Adg97747 scFV VHCD	653	31	57.4	130	8	ADM78043	Adm78043 Human SKB
581	31	57.4	31	9	AEA54170	Aea54170 Novel hum	654	31	57.4	130	8	ADO05872	Ado05872 C. jacchu
582	31	57.4	34	4	ABB38023	Abb38023 Peptide #	655	31	57.4	130	9	ABE15491	Abe15491 Anti-teta
583	31	57.4	34	4	AAW31437	Aaw31437 Peptide #	656	31	57.4	132	9	ADM04762	Adm04762 PAPP-A im
584	31	57.4	34	4	AAW71156	Aaw71156 Human bon	657	31	57.4	133	3	ABM24760	Abm24760 Plant SDF
585	31	57.4	34	4	AAW58650	Aaw58650 Human bra	658	31	57.4	133	9	ABAS3208	Abas3208 Novel hum
586	31	57.4	34	4	ABG52868	Abg52868 Human liv	659	31	57.4	136	3	AAW77600	Aaw77600 Anti-huma
587	31	57.4	34	5	ABG40953	Abg40953 Human pep	660	31	57.4	136	3	AAW77593	Aaw77593 Anti-huma
588	31	57.4	37	9	AEA54194	Aea54194 Novel hum	661	31	57.4	136	3	AAW77596	Aaw77596 Anti-huma
589	31	57.4	45	2	AAW77720	Aaw77720 Staphyloc	662	31	57.4	136	4	ABM78869	Abm78869 Anti-huma
590	31	57.4	45	3	AAW02710	Aaw02710 Human sec	663	31	57.4	136	4	ABM78862	Abm78862 Anti-huma
591	31	57.4	56	2	AAW02491	Aaw02491 Clone sel	664	31	57.4	136	4	ABM78865	Abm78865 Anti-huma
592	31	57.4	63	4	AAO12871	Aao12871 Human pol	665	31	57.4	138	6	AAO23064	Aao23064 Murine K8
593	31	57.4	69	6	ABU31139	Abu31139 Protein e	666	31	57.4	138	7	ABR62341	AbR62341 Anti-HLA-
594	31	57.4	77	5	ABP08163	Abp08163 Human ORF	667	31	57.4	138	7	ADD28324	Add28324 Human het
595	31	57.4	80	9	ADZ59996	Adz59996 CAB1 cons	668	31	57.4	138	8	ADX75833	Adx75833 Plant ful
596	31	57.4	82	2	AAW60534	Aaw60534 Human nor	669	31	57.4	139	2	AAW65774	Aaw65774 Anti-huma
597	31	57.4	82	6	ABM71378	Abm71378 Staphyloc	670	31	57.4	139	2	AAW65773	Aaw65773 Anti-huma
598	31	57.4	82	6	ABM70825	Abm70825 Staphyloc	671	31	57.4	139	2	AAW62216	Aaw62216 Humanised
599	31	57.4	82	6	ABM71532	Abm71532 Staphyloc	672	31	57.4	139	2	AAW62204	Aaw62204 Humanised
600	31	57.4	92	7	ADC97482	Adc97482 E. faeciu	673	31	57.4	139	2	AAW62211	Aaw62211 Humanised
601	31	57.4	95	4	AAW78911	Aaw78911 Human pro	674	31	57.4	139	2	AAW62215	Aaw62215 Humanised
602	31	57.4	97	2	AAW80371	Aaw80371 Heavy cha	675	31	57.4	139	2	AAW62199	Aaw62199 Humanised
603	31	57.4	97	6	ABO04834	AbO04834 Human epi	676	31	57.4	139	2	AAW62214	Aaw62214 Humanised
604	31	57.4	97	9	AEA17748	Aea17748 Hybridoma	677	31	57.4	139	2	AAW62217	Aaw62217 Humanised
605	31	57.4	98	3	AAW25120	Aaw25120 Euclalyptu	678	31	57.4	139	2	AAW62196	Aaw62196 Humanised
606	31	57.4	99	2	AAW13816	Aaw13816 Carboxyl-	679	31	57.4	139	2	AAW62188	Aaw62188 Mouse ant
607	31	57.4	104	4	ABB11159	Abb11159 Human GTP	680	31	57.4	139	2	AAW62201	Aaw62201 Humanised
608	31	57.4	107	5	AAE23396	Aae23396 Human MOG	681	31	57.4	139	2	AAW62210	Aaw62210 Humanised

682	31	57.4	139	2	AAW622205	Aaw622205 Humanised	755	31	57.4	256	5	ABP45274	Abp45274 Human Bly
683	31	57.4	139	2	AAW622206	Aaw622206 Humanised	756	31	57.4	256	7	ADG96101	Adg96101 Single ch
684	31	57.4	139	2	AAW622209	Aaw622209 Humanised	757	31	57.4	268	8	Adx80246	Adx80246 Plant ful
685	31	57.4	139	2	AAW622198	Aaw622198 Humanised	758	31	57.4	270	2	Aar75719	Aar75719 MFE-23 an
686	31	57.4	139	2	AAW622218	Aaw622218 Humanised	759	31	57.4	270	3	AAW75719	AAW75719
687	31	57.4	139	2	AAW622197	Aaw622197 Humanised	760	31	57.4	276	3	AAW57344	AAW57344 Arabidops
688	31	57.4	139	2	AAW622202	Aaw622202 Humanised	761	31	57.4	276	8	Adn72875	Adn72875 Thale cre
689	31	57.4	139	2	AAW62212	Aaw62212 Humanised	762	31	57.4	280	2	AAW54379	AAW54379 Cell divi
690	31	57.4	139	2	AAW622200	Aaw622200 Humanised	763	31	57.4	282	9	Aeb40350	Aeb40350 L. pneumo
691	31	57.4	139	2	AAW622203	Aaw622203 Humanised	764	31	57.4	283	6	ABU29187	ABU29187 Protein e
692	31	57.4	139	2	AAW622213	Aaw622213 Humanised	765	31	57.4	285	9	ABU17984	ABU17984 Humanized
693	31	57.4	139	2	AAW77295	Aaw77295 HM1.24 an	766	31	57.4	285	9	ABU17986	ABU17986 Humanized
694	31	57.4	139	2	AAW702557	Aay02557 Humanised	767	31	57.4	287	9	ABU18012	ABU18012 Humanized
695	31	57.4	139	2	AAW02568	Aay02568 Humanised	768	31	57.4	287	9	ABU18011	ABU18011 Humanized
696	31	57.4	139	2	AAW02573	Aay02573 Humanised	769	31	57.4	292	4	AAU35101	AAU35101 Enterococ
697	31	57.4	139	2	AAW02561	Aay02561 Humanised	770	31	57.4	293	2	AAW14481	AAW14481 Ramp-1. 5
698	31	57.4	139	2	AAW02558	Aay02558 Humanised	771	31	57.4	293	6	ABU08258	ABU08258 Human C-4
699	31	57.4	139	2	AAW02546	Aay02546 H chain V	772	31	57.4	293	7	ADE56528	ADE56528 Human Pro
700	31	57.4	139	2	AAW02570	Aay02570 Humanised	773	31	57.4	293	7	ADE56526	ADE56526 Rat Prote
701	31	57.4	139	2	AAW02575	Aay02575 Humanised	774	31	57.4	293	7	ADE31647	ADE31647 Human 616
702	31	57.4	139	2	AAW02564	Aay02564 Humanised	775	31	57.4	293	8	ADK46497	ADK46497 Streptoco
703	31	57.4	139	2	AAW02565	Aay02565 Humanised	776	31	57.4	293	8	ADL82961	ADL82961 Human PRO
704	31	57.4	139	2	AAW02572	Aay02572 Humanised	777	31	57.4	293	8	ADN04388	ADN04388 Antipsori
705	31	57.4	139	2	AAW02571	Aay02571 Humanised	778	31	57.4	293	8	ADO19683	ADO19683 Human PRO
706	31	57.4	139	2	AAW02555	Aay02555 Humanised	779	31	57.4	293	8	ADQ88178	ADQ88178 Human 616
707	31	57.4	139	2	AAW02559	Aay02559 Humanised	780	31	57.4	293	8	ADP56122	ADP56122 Human PRO
708	31	57.4	139	2	AAW02560	Aay02560 Humanised	781	31	57.4	293	8	ADR68904	ADR68904 Human C-4
709	31	57.4	139	2	AAW02563	Aay02563 Humanised	782	31	57.4	293	8	ADP24211	ADP24211 PRO poly
710	31	57.4	139	2	AAW02567	Aay02567 Humanised	783	31	57.4	293	9	AEB36989	AEB36989 L. pneumo
711	31	57.4	139	2	AAW02566	Aay02566 Humanised	784	31	57.4	297	9	AEA58980	AEA58980 Streptoco
712	31	57.4	139	2	AAW02574	Aay02574 Humanised	785	31	57.4	297	9	AAW39142	AAW39142 Human pol
713	31	57.4	139	2	AAW02562	Aay02562 Humanised	786	31	57.4	298	4	AAW58101	AAW58101 Haemortha
714	31	57.4	139	2	AAW02556	Aay02556 Humanised	787	31	57.4	300	3	AAW58101	AAW58101 Haemortha
715	31	57.4	139	2	AAW02569	Aay02569 Humanised	788	31	57.4	305	6	ADA34782	ADA34782 Human T2R
716	31	57.4	139	2	AAW32771	Aay32771 Anti-HM1.	789	31	57.4	317	4	AAW87744	AAW87744 Human T2R
717	31	57.4	139	2	AAW32770	Aay32770 Anti-HM1.	790	31	57.4	317	7	ADH86802	ADH86802 Enterococ
718	31	57.4	139	2	AAW05487	Aay05487 H chain V	791	31	57.4	317	8	ADJ84507	ADJ84507 Human T2R
719	31	57.4	139	2	AAW05486	Aay05486 H chain V	792	31	57.4	317	8	ADK47596	ADK47596 Streptoco
720	31	57.4	139	5	AAW52354	Aam52354 H chain V	793	31	57.4	317	8	ADR29087	ADR29087 Taste rec
721	31	57.4	139	5	AAW52355	Aam52355 H chain V	794	31	57.4	317	8	ADM33327	ADM33327 Human bit
722	31	57.4	139	6	ABG71946	ABG71946 Human res	795	31	57.4	317	9	ADM74528	ADM74528 Human bit
723	31	57.4	139	8	ADG60011	H chain V	796	31	57.4	317	9	ADM74530	ADM74530 Human bit
724	31	57.4	139	8	ADG60010	H chain V	797	31	57.4	317	9	ADM74408	ADM74408 Human bit
725	31	57.4	140	2	AAW677294	Aaw677294 HM1.24 an	798	31	57.4	317	9	ADW74526	ADW74526 Human bit
726	31	57.4	148	8	ADM46624	ADM46624 Mouse 7F4	799	31	57.4	321	8	ADR94260	ADR94260 Novel S.
727	31	57.4	148	8	ADP02855	ADP02855 Solanum a	800	31	57.4	321	9	AEA58130	AEA58130 Streptoco
728	31	57.4	174	8	ADU25582	ADu25582 L. acidop	801	31	57.4	322	6	ABRS8041	ABRS8041 Human GI
729	31	57.4	176	2	AAW80254	Aaw80254 Amino aci	802	31	57.4	323	7	ADC46685	ADC46685 Thalecres
730	31	57.4	176	8	ADP57551	ADf57551 Mouse ymk	803	31	57.4	323	8	ADO01701	ADO01701 Thalecres
731	31	57.4	176	8	ADM46623	ADM46623 Mouse 7F4	804	31	57.4	339	4	ABB64705	ABB64705 Drosophil
732	31	57.4	180	8	ADW27331	ADw27331 Bacterial	805	31	57.4	344	5	ABB49083	ABB49083 Listeria
733	31	57.4	180	8	ADS26602	ADS26602 Bacterial	806	31	57.4	358	8	ADW78536	ADW78536 Plant ful
734	31	57.4	180	8	ADS26977	ADS26977 Bacterial	807	31	57.4	359	5	ABB90660	ABB90660 Chlamydia
735	31	57.4	186	3	AAW24759	AAw24759 Plant SDF	808	31	57.4	359	9	ABE39703	ABE39703 L. pneumo
736	31	57.4	192	2	ADR12257	ADR12257 HIV-1 str	809	31	57.4	367	2	RAY35144	RAY35144 Chlamydia
737	31	57.4	192	9	ADX40509	ADx40509 HIV Vif p	810	31	57.4	368	8	ADS42877	ADS42877 Bacterial
738	31	57.4	195	7	ABO65825	ABO65825 Klebsiell	811	31	57.4	369	9	ABE36286	ABE36286 L. pneumo
739	31	57.4	199	4	AAU43144	AAu43144 Propionib	812	31	57.4	371	9	ABM94477	ABM94477 M. xanthu
740	31	57.4	199	6	ABM39663	ABm39663 Propionib	813	31	57.4	383	4	ABW4398	ABW4398 Amino aci
741	31	57.4	203	3	AAW24758	AAw24758 Plant SDF	814	31	57.4	383	4	AAW94899	AAW94899 Human pro
742	31	57.4	203	3	AAW57345	AAW57345 Arabidops	815	31	57.4	383	4	AAW95272	AAW95272 Human pro
743	31	57.4	223	4	AAW08638	AAW08638 Ciona int	816	31	57.4	383	6	AAE37143	AAE37143 Human sal
744	31	57.4	225	8	AAW10451	AAw10451 Vibrio ch	817	31	57.4	383	8	ADJ75477	ADJ75477 Marker ge
745	31	57.4	230	2	AAW14072	AAW14072 S.thermop	818	31	57.4	383	8	ADP24921	ADP24921 PRO poly
746	31	57.4	230	2	AAW22171	AAW22171 S.thermop	819	31	57.4	386	8	ADJ76245	ADJ76245 Marker ge
747	31	57.4	230	3	AAW43769	AAW43769 Amino aci	820	31	57.4	388	4	ABG25142	ABG25142 Novel hum
748	31	57.4	230	3	AAW54067	AAW54067 Enzyme EP	821	31	57.4	391	7	ADH88325	ADH88325 Enterococ
749	31	57.4	244	5	ABP45870	ABp45870 Human Bly	822	31	57.4	392	4	ABB61101	ABB61101 Drosophil
750	31	57.4	244	7	ADG96697	ADg96697 Single ch	823	31	57.4	393	7	ADC96383	ADC96383 E. faeciu
751	31	57.4	244	8	ADK18141	ADK18141 CAB1-scfv	824	31	57.4	396	8	ADF57557	ADF57557 Mouse ymk
752	31	57.4	244	8	ADJ54093	ADJ54093 CAB-1 scf	825	31	57.4	398	4	AAW40928	AAW40928 Human pol
753	31	57.4	244	9	ABE17982	ABE17982 Mouse scf	826	31	57.4	398	7	ADF60215	ADF60215 Human con
754	31	57.4	251	8	ADX95232	ADx95232 Plant ful	827	31	57.4	403	6	ABO14691	ABO14691 Novel hum

828	31	57.4	406	6	ABU29736	Abu29736 Protein e	901	31	57.4	561	8	ADR89406	Adr89406 AXMI-0080
829	31	57.4	409	7	ADH87200	Adh87200 Enterococ	902	31	57.4	568	6	ADB10594	Adb10594 Alloiococ
830	31	57.4	411	8	ADU87524	Adu87524 Mycoplasma	903	31	57.4	571	6	ADB10592	Adb10592 Alloiococ
831	31	57.4	411	8	ADY13574	Ady13574 Plant ful	904	31	57.4	573	2	AAW18303	Aaw18303 Photorhab
832	31	57.4	420	6	ADC94418	Adc94418 E. faeciu	905	31	57.4	573	2	AAW56559	Aaw56559 Toxin Tcb
833	31	57.4	428	6	ADB08200	Adb08200 Alloiococ	906	31	57.4	576	8	ADS226183	Ada226183 Bacterial
834	31	57.4	431	4	AAU35440	Aau35440 Haemophil	907	31	57.4	576	8	ADS22664	Ada22664 Bacterial
835	31	57.4	451	4	AAW79843	Aaw79843 Human pro	908	31	57.4	576	8	ADS25707	Ada25707 Bacterial
836	31	57.4	452	6	ADA36582	Ada36582 Protein e	909	31	57.4	583	4	AAU37865	Aau37865 Streptoco
837	31	57.4	452	6	ADA36582	Ada36582 Acinetoba	910	31	57.4	583	6	ABU02324	Abu02324 S. pneumo
838	31	57.4	455	6	ADB08202	Adb08202 Alloiococ	911	31	57.4	583	6	ABP81636	Abp81636 Streptoco
839	31	57.4	455	7	ADBS8778	Adbs8778 Rat prote	912	31	57.4	583	6	ABU46225	Abu46225 Protein e
840	31	57.4	456	5	ABG91778	Abg91778 Purine/py	913	31	57.4	605	9	AEA99619	Aea99619 Human CAB
841	31	57.4	456	7	ABJ72183	Abj72183 B subtili	914	31	57.4	605	9	AEA99702	Aea99702 Human CAB
842	31	57.4	457	5	ABR47683	Abra47683 Listeria	915	31	57.4	605	9	AEA99620	Aea99620 Human CAB
843	31	57.4	457	6	ABU32986	Abu32986 Protein e	916	31	57.4	605	9	AEA99617	Aea99617 Human CAB
844	31	57.4	459	6	ABU17815	Abu17815 Protein e	917	31	57.4	605	9	AEA99647	Aea99647 Human CAB
845	31	57.4	463	2	AAW43010	Aaw43010 Truncated	918	31	57.4	605	9	AEA99649	Aea99649 Human CAB
846	31	57.4	463	2	AAW51803	Aaw51803 H. influe	919	31	57.4	605	9	AEA99663	Aea99663 Human CAB
847	31	57.4	466	5	ABP74041	Abp74041 Candida a	920	31	57.4	619	4	AAU91554	Aau91554 C. glutami
848	31	57.4	481	8	ADN01952	Adn01952 Staphyloc	921	31	57.4	619	7	ADU87437	Adu87437 DNA repli
849	31	57.4	481	8	ADN01939	Adn01939 Staphyloc	922	31	57.4	631	2	AAU77896	Aau77896 Bacterial
850	31	57.4	481	8	ADN01953	Adn01953 Staphyloc	923	31	57.4	631	2	AAU77894	Aau77894 Bacterial
851	31	57.4	481	8	ADN01953	Adn01953 Staphyloc	924	31	57.4	631	2	AAU08968	Aau08968 Amino aci
852	31	57.4	481	8	ADN01946	Adn01946 Staphyloc	925	31	57.4	631	2	AAU08970	Aau08970 Amino aci
853	31	57.4	486	6	AEW71573	Aew71573 Staphyloc	926	31	57.4	631	2	AAU51782	Aay51782 H. influe
854	31	57.4	490	2	AAW89764	Aaw89764 Staphyloc	927	31	57.4	631	2	AAU51784	Aay51784 H. influe
855	31	57.4	490	8	ADN01954	Adn01954 Staphyloc	928	31	57.4	631	2	AAW54126	Aaw54126 H. influe
856	31	57.4	493	8	ADN22942	Adn22942 Bacterial	929	31	57.4	631	2	AAW54128	Aaw54128 H. influe
857	31	57.4	494	8	ADN26298	Adn26298 Bacterial	930	31	57.4	631	3	AAU80364	Aay80364 H. influe
858	31	57.4	496	2	AAW94309	Aaw94309 Thermus f	931	31	57.4	631	3	AAU80366	Aay80366 H. influe
859	31	57.4	496	7	ADK70725	Adk70725 Heat-resi	932	31	57.4	647	2	AAW43014	Aaw43014 Truncated
860	31	57.4	503	2	AAU00189	Aay00189 Enterococ	933	31	57.4	647	2	AAU51800	Aay51800 H. influe
861	31	57.4	503	2	AAU53536	Aay53536 Amino aci	934	31	57.4	649	4	AAU96494	Aau96494 Putative
862	31	57.4	503	5	ABP43408	Abp43408 E. faecali	935	31	57.4	654	2	AAU77889	Aau77889 Bacterial
863	31	57.4	503	6	ABU88436	Abu88436 E. faecal	936	31	57.4	654	2	AAU08964	Aau08964 Amino aci
864	31	57.4	503	6	ABU13687	Abu13687 Enterococ	937	31	57.4	654	2	AAU51694	Aay51694 H. influe
865	31	57.4	503	9	ADK39094	Adk39094 Novel Ent	938	31	57.4	654	2	AAU53049	Aay53049 H. influe
866	31	57.4	503	9	AEBA1930	Aeb41930 L. pneumo	939	31	57.4	654	3	AAU80360	Aay80360 H. influe
867	31	57.4	508	6	ABU32133	Abu32133 Protein e	940	31	57.4	660	2	AAU77885	Aau77885 Bacterial
868	31	57.4	514	9	AEBS38701	Aeb38701 L. pneumo	941	31	57.4	660	2	AAU77887	Aau77887 Bacterial
869	31	57.4	522	8	ADK79210	Adk79210 Plant ful	942	31	57.4	660	2	AAU96970	Aau96970 Bacterial
870	31	57.4	523	2	AAW43011	Aaw43011 Truncated	943	31	57.4	660	2	AAU08960	Aau08960 Amino aci
871	31	57.4	524	3	AAU46112	Aag46112 Arabidops	944	31	57.4	660	2	AAU08962	Aau08962 Amino aci
872	31	57.4	529	2	AAW43012	Aaw43012 Truncated	945	31	57.4	660	2	AAU51692	Aay51692 H. influe
873	31	57.4	529	2	AAU51802	Aay51802 H. influe	946	31	57.4	660	2	AAU51690	Aay51690 H. influe
874	31	57.4	533	3	AEA55100	Aea55100 Yeast unn	947	31	57.4	660	2	AAU53047	Aaw53047 H. influe
875	31	57.4	534	3	AAU46111	Aag46111 Arabidops	948	31	57.4	660	2	AAU53045	Aaw53045 H. influe
876	31	57.4	537	4	AAU95734	Aab95734 Human pro	949	31	57.4	660	3	AAU80358	Aay80358 H. influe
877	31	57.4	540	6	ABR52536	Abr52536 Protein s	950	31	57.4	660	3	AAU80356	Aay80356 H. influe
878	31	57.4	540	6	ABR47712	Abr47712 Human sec	951	31	57.4	673	6	ABU25846	Abu25846 Protein e
879	31	57.4	540	6	ABR00059	Abr00059 Human gen	952	31	57.4	681	3	AAU46110	Aag46110 Arabidops
880	31	57.4	540	7	ADB91515	Adb91515 Human sec	953	31	57.4	683	4	AAU83282	Aag83282 Chlamydia
881	31	57.4	540	7	ADB85510	Adb85510 Human RGA	954	31	57.4	683	5	ABU94253	Abu94253 Chlamydia
882	31	57.4	540	7	ADC16718	Adc16718 Human mod	955	31	57.4	708	6	ABU64972	Abu64972 Propionib
883	31	57.4	540	7	ADC74095	Adc74095 Human sec	956	31	57.4	713	6	ABU18932	Abu18932 Protein e
884	31	57.4	540	8	ADM64750	Adm64750 Disease t	957	31	57.4	721	6	ADU55497	Adu55497 Human pro
885	31	57.4	540	8	ADM81443	Adm81443 Tumour-as	958	31	57.4	742	9	ADM93593	Adm93593 Magnapor
886	31	57.4	541	2	AAW67820	Aaw67820 Human sec	959	31	57.4	743	8	ADU88179	Adu88179 Streptoco
887	31	57.4	543	6	ADB10596	Adb10596 Alloiococ	960	31	57.4	743	8	ADU79432	Adu79432 Streptoco
888	31	57.4	543	9	ABM96415	Abm96415 M. xantho	961	31	57.4	752	4	AAU67614	Aau67614 Propionib
889	31	57.4	547	2	AAW43013	Aaw43013 Truncated	962	31	57.4	752	6	ABM64133	Abm64133 Propionib
890	31	57.4	547	2	AAU51801	Aay51801 H. influe	963	31	57.4	754	8	ADN22721	Adn22721 Bacterial
891	31	57.4	549	7	ABO67262	Abob67262 Klebsiell	964	31	57.4	775	6	ABM67512	Abm67512 Photorhab
892	31	57.4	550	4	ABB66629	Abb66629 Drosophil	965	31	57.4	782	4	ABU46720	Abu46720 ACNV DNA
893	31	57.4	553	2	AAW11508	Aaw11508 Single ch	966	31	57.4	795	8	ADR08555	Adr08555 Human pro
894	31	57.4	553	2	AAW73223	Aaw73223 H22-anti-	967	31	57.4	796	7	ADC97438	Adc97438 E. faeciu
895	31	57.4	553	4	AAU61960	Abu61960 Bispecifi	968	31	57.4	800	9	AEA94231	Aea94231 L. rhanno
896	31	57.4	553	4	ABH85455	Abh85455 Bispecifi	969	31	57.4	801	8	ADJ38207	Adj38207 Plaetid d
897	31	57.4	553	8	ADS25287	Ads25287 Bacterial	970	31	57.4	801	8	ADJ38211	Adj38211 Plaetid d
898	31	57.4	555	7	ADH86021	Adh86021 Enterococ	971	31	57.4	801	8	ADJ38202	Adj38202 Arabidops
899	31	57.4	556	4	AAU80040	Aau80040 scFv-rear	972	31	57.4	801	8	ADJ38209	Adj38209 Plaetid d
900	31	57.4	556	4	AAU97935	Aau97935 scFv-rear	973	31	57.4	801	8	ADT55694	Adt55694 Plant pol

974 31 57.4 824 5 AAU81516 Human int  
975 31 57.4 848 6 ADA38354 Ada38354 Vibrio ha  
976 31 57.4 857 6 ABU48441 Abu48441 Protein e  
977 31 57.4 884 9 AEB44578 Aeb44578 Sleep dis  
978 31 57.4 888 8 ADX82497 Adx82497 Leptospir  
979 31 57.4 892 2 AAY37822 Aay37822 Chlamydia  
980 31 57.4 910 7 ADH86403 Adh86403 Enterococ  
981 31 57.4 913 4 ABB63115 Abb63115 Drosophil  
982 31 57.4 918 4 ABB59892 Abb59892 Drosophil  
983 31 57.4 928 6 ABU26723 Abu26723 Protein e  
984 31 57.4 942 6 ABU29797 Abu29797 Protein e  
985 31 57.4 948 3 AAB13643 Aab13643 C. tracho  
986 31 57.4 948 4 AAG83211 Aag83211 Protein e  
987 31 57.4 948 5 ABB94182 Abb94182 Chlamydia  
988 31 57.4 978 6 ABU26455 Abu26455 Protein e  
989 31 57.4 983 8 ADR09058 Adr09058 Human pro  
990 31 57.4 1014 3 AAB25488 Aab25488 Eucalyptu  
991 31 57.4 1024 5 ABB04863 Abb04863 LDL recep  
992 31 57.4 1045 2 ABP60399 Abp60399 Yeast HMG  
993 31 57.4 1045 2 AAR58611 Aar58611 Yeast HMG  
994 31 57.4 1045 8 ADM98779 Adm98779 HMG-CoA r  
995 31 57.4 1045 8 ADM98798 Adm98798 HMG-CoA r  
996 31 57.4 1045 8 ADM98844 Adm98844 HMG-CoA r  
997 31 57.4 1045 8 ADM98916 Adm98916 HMG-CoA r  
998 31 57.4 1045 8 ADM98889 Adm98889 HMG-CoA r  
999 31 57.4 1045 8 ADN19183 Adn19183 Bacterial  
1000 31 57.4 1074 2 AAY00188 Aay00188 Enterococ

# ALIGNMENTS

RESULT 1  
AAB81981  
ID AAB81981 standard; peptide; 10 AA.  
XX  
AC AAB81981;  
XX  
DT 03-JUL-2001 (first entry)  
XX  
DE Ganglioside GD3 specific antibody related peptide SEQ ID NO: 5.  
XX  
KW Ganglioside; GD3; complementarity determining region; CDR; antibody;  
KW cancer.  
XX  
OS Mus musculus.  
XX  
FN WO200123432-A1.  
XX  
PD 05-APR-2001.  
XX  
PF 29-SEP-2000; 2000WO-JP006774.  
XX  
PR 30-SEP-1999; 99JP-00278291.  
PR 06-APR-2000; 2000JP-00105088.  
XX  
PA (KYOW ) KYOWA HAKKO KOGYO KK.  
XX  
PI Hanai N, Shitara K, Nakamura K, Niwa R;  
XX  
DR WPI; 2001-266143/27.  
XX  
PT New human type complementation-determining region-transplanted antibody  
PT and derivatives against ganglioside GD3; useful in diagnosis and therapy  
PT of e.g. tumors, with low antigenicity, little side effects but potent  
PT activity in cancer.  
XX  
PS Claim 5; Page 141; 183pp; Japanese.  
XX  
CC The present invention describes a monoclonal antibody which can react  
CC specifically with ganglioside GD3. The antibody and its derivatives are  
CC useful in the diagnosis and therapy of tumors, particularly cancer  
CC diagnosis. The present sequence is a protein used in the exemplification

CC of the invention  
XX  
SQ Sequence 10 AA;  
Query Match 100.0%; Score 54; DB 4; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.0019;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 VKLGTYTFDS 10  
Db 1 VKLGTYTFDS 10  
RESULT 2  
AABU1006  
ID AABU1006 standard; peptide; 10 AA.  
XX  
AC AABU1006;  
XX  
DT 04-FEB-2003 (first entry)  
XX  
DE Modified ganglioside GD3 antibody associated peptide #3.  
XX  
KW Ganglioside GD3; anti-ganglioside GD3 antibody; tumour; melanoma.  
XX  
OS Mus musculus.  
XX  
FN WO200278739-A1.  
XX  
PD 10-OCT-2002.  
XX  
PF 29-MAR-2002; 2002WO-JP003170.  
XX  
PR 29-MAR-2001; 2001JP-00097483.  
XX  
PA (KYOW ) KYOWA HAKKO KOGYO KK.  
XX  
PI Shitara K, Niwa R, Kanazawa J, Asada M;  
XX  
DR WPI; 2003-067410/06.  
XX  
PT Drugs containing genetically-modified antibody against ganglioside GD3,  
PT its fragment, immunocompetent cell activators or/and antitumor agents in  
PT combination, applicable in treating malignant tumor like melanoma.  
XX  
PS Claim 6; Page 98; 121pp; Japanese.  
XX  
CC The invention describes drugs contain a genetically-modified antibody  
CC against ganglioside GD3 or its fragment and at least 1 of a substance  
CC capable of activating immunocompetent cells and a substance having an  
CC antitumor activity in combination. The drugs can be used to treat tumour  
CC like melanoma and can provide a treatment with enhanced therapeutic  
CC effect and little side-reactions, particularly to relieve problems of  
CC side-effects during the conventional single administration. This sequence  
CC represents a peptide associated with the anti- ganglioside GD3 antibody  
XX  
SQ Sequence 10 AA;  
Query Match 100.0%; Score 54; DB 6; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.0019;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 VKLGTYTFDS 10  
Db 1 VKLGTYTFDS 10  
RESULT 3  
ADZ57812  
ID ADZ57812 standard; peptide; 10 AA.  
XX  
AC ADZ57812;  
XX





PT New human type complementation-determining region-transplanted antibody  
PT and derivatives against ganglioside GD3, useful in diagnosis and therapy  
PT of e.g. tumors, with low antigenicity, little side effects but potent  
PT activity in cancer.

XX Claim 10; Page 173-174; 183pp; Japanese.

XX The present invention describes a monoclonal antibody which can react  
CC specifically with ganglioside GD3. The antibody and its derivatives are  
CC useful in the diagnosis and therapy of tumors, particularly cancer  
CC diagnosis. The present sequence is a protein used in the exemplification  
CC of the invention

XX Sequence 119 AA;

Query Match 100.0%; Score 54; DB 4; Length 119;  
Best Local Similarity 100.0%; Pred. No. 0.028;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VKLGTYTFDS 10  
| | | | | | | |  
Db 99 VKLGTYTFDS 108

#### RESULT 6

ABU11012  
ID ABU11012 standard; protein; 119 AA.

XX AC ABU11012;

DT 04-FEB-2003 (first entry)

DE Modified ganglioside GD3 antibody associated protein #5.

KW Ganglioside GD3; anti-ganglioside GD3 antibody; tumour; melanoma.

XX OS Mus musculus.

XX PN WO200278739-A1.

PD 10-OCT-2002.

XX PF 29-MAR-2002; 2002WO-JP003170.

XX PR 29-MAR-2001; 2001JP-00097483.

XX PA (KYOW ) KYOWA HAKKO KOGYO KK.

XX PI Shitara K, Niwa R, Kanazawa J, Asada M;

XX DR WPI; 2003-067410/06.

XX Drugs containing genetically-modified antibody against ganglioside GD3,  
PT its fragment, immunocompetent cell activators or/and antitumor agents in  
PT combination, applicable in treating malignant tumor like melanoma.

XX Claim 7; Page 112-113; 121pp; Japanese.

XX The invention describes drugs contain a genetically-modified antibody  
CC against ganglioside GD3 or its fragment and at least 1 of a substance  
CC capable of activating immunocompetent cells and a substance having an  
CC antitumor activity in combination. The drugs can be used to treat tumour  
CC like melanoma and can provide a treatment with enhanced therapeutic  
CC effect and little side-reactions, particularly to relieve problems of  
CC side-effects during the conventional single administration. This sequence  
CC represents a protein associated with the anti- ganglioside GD3 antibody

XX Sequence 119 AA;

Query Match 100.0%; Score 54; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 0.028;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VKLGTYTFDS 10  
| | | | | | | |  
Db 99 VKLGTYTFDS 108

#### RESULT 7

ABU11010  
ID ABU11010 standard; protein; 119 AA.

XX AC ABU11010;

DT 04-FEB-2003 (first entry)

DE Modified ganglioside GD3 antibody associated protein #3.

KW Ganglioside GD3; anti-ganglioside GD3 antibody; tumour; melanoma.

XX OS Synthetic.

XX PN WO200278739-A1.

XX PD 10-OCT-2002.

XX PF 29-MAR-2002; 2002WO-JP003170.

XX PR 29-MAR-2001; 2001JP-00097483.

XX PA (KYOW ) KYOWA HAKKO KOGYO KK.

XX PI Shitara K, Niwa R, Kanazawa J, Asada M;

XX DR WPI; 2003-067410/06.

XX Drugs containing genetically-modified antibody against ganglioside GD3,  
PT its fragment, immunocompetent cell activators or/and antitumor agents in  
PT combination, applicable in treating malignant tumor like melanoma.

XX Claim 8; Page 99; 121pp; Japanese.

XX The invention describes drugs contain a genetically-modified antibody  
CC against ganglioside GD3 or its fragment and at least 1 of a substance  
CC capable of activating immunocompetent cells and a substance having an  
CC antitumor activity in combination. The drugs can be used to treat tumour  
CC like melanoma and can provide a treatment with enhanced therapeutic  
CC effect and little side-reactions, particularly to relieve problems of  
CC side-effects during the conventional single administration. This sequence  
CC represents a protein associated with the anti- ganglioside GD3 antibody

XX Sequence 119 AA;

Query Match 100.0%; Score 54; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 0.028;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VKLGTYTFDS 10  
| | | | | | | |  
Db 99 VKLGTYTFDS 108

#### RESULT 8

ADZ57816  
ID ADZ57816 standard; protein; 119 AA.

XX AC ADZ57816;

DT 30-JUN-2005 (first entry)

DE Ganglioside GD3 binding antibody associated protein SEQ ID NO 20.

KW cytostatic; antibody engineering; cancer; neoplasm; ganglioside; GD3;  
XX pharmaceutical.

XX OS Mus musculus.



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XX PN WO2005035577-A1.
XX PD 21-APR-2005.
XX PF 08-OCT-2004; 2004WO-JP015314.
XX PR 08-OCT-2003; 2003JP-00350161.
XX PA (KYOW ) KYOWA HAKKO KOGYO KK.
XX PI Iida S, Satoh M, Urakubo M, Wakitani M, Uchida K, Niwa R;
XX PI Shitara K;
XX DR WPI; 2005-346195/35.
XX PT Antibody composition for treating ganglioside GD3 associated disease e.g.
XX PT cancer, comprises genetically modified antibody molecule, which
XX PT specifically binds to ganglioside GD3 and has N-glycoside-binding sugar
XX PT chain in its Fc domain.
XX PS Claim 13; SEQ ID NO 20; 124pp; Japanese.
XX CC The invention describes an antibody composition (I), comprising a
XX CC genetically modified antibody molecule which specifically binds to
XX CC ganglioside GD3 and has an N-glycoside-binding complex sugar chain in its
XX CC Fc domain, where the N-glycoside-binding complex sugar chain is a sugar
XX CC chain having no fucose attached to N-acetylglucosamine at the reducing
XX CC end of the sugar chain. Also described are: a transformant (II) capable
XX CC of producing (I), obtained by introducing DNA that encodes the antibody
XX CC molecule which specifically binds with ganglioside GD3, to a host cell;
XX CC producing (II), involving cultivating (I) in a culture medium, such that
XX CC C1 (sic) is produced and accumulated in the culture, extracting and
XX CC purifying C1 from the culture medium; a pharmaceutical (III) containing
XX CC GD3 associated disease, comprising C1 as an active ingredient. (I) is
XX CC useful for treating GD3 associated disease, which involves administering
XX CC (I), where the GD3 associated disease is cancer. (AI) is also useful for
XX CC treating GD3 associated disease. (II) is useful for producing (I). (I) is
XX CC useful for manufacturing a therapeutic agent for GD3 associated disease.
XX CC This sequence represents a ganglioside GD3 binding antibody associated
XX CC protein.
XX SQ Sequence 119 AA;

Query Match 100.0%; Score 54; DB 9; Length 119;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VKLGTYYPDS 10
Db |||||
99 VKLGTYYPDS 108

RESULT 9
ADZ57818
ID ADZ57818 standard; protein; 119 AA.
XX AC ADZ57818;
XX DT 30-JUN-2005 (first entry)
XX DE Ganglioside GD3 binding antibody associated protein SEQ ID NO 22.
XX KW Cytostatic; antibody engineering; cancer; neoplasm; ganglioside; GD3;
XX KW pharmaceutical.
XX OS Synthetic.
XX PN WO2005035577-A1.
XX PD 21-APR-2005.
XX PF 08-OCT-2004; 2004WO-JP015314.
XX PR 08-OCT-2003; 2003JP-00350161.
XX PA (KYOW ) KYOWA HAKKO KOGYO KK.

Query Match 100.0%; Score 54; DB 9; Length 119;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VKLGTYYPDS 10
Db |||||
99 VKLGTYYPDS 108

RESULT 10
ADZ57821
ID ADZ57821 standard; protein; 119 AA.
XX AC ADZ57821;
XX DT 30-JUN-2005 (first entry)
XX DE Ganglioside GD3 binding antibody associated protein SEQ ID NO 25.
XX KW Cytostatic; antibody engineering; cancer; neoplasm; ganglioside; GD3;
XX KW pharmaceutical.
XX OS Synthetic.
XX PN WO2005035577-A1.
XX PD 21-APR-2005.
XX PF 08-OCT-2004; 2004WO-JP015314.
XX PR 08-OCT-2003; 2003JP-00350161.
XX PA (KYOW ) KYOWA HAKKO KOGYO KK.

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XX Iida S, Satoh M, Urakubo M, Wakitani M, Uchida K, Niwa R;  
PI Shitara K;  
XX WPI; 2005-346195/35.  
DR  
XX Antibody composition for treating ganglioside GD3 associated disease e.g.  
PT cancer, comprises genetically modified antibody molecule, which  
PT specifically binds to ganglioside GD3 and has N-glycoside-binding sugar  
PT chain in its Fc domain.  
XX  
XX Claim 24; SEQ ID NO 25; 124pp; Japanese.  
PS  
XX The invention describes an antibody composition (I), comprising a  
CC genetically modified antibody molecule which specifically binds to  
CC ganglioside GD3 and has an N-glycoside-binding complex sugar chain in its  
CC Fc domain, where the N-glycoside-binding complex sugar chain is a sugar  
CC chain having no fucose attached to N-acetylglucosamine at the reducing  
CC end of the sugar chain. Also described are: a transformant (II) capable  
CC of producing (I), obtained by introducing DNA that encodes the antibody  
CC molecule which specifically binds with ganglioside GD3, to a host cell;  
CC producing (I), involving cultivating (I) in a culture medium, such that  
CC C1 (sic) is produced and accumulated in the culture, extracting and  
CC purifying C1 from the culture medium; a pharmaceutical (III) containing  
CC C1 as an active ingredient; and a therapeutic agent (A1) for ganglioside  
CC GD3 associated disease, comprising C1 as an active ingredient. (I) is  
CC useful for treating GD3 associated disease, which involves administering  
CC (II), where the GD3 associated disease is cancer. (A1) is also useful for  
CC treating GD3 associated disease. (II) is useful for producing (I). (I) is  
CC useful for manufacturing a therapeutic agent for GD3 associated disease.  
CC This sequence represents a ganglioside GD3 binding antibody associated  
CC protein.  
XX  
XX Sequence 119 AA;  
SQ  
Query Match 100.0%; Score 54; DB 9; Length 119;  
Best Local Similarity 100.0%; Pred. No. 0.028;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 VKLGTYYFDS 10  
DB 99 VKLGTYYFDS 108  
RESULT 11  
AAR33256  
ID AAR33256 standard; protein; 130 AA.  
XX  
XX AAR33256;  
XX  
XX 25-MAR-2003 (revised)  
DT 12-JUL-1993 (first entry)  
XX  
XX Rat immunoglobulin H chain variable region of pKM641HA3.  
XX  
XX Promoter; variable; region; rat; immunoglobulin; heavy; H; chain;  
KW humanised; chimeric; antibody; expression vector.  
XX  
XX Rattus rattus.  
OS  
XX  
XX Key Location/Qualifiers  
FH Peptide 1..10  
FT Protein /note= "Signal peptide"  
FT Protein 11..130  
FT Protein /note= "Mature protein"  
XX  
XX EP533199-A2.  
PN  
XX  
XX 24-MAR-1993.  
PD  
XX 18-SEP-1992; 92EP-00116026.  
PF  
XX 18-SEP-1991; 91JP-00238375.  
PR

XX (KYOW ) KYOWA HAKKO KOGYO CO LTD.  
XX  
XX Shitara K, Hanai N, Hasegawa M, Miyaji H, Kuwana Y;  
XX  
XX WPI; 1993-095510/12.  
DR N-PSDB; AAQ33257.  
XX  
XX Humanised chimeric antibody prodn. against ganglioside GD3 - for treating  
PT cancers, such as melanoma, neuroblastoma, etc.  
PT  
XX  
XX Claim 6; Page 29-30; 63pp; English.  
PS  
XX The sequences given in AAR33256-57 represent rat heavy and light chain  
CC variable regions respectively. The DNA sequences encoding these proteins  
CC were used in the construction of humanised chimeric antibody expression  
CC vectors. In these humanised antibodies none of the amino acids of the non  
CC -human animal AB variable region have been changed. (Updated on 25-MAR-  
CC 2003 to correct PN field.)  
XX  
XX Sequence 130 AA;  
SQ  
Query Match 100.0%; Score 54; DB 2; Length 130;  
Best Local Similarity 100.0%; Pred. No. 0.031;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 VKLGTYYFDS 10  
DB 109 VKLGTYYFDS 118  
RESULT 12  
AAR53341  
ID AAR53341 standard; protein; 130 AA.  
XX  
XX AAR53341;  
XX  
XX 18-NOV-1994 (first entry)  
DT  
XX  
XX KM641 L chain variable region.  
DE  
XX  
XX Monoclonal antibody; Ab; ganglioside GM2; chimera; chimeric antibody;  
KW expression vector; heavy; light; chain; hypervariable region; CDR;  
KW constant region; hybridoma; Ig; immunoglobulin; promoter; enhancer.  
XX  
XX Mus musculus.  
OS  
XX  
XX Key Location/Qualifiers  
FH Peptide 1..10  
FT Protein /label= sig\_peptide  
XX  
XX AU9346181-A.  
PN  
XX  
XX 17-MAR-1994.  
PD  
XX  
XX 07-SEP-1993; 93AU-00046181.  
PF  
XX  
XX 07-SEP-1992; 92JP-00238452.  
PR  
XX  
XX (KYOW ) KYOWA HAKKO KOGYO KK.  
PA  
XX  
XX Nakamura K, Koike M, Shitara K, Hanai N, Kuwana Y, Hasegawa M;  
PI  
XX  
XX WPI; 1994-126857/16.  
DR N-PSDB; AAQ45439.  
XX  
XX Humanised antibody specific for ganglioside GM2 - used for producing a  
PT cytotoxic effect on cancers such as melanoma, neuroblastoma and glioma.  
PT  
XX  
XX Example 2; Page 116-117; 191pp; English.  
PS  
XX  
XX Example 2 describes the construction of the vector pChi641HA1 for  
CC chimeric human antibody H chain expression. mRNA from mouse anti-GD3

```
CC monoclonal Ab KM641-producing cells was isolated and KM641 H and L chain
CC cDNAs isolated. The base sequences of the Ig variable regions in KM641 H
CC chain cDNA (pKM641HA3) and KM641 L chain cDNA (pKM641LA2) are given in
CC AAQ45438-39. A KM641-derived chimeric human Ab H chain expression vector
CC was constructed by joining the H chain variable region gene from
CC pKM641HA3 to a vector for chimeric human Ab H chain expression using the
CC synthetic DNAs given in AAQ63439 and AAQ63440
XX
XX Sequence 130 AA;
SQ
Query Match 100.0%; Score 54; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VKLGTYYPDS 10
DB 109 VKLGTYYPDS 118
RESULT 13
AAZY28369
ID AAY28369 standard; protein; 130 AA.
XX
XX AAY28369;
XX
XX 04-NOV-1999 (first entry)
DT
DE pKM641 HA3 immunoglobulin heavy chain.
XX
XX antibody; nucleotide; genomic; hypervariable region; chimeric;
KW light chain; amino acid.
XX
XX Mus sp.
XX
XX US5939532-A.
XX
XX 17-AUG-1999.
XX
XX 07-JUN-1995; 95US-00483528.
XX
XX 07-SEP-1993; 93US-00116778.
XX
XX (KYOW ) KYOWA HAKKO KOGYO KK.
XX
XX Nakamura K, Hanai N, Kuwana Y, Hasegawa M, Koike M, Shitara K;
XX
XX WPI: 1999-468416/39.
XX
XX N-PSDB; AAX99482.
XX
XX Chimeric human antibody expression vectors.
XX
XX Example 1; Col 99-101; 188pp; English.
XX
XX This immunoglobulin region was isolated from pKM641HA3. This sequence has
XX no methionine initiation codon and the leader sequence was partly
XX lacking. The chimeric human antibodies are useful in the treatment of
XX cancer, especially that which is of neural ectodermal origin. In contrast
XX to prior art constructs based on mouse monoclonal antibodies, the
XX chimeric human antibodies do not cause anti-mouse immunoglobulin
XX production. The chimeric human antibodies have a prolonged half-life and
XX a reduced frequency of adverse effects when compared to mouse monoclonal
XX antibodies
XX
XX Sequence 130 AA;
SQ
Query Match 100.0%; Score 54; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VKLGTYYPDS 10
DB 109 VKLGTYYPDS 118
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RESULT 14
AAB01627
ID AAB01627 standard; protein; 130 AA.
XX
XX AAB01627;
XX
XX 07-DEC-2000 (first entry)
DT
DE Murine immunoglobulin heavy chain variable region.
XX
XX Mouse; immunoglobulin; H chain; heavy chain; variable region; cancer;
KW humanised antibody.
XX
XX Mus sp.
XX
XX Key Location/Qualifiers
XX FT Peptide 1..10
XX FT /label= signal_peptide
XX FT Protein 11..130
XX FT /label= mature_immunoglobulin_heavy_chain_variable_region
XX
XX EP1013761-A2.
XX
XX 28-JUN-2000.
XX
XX 18-SEP-1992; 99EP-00124345.
XX
XX 18-SEP-1991; 91JP-00238375.
XX
XX 18-SEP-1992; 92EP-00116026.
XX
XX (KYOW ) KYOWA HAKKO KOGYO KK.
XX
XX Shitara K, Hanai N, Hasegawa M, Miyaji H, Kuwana Y;
XX
XX WPI: 2000-402204/35.
XX
XX N-PSDB; AAS1003.
XX
XX New humanized chimera antibody KM-871 useful for treating cancer,
XX comprises variable region of mouse monoclonal antibody, reactive with
XX ganglioside and human antibody constant region.
XX
XX Claim 14; Page 27-28; 65pp; English.
XX
XX The present sequence is a murine immunoglobulin heavy chain variable
XX region from plasmid KM-641. The coding sequence was used in the creation
XX of an expression vector, along with the sequence for a human antibody, to
XX produce humanised chimaeric antibodies, which can be used to treat
XX cancer. Humanised chimaeric antibodies are more effective than mouse
XX antibodies as they do not provoke a reaction in the human and side
XX effects, such as the formation of anti-mouse immunoglobulin antibody and
XX the rapid half-life of the immunoglobulins, do not occur
XX
XX Sequence 130 AA;
SQ
Query Match 100.0%; Score 54; DB 3; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VKLGTYYPDS 10
DB 109 VKLGTYYPDS 118
RESULT 15
AAB81977
ID AAB81977 standard; protein; 138 AA.
XX
XX AAB81977;
XX
XX 03-JUL-2001 (first entry)
DT
XX Ganglioside GD3 specific antibody related protein SEQ ID NO: 1.
DE
```

XX Ganglioside; GD3; complementarity determining region; CDR; antibody;  
 KW cancer.  
 XX  
 OS Mus musculus.  
 XX  
 PN WO200123432-A1.  
 XX  
 PD 05-APR-2001.  
 XX  
 PF 29-SEP-2000; 2000WO-JP006774.  
 XX  
 PR 30-SEP-1999; 99JP-00278291.  
 XX  
 PR 06-APR-2000; 2000JP-00105088.  
 XX  
 PA (KYOW ) KYOWA HAKKO KOGYO KK.  
 XX  
 PI Hanai N, Shitara K, Nakamura K, Niwa R;  
 XX  
 XX WPI; 2001-266143/27.  
 XX  
 XX New human type complementation-determining region-transplanted antibody  
 PT and derivatives against ganglioside GD3, useful in diagnosis and therapy  
 PT of e.g. tumors, with low antigenicity, little side effects but potent  
 PT activity in cancer.  
 XX  
 PS Example 1; Page 138-139; 183pp; Japanese.  
 XX  
 XX The present invention describes a monoclonal antibody which can react  
 CC specifically with ganglioside GD3. The antibody and its derivatives are  
 CC useful in the diagnosis and therapy of tumours, particularly cancer  
 CC diagnosis. The present sequence is a protein used in the exemplification  
 CC of the invention  
 XX  
 SQ Sequence 138 AA;  
 Query Match 100.0%; Score 54; DB 4; Length 138;  
 Best Local Similarity 100.0%; Pred. No. 0.033;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 VKLGTYYFDS 10  
 |||||  
 Db 118 VKLGTYYFDS 127  
 |||||  
 RESULT 16  
 ABU11002  
 ID ABU11002 standard; protein; 138 AA.  
 XX  
 AC ABU11002;  
 XX  
 DT 04-FEB-2003 (first entry)  
 XX  
 DE Modified ganglioside GD3 antibody associated protein #1.  
 XX  
 KW Ganglioside GD3; anti-ganglioside GD3 antibody; tumour; melanoma.  
 XX  
 OS Mus musculus.  
 XX  
 PN WO200278739-A1.  
 XX  
 PD 10-OCT-2002.  
 XX  
 PF 29-MAR-2002; 2002WO-JP003170.  
 XX  
 PR 29-MAR-2001; 2001JP-00097483.  
 XX  
 PA (KYOW ) KYOWA HAKKO KOGYO KK.  
 XX  
 PI Shitara K, Niwa R, Kanazawa J, Asada M;  
 XX  
 XX WPI; 2003-067410/06.  
 XX

PT Drugs containing genetically-modified antibody against ganglioside GD3,  
 PT its fragment, immunocompetent cell activators or/and antitumor agents in  
 PT combination, applicable in treating malignant tumor like melanoma.  
 XX  
 PS Example 3; Page 97; 121pp; Japanese.  
 XX  
 XX The invention describes drugs contain a genetically-modified antibody  
 CC against ganglioside GD3 or its fragment and at least 1 of a substance  
 CC capable of activating immunocompetent cells and a substance having an  
 CC antitumor activity in combination. The drugs can be used to treat tumour  
 CC like melanoma and can provide a treatment with enhanced therapeutic  
 CC effect and little side-reactions, particularly to relieve problems of  
 CC side-effects during the conventional single administration. This sequence  
 CC represents a protein associated with the anti- ganglioside GD3 antibody  
 XX  
 SQ Sequence 138 AA;  
 Query Match 100.0%; Score 54; DB 6; Length 138;  
 Best Local Similarity 100.0%; Pred. No. 0.033;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 VKLGTYYFDS 10  
 |||||  
 Db 118 VKLGTYYFDS 127  
 |||||  
 RESULT 17  
 AAB81987  
 ID AAB81987 standard; protein; 582 AA.  
 XX  
 AC AAB81987;  
 XX  
 DT 03-JUL-2001 (first entry)  
 XX  
 DE Ganglioside GD3 specific antibody related protein SEQ ID NO: 53.  
 XX  
 KW Ganglioside; GD3; complementarity determining region; CDR; antibody;  
 KW cancer.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200123432-A1.  
 XX  
 PD 05-APR-2001.  
 XX  
 PF 29-SEP-2000; 2000WO-JP006774.  
 XX  
 PR 30-SEP-1999; 99JP-00278291.  
 XX  
 PR 06-APR-2000; 2000JP-00105088.  
 XX  
 PA (KYOW ) KYOWA HAKKO KOGYO KK.  
 XX  
 PI Hanai N, Shitara K, Nakamura K, Niwa R;  
 XX  
 XX WPI; 2001-266143/27.  
 XX  
 XX New human type complementation-determining region-transplanted antibody  
 PT and derivatives against ganglioside GD3, useful in diagnosis and therapy  
 PT of e.g. tumors, with low antigenicity, little side effects but potent  
 PT activity in cancer.  
 XX  
 PS Claim 41; Page 168-172; 183pp; Japanese.  
 XX  
 XX The present invention describes a monoclonal antibody which can react  
 CC specifically with ganglioside GD3. The antibody and its derivatives are  
 CC useful in the diagnosis and therapy of tumours, particularly cancer  
 CC diagnosis. The present sequence is a protein used in the exemplification  
 CC of the invention  
 XX  
 SQ Sequence 582 AA;  
 Query Match 100.0%; Score 54; DB 4; Length 582;  
 Best Local Similarity 100.0%; Pred. No. 0.16;

```

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VKLGTYYFDS 10
Db 99 VKLGTYYFDS 108

RESULT 18
AAB81991
ID AAB81991 standard; protein; 582 AA.
XX AC
XX AC AAB81991;
XX 03-JUL-2001 (first entry)
XX DE Ganglioside GD3 specific antibody related protein SEQ ID NO: 57.
XX KW Ganglioside; GD3; complementarity determining region; CDR; antibody;
XX KW cancer.
XX OS Synthetic.
XX PN WO200123432-A1.
XX PD 05-APR-2001.
XX PF 29-SEP-2000; 2000WO-JP006774.
XX PR 30-SEP-1999; 99JP-00278291.
XX PR 06-APR-2000; 2000JP-00105088.
XX PA (KYOW ) KYOWA HAKKO KOGYO KK.
XX PI Hanai N, Shitara K, Nakamura K, Niwa R;
XX WPI; 2001-266143/27.
XX DR
XX PT New human type complementation-determining region-transplanted antibody
XX PT and derivatives against ganglioside GD3, useful in diagnosis and therapy
XX PT of e.g. tumors, with low antigenicity, little side effects but potent
XX PT activity in cancer.
XX PS Claim 39; Page 175-179; 183pp; Japanese.
XX CC The present invention describes a monoclonal antibody which can react
XX CC specifically with ganglioside GD3. The antibody and its derivatives are
XX CC useful in the diagnosis and therapy of tumors, particularly cancer
XX CC diagnosis. The present sequence is a protein used in the exemplification
XX CC of the invention
XX SQ Sequence 582 AA;

Query Match 100.0%; Score 54; DB 4; Length 582;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VKLGTYYFDS 10
Db 99 VKLGTYYFDS 108

RESULT 19
AAR34284
ID AAR34284 standard; protein; 120 AA.
XX AC
XX AC AAR34284;
XX 25-MAR-2003 (revised)
XX DT 26-JUL-1993 (first entry)
XX DE Human TNF binding antibody heavy chain VHLM2.
XX KW Monoclonal antibody; anti-globulin response; VH gene; chimeric;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VKLGTYYFDS 10
Db 99 VKLGTYYFDS 108

Query Match 100.0%; Score 54; DB 4; Length 582;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VKLGTYYFDS 10
Db 99 VKLGTYYFDS 108

Query Match 77.8%; Score 42; DB 2; Length 120;
Best Local Similarity 87.5%; Pred. No. 5.6;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 LGTTYFDS 10
Db 101 LGTTYFDS 108

RESULT 20
ADU25526
ID ADU25526 standard; protein; 368 AA.
XX AC
XX AC ADU25526;
XX 27-JAN-2005 (first entry)
XX DT
XX
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KW mouse-human antibodies; antibody; prevention; tumour necrosis factor.
XX OS Homo sapiens.
XX PH Key
XX FT Region
XX FT Location/Qualifiers
XX FT 1..30
XX FT /note= "Framework region FR1"
XX FT 31..35
XX FT /note= "Complementarity determining region CDR1"
XX FT 36..49
XX FT /note= "Framework region FR2"
XX FT 50..66
XX FT /note= "Complementarity determining region CDR2"
XX FT 67..98
XX FT /note= "Framework region FR3"
XX FT 99..116
XX FT /note= "Complementarity determining region CDR3"
XX FT 117..120
XX FT /note= "Framework region FR4"
XX PN WO9306213-A1.
XX PD 01-APR-1993.
XX PF 23-SEP-1992; 92WO-GB001755.
XX PR 23-SEP-1991; 91GB-00020252.
XX PR 25-SEP-1991; 91GB-00020377.
XX PR 24-MAR-1992; 92GB-00006318.
XX PR 24-MAR-1992; 92GB-00006372.
XX PR 15-MAY-1992; 92WO-GB000883.
XX (MEDI-) MEDICAL RES COUNCIL.
XX PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX PI Hoogenboom HRJM, Baier M, Jespers LSAT, Winter GP;
XX WPI; 1993-117534/14.
XX PT Producing human antibody polypeptide dimer specific for antigen -
XX PT comprises use of chain shuffling using phage expression, useful for
XX PT reducing anti globulin responses in humans for increased human
XX PT characteristics.
XX PS Example; Fig 6; 109pp; English.
XX CC The sequence is that of the heavy chain VHLM2 which shows minimal
XX CC differences compared with the germline DP-46, which is of the VH3 family.
XX CC It may be used as part of a method of producing chimeric mouse-human
XX CC antibodies or fragments which have the same binding specificity as a
XX CC parent Ab but have increased human characteristics, preventing anti-
XX CC globulin response in humans. (Updated on 25-MAR-2003 to correct PN
XX CC field.)
XX SQ Sequence 120 AA;

```

DE L. acidophilus cell surface protein homologue #51.  
 KW Cell wall; cell surface; secreted protein; gastrointestinal disorder;  
 KW inflammatory bowel disease; Crohn's disease; ulcerative colitis;  
 KW irritable bowel syndrome; diarrhoea; antibiotic-associated diarrhoea;  
 KW constipation; small bowel bacterial overgrowth; antiinflammatory.  
 XX  
 OS Lactobacillus acidophilus.  
 XX  
 XX WO2004096992-A2.  
 XX  
 XX 11-NOV-2004.  
 PD  
 XX 23-APR-2004; 2004WO-US012717.  
 XX  
 XX 25-APR-2003; 2003US-0465621P.  
 PR  
 XX (UYNC-) UNIV NORTH CAROLINA STATE.  
 PA  
 XX Klaenhammer TR, Russell WM, Alterman E, Cano RJ, Hamrick A;  
 PI  
 XX WPI; 2004-804747/79.  
 DR  
 XX N-PSDB; ADU25525.  
 DR  
 XX  
 PT New cell wall, cell surface and secreted protein nucleic acid molecules  
 PT and polypeptides, useful for treating gastrointestinal disorders, e.g.  
 PT inflammatory bowel disease, Crohn's disease, ulcerative colitis, or  
 PT diarrhea.  
 PT  
 PS Claim 6; SEQ ID NO 102; 722pp; English.  
 XX  
 CC The invention relates to Lactobacillus acidophilus cell wall, cell  
 CC surface and secreted protein nucleic acid molecules comprising any of the  
 CC 154 nucleotide sequences, fully defined in the specification, and the  
 CC polypeptide sequences encoded by them. Also disclosed are a vector  
 CC comprising the nucleic acid molecule, a host cell that contains the  
 CC vector, an isolated polypeptide as encoded by the nucleic acid molecule,  
 CC an antibody that selectively binds to the polypeptide, and a  
 CC Lactobacillus acidophilus bacterial strain with a modified ability for  
 CC modulating the immune system of a host, as compared to a wild-type  
 CC Lactobacillus acidophilus, where the modified ability is due to  
 CC expression of at least one of the polypeptides cited above. The nucleic  
 CC acid molecules and polypeptides are useful for treating gastrointestinal  
 CC disorders, e.g. inflammatory bowel disease, Crohn's disease, ulcerative  
 CC colitis, irritable bowel syndrome, diarrhoea, antibiotic-associated  
 CC diarrhoea, constipation, and small bowel bacterial overgrowth. This  
 CC sequence represents a L. acidophilus polypeptide sequence of the  
 CC invention.  
 XX  
 SQ Sequence 368 AA;  
 Query Match 75.9%; Score 41; DB 8; Length 368;  
 Best Local Similarity 100.0%; Pred. No. 30;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 GTTYFDS 10  
 DB 229 GTTYFDS 235  
 |||||  
 RESULT 21  
 ID ADT59951  
 ID ADT59951 standard; protein; 446 AA.  
 XX  
 AC ADT59951;  
 XX  
 DT 13-JAN-2005 (first entry)  
 XX  
 DE Plant polypeptide, SEQ ID 10028.  
 XX  
 KW Plant; transgenic; cold tolerance; growth rate; drought tolerance;  
 KW disease resistance; galactomannan production; plant growth regulator;  
 KW heat tolerance; herbicide tolerance; lignin production;

KW extreme osmotic condition tolerance; pathogens resistance;  
 KW pest resistance; yield improvement; seed oil yield; seed protein yield.  
 XX Viridiplantae.  
 OS  
 XX US2004216190-A1.  
 PN  
 XX 28-OCT-2004.  
 PD  
 XX 18-DEC-2003; 2003US-00739930.  
 PF  
 XX 28-APR-2003; 2003US-00424599.  
 PR  
 XX 28-APR-2003; 2003US-00425115.  
 PR  
 XX (KOVA/) KOVALIC D K.  
 PA  
 XX Kovalic DK;  
 PI  
 XX WPI; 2004-757369/74.  
 DR  
 XX New recombinant DNA constructs useful in the field of biochemistry and  
 PT genetics, and in particular for producing transgenic plants with improved  
 PT biological characteristics.  
 PT  
 PS Claim 2; SEQ ID NO 10028; 14pp; English.  
 XX  
 CC The invention relates a recombinant DNA construct comprising a  
 CC polynucleotide having any of 5544 nucleotide sequences (CDNAs SEQ ID NO:  
 CC 1-5544) and encoding a polypeptide with any of 5544 amino acid sequences  
 CC (SEQ ID NO: 5545-11088). The CDNAs and proteins are from corn, soybean,  
 CC Arabidopsis, wheat and rape but the specification does not indicate which  
 CC sequences is derived from which organism. Also included is a method of  
 CC producing a plant having an improved property, comprising transforming a  
 CC plant with a recombinant DNA construct comprising a promoter region  
 CC functional in a plant cell operably joined to a polynucleotide encoding a  
 CC polypeptide associated with the property, and growing the transformed  
 CC plant. The property is selected from improving plant cold tolerance, for  
 CC manipulating growth rate in plant cells by modification of the cell cycle  
 CC pathway, for improving plant drought tolerance, for providing increased  
 CC resistance to plant disease, for galactomannan production, for production  
 CC of plant growth regulators, for improving plant heat tolerance, for  
 CC improving plant tolerance to herbicides, for increasing the rate of  
 CC homologous recombination in plants, for lignin production, for improving  
 CC plant tolerance to extreme osmotic conditions, for improving plant  
 CC tolerance to pathogens or pests, for yield improvement by modification of  
 CC photosynthesis, for modifying seed oil yield and/or content, for  
 CC modifying seed protein yield and/or content, for yield improvement by  
 CC modification of carbohydrate, nitrogen or phosphorus use and/or uptake  
 CC and for yield improvement by providing improved plant growth and  
 CC development under at least one stress condition. The polynucleotide may  
 CC also encode a plant transcription factor. The methods and compositions of  
 CC the present invention are useful in the field of biochemistry and  
 CC genetics, in particular for producing transgenic plants with improved  
 CC biological characteristics such as increased yield, improved nitrogen  
 CC flow, increasing plant tolerance to cold or heat, improving plant  
 CC tolerance to extreme osmotic and drought conditions, and improving plant  
 CC tolerance to plant pests or pathogens. They can also be used in physical  
 CC arrays of molecules, plant breeding markers, computer-based storage and  
 CC analysis systems. The present sequence is one of the 5544 plant protein  
 CC sequences of the invention. Note: The sequence data for this patent did  
 CC not form part of the printed specification, but was obtained in  
 CC electronic format directly from USPTO at  
 CC seqdata.uspto.gov/sequence.html?DocID=20040216190.  
 CC  
 XX  
 SQ Sequence 446 AA;  
 Query Match 74.1%; Score 40; DB 8; Length 446;  
 Best Local Similarity 80.0%; Pred. No. 57;  
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 VKLGTYYFDS 10  
 DB 195 VILGQYYFDS 204  
 |||||

RESULT 22  
ADQ26346  
ID ADQ26346 standard; protein; 4130 AA.  
XX AC ADQ26346;  
XX DT 23-SEP-2004 (first entry)  
XX DE Chromobacterium violaceum CV44287 involved in haemolysin synthesis.  
XX KW Haemolysin; anticoagulant; CV44287.  
XX OS Chromobacterium violaceum.  
XX PN WO2004056960-A2.  
XX PD 08-JUL-2004.  
XX PF 16-DEC-2003; 2003WO-BR000207.  
XX PR 19-DEC-2002; 2002BR-00007239.  
XX PA (CNPQ-) CNPQ CONSELHO NACIONAL DESENVOLVIMENTO.  
XX PI De Vasconcelos ATR, Simpson AJG, Abreu HNS, De Almeida DF;  
PI Almeida FC, De Almeida R, Antonio RV, Araripe JR, De Araujo MFF;  
PI Bogo RM, Bonatto SL, Brígido MDM, De Brito CPA, Brochi M, Burity HA;  
PI Camargo A, Carraro D, Carvalho CMB, Cascado JCDM, Cavada BS;  
PI Chueire LMDO, Da Cunha MH, Fantinatti F, Farias IP, Felipe MSS;  
PI Ferrari LP, Ferro JA, Franco GR, De Freitas NSA, Furlan LR;  
PI Gattapaglia D, Gazzinelli RT, Gomes JAA, Gonçalves PR, Grangeiro TB;  
PI Grisard EC, Guimarães CT, Hanna ES, Jardim SN, Laurino JP, Lima LFA;  
PI De Lyra MDCPP, Madeira HMF, Maranhão AQ, Manfio GP, Martins WS;  
PI De Medeiros SRB, Meissner RDV, Moreira MA, Do Nascimento FF;  
PI Nicolas MF, De Oliveira JG, Oliveira SC, Paixão RFC, Parra J;  
PI Pasa TBC, Pedrosa FDO, Pena SDJP, Pereira JO, Pereira M, Pinto LSRC;  
PI Pinto LDS, Porto JIR, Potrich DP, Ramalho CE, Reis AMM;  
PI Rondinelli E, Sampaio AH, Dos Santos FR, Schneider MPC, Silva DW;  
PI Silva R, Soares CMA, De Souza EM, De Souza KRL, Souza RC;  
PI Steindel M, Teixeira SMR, Trevilato PB, Urmenyi TP, Wassén R;  
PI Azevedo V, Bartoletti LA, Batista JDS, Filho AS, Zaha A;  
PI Andrade EDM, Gonzaga L, Dos Santos EBP, Soares RDBA, Bataus LAM;  
PI Cardoso DDFDP, Parente JA, Rigo LU, Steffens MBR;  
XX WPI; 2004-500292/47.  
XX New gene-coding polynucleotides of the chromosome of Chromobacterium  
PT violaceum, useful for therapeutic, diagnostic or pharmacological  
PT applications, in control processes for environmental parameters or in  
PT enzyme synthesis.  
XX Claim 4; SEQ ID NO 19; 31pp; English.  
XX The present sequence is that of the protein encoded by the CV44287 gene  
CC of Chromobacterium violaceum strain ATCC 12472 (NCIB 9131, NCTC 9757, JCM  
CC 1249, DSM 30191, IAM 12470, LMG 1267). The invention relates to 29  
CC polynucleotides that have been identified by sequencing the genome of  
CC this strain, to the polypeptides ADQ26328-ADQ26356 encoded by these  
CC polynucleotides, and to the uses of the polynucleotides and polypeptides  
CC for therapeutic, diagnostic, medicinal, pharmacological and  
CC pharmacognostic applications, in control processes for environmental  
CC parameters, and in enzyme synthetic processes. The CV44287 gene is  
CC involved in haemolytic activity. The gene and the encoded polypeptide can  
CC be used in the production of haemolysins for pharmaceutical use as  
CC anticoagulants.  
XX Sequence 4130 AA;  
SQ Query Match 74.1%; Score 40; DB 8; Length 4130;  
Best Local Similarity 70.0%; Pred. No. 6.4e+02;  
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 VKLGTYYFDS 10  
|||::|||  
Db 2460 VKYGTFFDS 2469  
RESULT 23  
ADX77421  
ID ADX77421 standard; protein; 427 AA.  
XX AC ADX77421;  
XX DT 21-APR-2005 (first entry)  
XX DE Plant full length insert polypeptide seqid 46787.  
XX KW plant protectant; plant growth regulant; gene therapy; plant;  
KW recombinant DNA construct; physical array; plant breeding marker;  
KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;  
KW extreme osmotic condition; pathogen tolerance; pest tolerance;  
KW growth rate; cell cycle pathway; disease resistance;  
KW galactomannan production; lignin production; plant growth regulator;  
KW yield; plant growth; plant development; seed oil; protein yield;  
KW protein content.  
XX OS Unidentified.  
XX PN US2004034888-A1.  
XX PD 19-FEB-2004.  
XX PF 28-APR-2003; 2003US-00425114.  
XX PR 06-MAY-1999; 99US-00304517.  
XX PR 05-NOV-2001; 2001US-00985678.  
XX PA (LIUJ/) LIU J.  
PA (ZHOU/) ZHOU Y.  
PA (KOVA/) KOVALIC D K.  
PA (SCRE/) SCREEN S E.  
PA (TAB/) TABASKA J E.  
PA (CAOY/) CAO Y.  
XX PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;  
XX WPI; 2004-180133/17.  
XX New recombinant DNA construct, useful for improving plant tolerance to  
PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or  
PT pests, for conferring increased resistance to plant disease, or for  
PT improving yield.  
XX Claim 1; SEQ ID NO 46787; 15pp; English.  
XX The invention describes a recombinant DNA construct comprising a  
CC polynucleotide consisting of a sequence encoding an amino acid sequence  
CC available in electronic form from the US Patent Office at  
CC ftp.segdata.uspto.gov/sequence.html?docID:2004034888. The polynucleotide  
CC of the invention are also useful in physical arrays of molecules and as  
CC plant breeding markers. The recombinant DNA construct is useful for  
CC improving plant tolerance to cold, heat, drought, herbicides, extreme  
CC osmotic conditions, pathogens or pests, for manipulating growth rate in  
CC plant cells by modification of the cell cycle pathway, for conferring  
CC increased resistance to plant disease, for producing galactomannan,  
CC lignin or plant growth regulators, for increasing the rate of homologous  
CC recombination in plants, for improving yield by modification of  
CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake  
CC or by providing improved plant growth and development under at least one  
CC stress condition or for modifying seed oil or protein yield and/or  
CC content. This is the amino acid sequence of a plant full length insert  
CC polypeptide that can be used in the recombinant DNA construct of the  
CC invention.

SQ Sequence 427 AA;

Query Match 72.2%; Score 39; DB 8; Length 427;  
Best Local Similarity 87.5%; Pred. No. 84;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 LGTYFFDS 10  
|||  
Db 150 LGQYFFDS 157

RESULT 24

ABM88891  
ID ABM88891 standard; protein; 434 AA.

XX AC ABM88891;

XX DT 02-JUN-2005 (first entry)

XX DE Rice abiotic stress responsive polypeptide SEQ ID NO:7137.

XX KW abiotic stress tolerance; transgenic plant; plant; cereal; agriculture.

XX OS Oryza sativa.

XX PN WO2003008540-A2.

XX PD 30-JAN-2003.

XX PF 21-JUN-2002; 2002WO-US019668.

XX PR 22-JUN-2001; 2001US-0300112P.

XX PR 24-AUG-2001; 2001US-0314662P.

XX PR 26-SEP-2001; 2001US-0325277P.

XX PR 21-NOV-2001; 2001US-0332132P.

XX PA (SYGN ) SYNGENTA PARTICIPATIONS AG.

XX PI Krepis J, Briggs SP, Cooper B, Glazebrook J, Goff SA, Katagiri F;  
XX PI Moughamer T, Provart N, Ricke D, Zhu T;

XX DR WPI; 2003-248011/24.

XX PT New stress-responsive nucleic acid, useful for altering the  
XX PT responsiveness of a plant, e.g. cereal, to an abiotic stress such as cold  
XX PT stress, salt stress or osmotic stress.

XX PS Claim 1; SEQ ID NO 7137; 89pp; English.

XX CC The invention relates to novel abiotic stress responsive polynucleotides  
XX CC and polypeptides. Also disclosed are vectors, expression cassettes, host  
XX CC cells, and plants containing such polynucleotides. Also disclosed are  
XX CC methods for using the polynucleotides and polypeptides to alter the  
XX CC responsiveness of a plant to abiotic stress. The invention is useful in  
XX CC agriculture. The nucleic acid is useful for determining whether a test  
XX CC plant has been exposed to an abiotic stress condition. It is also useful  
XX CC for selecting an agent that alters abiotic stress regulated  
XX CC polynucleotide expression in a plant cell, and to identify a homolog or  
XX CC ortholog to an abiotic stress responsive polynucleotide. The nucleic acid  
XX CC molecule and the polypeptide encoded by it are useful in altering the  
XX CC responsiveness of a plant to an abiotic stress, such as cold stress, salt  
XX CC stress, osmotic stress or any of their combinations. The present sequence  
XX CC is used in the exemplification of the invention

SQ Sequence 434 AA;

Query Match 72.2%; Score 39; DB 7; Length 434;  
Best Local Similarity 87.5%; Pred. No. 85;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 LGTYFFDS 10  
|||  
Db 145 LGQYFFDS 152

RESULT 25

AAU74519  
ID AAU74519 standard; protein; 1781 AA.

XX AC AAU74519;

XX DT 09-APR-2002 (first entry)

XX DE Lactobacillus reuteri glucosyltransferase A (gtfa) polypeptide.

XX KW Glucosyltransferase A; gtfa; glucan; anhydroglucose; sucrose;  
XX KW oligosaccharide; polysaccharide; sucrose; fructan; symbiotic; probiotic.

XX OS Lactobacillus reuteri.

XX PN WO200190372-A1.

XX PD 29-NOV-2001.

XX PF 23-MAY-2001; 2001WO-NL000393.

XX PR 25-MAY-2000; 2000EP-00201871.

XX PA (NEDE ) NEDERLANDSE ORG TOEGEPAST.

XX PI Van Geel Schutten GH, Dijkhuizen L, Rahaoui H, Leer RJ;

XX DR WPI; 2002-147583/19.

XX DR N-ESDB; AAS20540.

XX PT Protein with glucosyltransferase activity derived from Lactobacillus  
XX PT Reuteri.

XX PS Claim 3; Page 48-55; 59pp; English.

XX CC The invention relates to a Lactobacillus reuteri glucosyltransferase A  
XX CC (gtfa) polypeptide. This polypeptide produces a glucan with a unique  
XX CC structure having 4-linked, 6-linked and 4,6-linked anhydroglucose units  
XX CC or, in the presence of suitable acceptors, oligosaccharides. The protein  
XX CC can be used to produce an oligosaccharide or polysaccharide of interest,  
XX CC for example, to produce a glucan with sucrose as a substrate and  
XX CC optionally a fructan as a probiotic or symbiotic. This sequence  
XX CC represents L. reuteri glucosyltransferase A

SQ Sequence 1781 AA;

Query Match 70.4%; Score 38; DB 5; Length 1781;  
Best Local Similarity 85.7%; Pred. No. 6.2e+02;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GTTYFFDS 10

|||||  
Db 1724 GTTYFFDN 1730

RESULT 26

ADF06503

ID ADF06503 standard; protein; 94 AA.

XX AC ADF06503;

XX DT 12-FEB-2004 (first entry)

XX DE Bacterial polypeptide #2616.

XX KW Proteus mirabilis infection; bacterial infection; antibacterial;  
XX KW immunostimulant.

XX OS Proteus mirabilis.

XX PN US6605709-B1.



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XX PD 12-AUG-2003.
XX PF 05-APR-2000; 2000US-00543681.
XX PR 09-APR-1999; 99US-0128706P.
XX (GENO-) GENOME THERAPEUTICS CORP.
XX PA Breton GL;
XX PI
XX WPI; 2003-895291/82.
XX DR N-PSDB; ADF02331.
XX New Proteus mirabilis polypeptides and polynucleotides, useful as
PT reagents for diagnosis of bacterial disease, as components of
PT antibacterial vaccines, as targets for antibacterial drugs, or as
PT biocontrol agents for plants.
XX Disclousure; SEQ ID NO 6788; 870pp; English.
XX The invention relates to new Proteus mirabilis polypeptides and
CC polynucleotides. The invention also relates to antibodies against the
CC polypeptides, methods for producing the polypeptides, a method of
CC generating vaccines for immunising an individual against P. mirabilis, a
CC method for evaluating a compound for the ability to bind a P. mirabilis
CC polypeptide and a method for screening test compounds for anti-bacterial
CC activity. The polypeptides and polynucleotides are useful as molecular
CC targets for diagnosing, preventing and treating pathological conditions
CC resulting from bacterial infection, as reagents for diagnosis of
CC bacterial diseases, as components of antibacterial vaccines, as targets
CC for antibacterial drugs or as bio-control agents for plants. This
CC sequence represents a Proteus mirabilis polypeptide of the invention.
XX Sequence 94 AA;
SQ
Query Match 68.5%; Score 37; DB 7; Length 94;
Best Local Similarity 75.0%; Pred. No. 39;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 3 LGTYFYFDS 10
DB 21 LGTYFYNS 28
RESULT 27
ADC96455
ID ADC96455 standard; protein; 137 AA.
XX ADC96455;
XX 01-JAN-2004 (first entry)
XX E. faecium protein sequence SEQ ID 6082.
XX Vaccine; urinary tract infection; bacteraemia; endocarditis; wound;
KW abdominal-pelvic infection.
XX Enterococcus faecium.
OS US6583275-B1.
XX US6583275-B1.
XX 24-JUN-2003.
XX 30-JUN-1998; 98US-00107532.
XX 02-JUL-1997; 97US-0051571P.
XX 14-MAY-1998; 98US-0085598P.
XX (GENO-) GENOME THERAPEUTICS CORP.
XX Doucette-Stamm LA, Bush D;
XX
WPI; 2003-799836/75.
DR N-PSDB; ADC92801.
XX New isolated nucleic acid derived from Enterococcus faecium encoding an
PT Enterococcus faecium polypeptide useful for detection, prevention and
PT treatment of a pathological condition resulting from a bacterial
PT infection.
XX Example 1; SEQ ID NO 6082; 243pp; English.
XX The invention relates to an isolated nucleic acid derived from
CC Enterococcus faecium encoding an Enterococcus faecium polypeptide having
CC one of 10 fully defined sequences given in the (or comprising 40
CC sequential nucleotides chosen from any of the nucleic acids, its
CC complement or sequences hybridising to it). Also included are a
CC recombinant vector comprising the nucleic acid operably linked to
CC transcription regulatory element, a cell comprising the vector and a
CC single-stranded probe comprising the nucleic acid. The nucleic acids are
CC chosen from 3654 disclosed sequences encoding 3654 disclosed proteins.
CC The nucleic acids is useful for diagnosing pathological conditions
CC resulting from E. faecium bacterial infection (e.g. urinary tract
CC infection, bacteraemia, endocarditis, wounds and abdominal-pelvic
CC infection) and for screening drugs such as agonists and antagonists. The
CC nucleic acid is useful for recombinant production of Candida albicans -
CC derived peptides or antisense polypeptides. Pharmaceutical compositions
CC and vaccines containing the nucleic acid are useful for preventing or
CC treating Enterococcus faecium infections. The present sequence represents
CC one if the disclosed E. faecium proteins.
XX Sequence 137 AA;
SQ
Query Match 68.5%; Score 37; DB 7; Length 137;
Best Local Similarity 75.0%; Pred. No. 58;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 2 KLGTYFYD 9
DB 124 KLGTYHYD 131
RESULT 28
ABO00524
ID ABO00524 standard; protein; 179 AA.
XX ABO00524;
XX 06-AUG-2003 (first entry)
XX Novel human polypeptide #111.
XX Human; angiogenesis; cytokine; cell proliferation; pluripotent;
KW cell differentiation; totipotent; stem cell; transplantation; bio-sensor;
KW neuroepithelial cell; autoimmune disease; neural cell; genetic disorder;
KW nerve; brain tissue; central nervous system disease;
KW peripheral nervous system disease; neuropathy; haematopoiesis; bone;
KW myeloid disorder; lymphoid cell disorder; platelet disorder; tendon;
KW regeneration; cartilage; tendon; ligament; nerve tissue growth;
KW tissue repair; wound healing; burn; ulcer; osteoporosis; cancer;
KW osteoarthritis; bone degenerative disorder; periodontal disease;
KW gut protection; liver fibrosis; liver fibrosis; reperfusion injury;
KW immune deficiency; infection; autoimmune disorder; allergic reaction;
KW thrombolytic; thrombosis; coagulation disorder; hereditary disorder;
KW biohythm; circadian cycle; fertility; metabolism; catabolism; anabolism;
KW neurotropic; neuroprotective; antiparkinsonian; anticonvulsant;
KW haemostatic; vulnery; antilucer; osteopathic; antiarthritic;
KW vasotropic; immunostimulant; antibacterial; fungicide; immunosuppressive;
KW antirheumatic; antidiabetic; antiasthmatic; cytostatic; virucide.
XX Homo sapiens.
XX WO2003023013-A2.
XX 20-MAR-2003.

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XX PF 13-SEP-2002; 2002WO-US029001.  
 XX PR 13-SEP-2001; 2001US-0322511P.  
 XX PR 12-SEP-2002; 2002US-00243552.  
 XX (HYSE-) HYSEQ INC.  
 XX PA Tang YT, Yang Y, Wang Z, Weng G, Ma Y;  
 XX PI WPI; 2003-313249/30.  
 XX DR N-PSDB; ACD05601.  
 XX PR Novel nucleic acids and polypeptides for diagnosis, treatment of central  
 XX PT and peripheral nervous system diseases and neuropathies, such as  
 XX PT Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic  
 XX PT lateral sclerosis.  
 XX PS Claim 20; SEQ ID NO 447; 300pp; English.  
 XX CC The present invention relates to the isolation of novel human  
 XX CC polynucleotide sequences and their encoding polypeptides. The novel  
 XX CC polypeptides exhibit activities relating to angiogenesis, cytokine, cell  
 XX CC proliferation, cell differentiation, antiinflammatory, and stem cell  
 XX CC growth factor activities. The polypeptides are involved in the  
 XX CC proliferation, differentiation and survival of pluripotent and totipotent  
 XX CC stem cells, and are useful for re-engineering damaged or diseased  
 XX CC tissues, transplantation, manufacture of bio-pharmaceuticals and  
 XX CC development of bio-sensors. The polypeptides can be used to manipulate  
 XX CC stem cells in culture to give rise to neuroepithelial cells that can be  
 XX CC used to augment or replace cells damaged by illness, autoimmune disease,  
 XX CC accidental damage or genetic disorders. The polypeptides induce the  
 XX CC proliferation of neural cells and regeneration of nerve and brain tissue  
 XX CC and are useful for the treatment of central and peripheral nervous system  
 XX CC diseases and neuropathies, such as Alzheimer's, Parkinson's disease,  
 XX CC Huntington's disease, amyotrophic lateral sclerosis (ALS). The  
 XX CC polypeptides are also involved in chemotactic or chemokinetic activity,  
 XX CC regulation of haematopoiesis and are useful for treating myeloid or  
 XX CC lymphoid cell disorders, platelet disorders such as thrombocytopaenia and  
 XX CC for regeneration of bone, cartilage, tendon, ligament and/or nerve tissue  
 XX CC growth, in tissue repair, healing of burns, incisions, ulcers, for  
 XX CC treating osteoporosis, osteoarthritis, bone degenerative disorders, and  
 XX CC periodontal disease. The polypeptides are also useful for gut protection  
 XX CC or regeneration and treatment of lung or liver fibrosis, reperfusion  
 XX CC injury in various tissues, various immune deficiencies and disorders  
 XX CC including severe combined immunodeficiency (SCID), bacterial or fungal  
 XX CC infections, autoimmune disorders (e.g. multiple sclerosis, rheumatoid  
 XX CC arthritis, diabetes mellitus, myasthenia gravis), allergic reactions and  
 XX CC conditions, such as asthma or other respiratory problems. The  
 XX CC polypeptides are involved in thrombolysis or thrombosis and are useful in  
 XX CC treatment of various coagulation disorders (including hereditary  
 XX CC disorders such as haemophilia) or to enhance coagulation and other  
 XX CC haemostatic events in treating wounds resulting from trauma, surgery or  
 XX CC other causes. The polypeptides exhibit immune stimulating or immune  
 XX CC suppressing activity, and are useful for treating autoimmune diseases or  
 XX CC cancer. They also inhibit the growth, infection or function of infectious  
 XX CC agents such as bacteria, fungi, viruses, effect biorythms or circadian  
 XX CC cycles of rhythms, fertility of male or female subjects, metabolism,  
 XX CC catabolism, and anabolism. ABO00414-ABO00749 represent the novel  
 XX CC polypeptides of the invention. Note: The sequence data for this patent  
 XX CC did not form part of the printed specification, but was obtained in  
 XX CC electronic format directly from WIPO at  
 XX CC ftp.wipo.int/pub/published\_pct\_sequences

RESULT 29  
 ADN46177  
 ID ADN46177 standard; protein; 222 AA.  
 XX AC ADN46177;  
 XX AC 01-JUL-2004 (first entry)  
 XX DT Thermococcus kodakaraensis KOD1 protein sequence SeqID55.  
 XX DE gene disruption; gene targeting; marker gene; transformation;  
 XX KW homologous recombination; hyperthermostable archaeobacterium; KOD1;  
 XX KW gene structure; gene function; enzyme activity; medicine;  
 XX KW forensic science; food; drug inspection; molecular biology; immunology.  
 XX OS Thermococcus kodakaraensis.  
 XX PN WO2004022736-A1.  
 XX PD 18-MAR-2004.  
 XX PF 29-AUG-2003; 2003WO-IB003597.  
 XX PR 30-AUG-2002; 2002JP-00319011.  
 XX PA (NTSC-) JAPAN SCI & TECHNOLOGY CORP.  
 XX PI Imanaka T, Atomi H;  
 XX PX WPI; 2004-257583/24.  
 XX PT Method for disrupting targeted gene in genome of organism particularly  
 XX PT thermostable bacterium and with genome chips for analysis, applicable in  
 XX PT studying gene structure and functions.  
 XX PS Claim 9; SEQ ID NO 55; 598pp; Japanese.  
 XX CC This invention relates to a novel method for targeting disruption of an  
 XX CC arbitrary gene in a genome of an organism which comprises providing the  
 XX CC whole sequential data of the genome of such organism, selecting at least  
 XX CC 1 arbitrary region in the sequence, providing a vector that contains a  
 XX CC sequence homologous with the selected region and a marker gene,  
 XX CC transformation, and homologous recombination. The genome is preferably  
 XX CC the genome of a hyperthermostable archaeobacterium, particularly  
 XX CC Thermococcus kodakaraensis KOD1. The method is for targeting the  
 XX CC disruption of a gene in the genome of an organism, which is applicable in  
 XX CC studying gene structure and functions as well as enzyme activities of  
 XX CC encoded proteins and useful in medicine, forensic science, food or drug  
 XX CC inspection, molecular biology and immunology. With this method, the  
 XX CC disruption of a gene at an arbitrary position in a genome can be achieved  
 XX CC efficiently and reliably. The present sequence is that of a protein  
 XX CC encoded by the genome of Thermococcus kodakaraensis which was derived  
 XX CC using the method of the invention. Note: The sequence data for this  
 XX CC patent did not form part of the printed specification, but was obtained  
 XX CC in electronic format directly from WIPO at  
 XX CC ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 222 AA;  
 Query Match 68.5%; Score 37; DB 8; Length 222;  
 Best Local Similarity 60.0%; Pred. No. 99;  
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 VKLGTYYFDS 10  
 :||||| :|  
 Db 145 LKLGTYVYDT 154

RESULT 30  
 AAE03835  
 ID AAE03835 standard; protein; 380 AA.

XX AAE03835;  
 XX  
 DT 08-AUG-2001 (first entry)  
 XX  
 DE Human gene 18 encoded secreted protein HFKHW50, SEQ ID NO: 81.  
 XX  
 KW Human; secreted protein; proliferative disorder; cancer; tumour; asthma;  
 KW foetal abnormality; developmental abnormality; haematopoietic disorder;  
 KW immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;  
 KW Parkinson's disease; cognitive disorder; schizophrenia; skin disorder;  
 KW psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder;  
 KW inflammation; neurological disorder; Alzheimer's disease; food additive;  
 KW anogenital disorder; kidney disorder; gastrointestinal disorder; allergy;  
 KW pregnancy-related disorder; endocrine disorder; infection; wound healing;  
 KW cell culture; chemotaxis; vulnery; binding partner identification;  
 KW gene therapy.  
 XX  
 OS Homo sapiens.  
 XX  
 XX Key Location/Qualifiers  
 FH Peptide 1..24  
 FT /label= Signal\_peptide  
 FT 25..380  
 FT Protein /note= "Mature secreted protein"  
 FT  
 FN WO200136440-A1.  
 XX  
 XX 25-MAY-2001.  
 PD  
 XX 15-NOV-2000; 2000WO-US031282.  
 PF  
 XX 19-NOV-1999; 99US-0166414P.  
 PR 21-JUL-2000; 2000US-0219665P.  
 XX  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 XX Ruben SM, Komatsoulis GA, Birse CE, Moore PA;  
 XX  
 DR WPI; 2001-343795/36.  
 XX  
 DR N-PSDB; AAD08300.  
 XX  
 XX Isolated nucleic acid molecule encoding a human secreted protein is used  
 PT in preventing, treating or ameliorating a medical condition.  
 XX  
 XX Claim 11; Page 496-498; 553pp; English.  
 XX  
 XX AAD08283-AAD08355 represent cDNAs corresponding to 23 human secreted  
 CC protein genes, and AAE03818-AAE03970 represent the proteins they encode.  
 CC AAE03871-AAE03896 represent human secreted protein fragments or variants.  
 CC The secreted proteins and their genes are useful for preventing, treating  
 CC or ameliorating medical conditions, e.g., by protein or gene therapy.  
 CC Pathological conditions can be diagnosed by determining the amount of the  
 CC new protein in a sample or by determining the presence of mutations in  
 CC the new genes. Specific uses are described for each of the 23 genes,  
 CC based on the tissues in which they are most highly expressed, and include  
 CC developing products for the diagnosis or treatment of proliferative  
 CC disorders, cancer, tumours, foetal and developmental abnormalities,  
 CC haematopoietic disorders, diseases of the immune system, AIDS, autoimmune  
 CC diseases (e.g., rheumatoid arthritis), inflammation, allergies,  
 CC neurological disorders (e.g., Alzheimer's disease, Parkinson's disease),  
 CC cognitive disorders, schizophrenia, asthma, skin disorders (e.g.,  
 CC psoriasis), sepsis, diabetes, atherosclerosis, cardiovascular disorders,  
 CC anogenital disorders, kidney disorders, gastrointestinal disorders,  
 CC pregnancy-related disorders, endocrine disorders, and infections. The  
 CC proteins can also be used to aid wound healing and epithelial cell  
 CC proliferation, to prevent skin aging due to sunburn, to maintain organs  
 CC before transplantation, for supporting cell culture of primary tissues,  
 CC to regenerate tissues, to identify their cognate ligands or binding  
 CC partners, and in chemotaxis, and can be used as a food additive or  
 CC preservative to modify storage properties. Antibodies specific for a  
 CC protein of the invention can be used in alleviating symptoms associated  
 CC with the disorders mentioned above, and in diagnostic immunoassays e.g.,

CC radioimmunoassay or enzyme linked immunosorbent assay (ELISA). The  
 CC present sequence represents a human secreted protein of the invention  
 XX  
 SQ Sequence 380 AA;  
 CC  
 Query Match 68.5%; Score 37; DB 4; Length 380;  
 Best Local Similarity 87.5%; Pred. No. 1.8e+02;  
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 3 LGTYFDS 10  
 Db 183 LGTYSDS 190  
 |||||  
 |||||  
 RESULT 31  
 ID ABG64570  
 XX ABG64570 standard; protein; 380 AA.  
 XX  
 AC ABG64570;  
 XX  
 DT 27-AUG-2002 (first entry)  
 XX  
 DE Human albumin fusion protein #1245.  
 XX  
 KW Albumin fusion protein; therapeutic protein X; human albumin; HA;  
 KW human serum albumin; HSA; cancer; reproductive disorder;  
 KW digestive disorder; immune disorder; endocrine disorder;  
 KW haematopoietic disorder; neural disorder; connective disorder;  
 KW cytostatic; antifertility; antiinflammatory; antiulcer;  
 KW immunomodulator; anti-HIV; antidiabetic; haemostatic; nootropic;  
 KW neuroprotective; antiparkinsonian; antimicrobial; neuroleptic;  
 KW osteopathic; antiarthritic.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 XX WO200177137-A1.  
 XX  
 PD 18-OCT-2001.  
 XX  
 XX 12-APR-2001; 2001WO-US011988.  
 PF  
 XX 12-APR-2000; 2000US-0229358P.  
 PR 25-APR-2000; 2000US-0199384P.  
 XX 21-DEC-2000; 2000US-0256931P.  
 XX  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 XX Rosen CA, Haseltine WA;  
 XX  
 DR WPI; 2002-010886/01.  
 XX  
 XX New fusion protein for treating disease e.g. diabetes comprises an  
 PT albumin fused to a therapeutic protein.  
 XX  
 XX Claim 1; Page 1335-1336; 2102pp; English.  
 XX  
 XX The present invention relates to albumin fusion proteins comprising a  
 CC therapeutic protein X and human albumin (HA, also known as human serum  
 CC albumin, HSA). The proteins are useful for treating a disease or disorder  
 CC that may be modulated by therapeutic protein X. The albumin extends the  
 CC shelf-life of protein X, and may increase its biological in vitro/in vivo  
 CC activity. The protein is useful for treating and diagnosing disorders  
 CC such as cancer, reproductive disorders, digestive disorders (e.g. Crohn's  
 CC disease, ulcerative colitis), immune disorders (e.g. acquired  
 CC immunodeficiency syndrome, AIDS), endocrine disorders (e.g. diabetes),  
 CC haematopoietic disorders, neural disorders (e.g. Alzheimer's,  
 CC Parkinson's, Creutzfeldt-Jacob disease, encephalomyelitis, meningitis,  
 CC schizophrenia), and connective disorders (e.g. osteoporosis, arthritis).  
 CC ABG63326-ABG65518 represent albumin fusion proteins of the invention  
 XX  
 XX Sequence 380 AA;

Query Match 68.5%; Score 37; DB 5; Length 380;  
 Best Local Similarity 87.5%; Pred. No. 1.8e+02;  
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 LGTYVDFS 10  
 DB 183 LGTYVDFS 190

RESULT 32  
 ADL77837  
 ID ADL77837 standard; protein; 380 AA.  
 AC ADL77837;  
 XX  
 DT 20-MAY-2004 (first entry)  
 XX  
 DE Albumin fusion protein related therapeutic protein X, SEQ ID NO 1319.  
 KW albumin fusion protein; cytostatic; antianaemic; antiarthritic;  
 KW antiasthmatic; anti-HIV; immunosuppressive; antiinflammatory;  
 KW antipsoriatic; antibacterial; osteopathic; dermatological; antigout;  
 KW immunomodulator; antiarrhythmic; cardiac; nootropic; antilipaeamic;  
 KW nephrotropic; uropathic; neuroprotective; antiparkinsonian; tranquilizer;  
 KW antidiabetic; anabolic; hypertensive; vulnary; gene therapy; cancer;  
 KW reproductive system disorder; therapeutic protein.  
 XX  
 OS Unidentified.  
 XX  
 PN US2004010134-A1.  
 XX  
 PD 15-JAN-2004.  
 XX  
 PF 12-APR-2001; 2001US-00833245.  
 XX  
 PR 12-APR-2000; 2000US-0229358P.  
 PR 25-APR-2000; 2000US-0199384P.  
 PR 21-DEC-2000; 2000US-0256931P.  
 XX  
 XX (ROSE/) ROSEN C A.  
 PA (HASE/) HASELTINE W A.  
 XX  
 XX Rosen CA, Haseltine WA;  
 XX WPI; 2004-090519/09.  
 XX  
 XX New albumin fusion proteins, useful for diagnosing, treating, preventing  
 PT or ameliorating diseases or disorders e.g. cancer, anemia, arthritis,  
 PT asthma, inflammatory bowel disease or Alzheimer's disease.  
 XX  
 PS Disclosure; SEQ ID NO 1319; 279pp; English.  
 XX

The invention relates to a novel albumin fusion protein. The invention  
 CC further relates to: a composition comprising the albumin fusion protein  
 CC and a pharmaceutical carrier; a kit comprising the composition of the  
 CC albumin fusion protein formula; a method of treating a disease or  
 CC disorder in a patient comprising the step of administering the albumin  
 CC fusion protein; a method of treating a patient with a disease or disorder  
 CC that is modulated by Therapeutic protein: X, or its fragment or variant;  
 CC a method of extending the shelf life of Therapeutic protein: X, or its  
 CC fragment or variant; a nucleic acid molecule comprising a polynucleotide  
 CC sequence encoding the albumin fusion protein; a vector comprising the  
 CC nucleic acid molecule of the albumin fusion protein; and a host cell  
 CC comprising the nucleic acid molecule of the albumin fusion protein. The  
 CC albumin fusion protein and its compositions have the following  
 CC activities: cytostatic, antianaemic, antiarthritic, antiasthmatic, anti-  
 CC HIV, immunosuppressive, antiinflammatory, antipsoriatic, antibacterial,  
 CC osteopathic, dermatological, antigout, immunomodulator, antiarrhythmic,  
 CC cardiac, nootropic, antilipaeamic, nephrotropic, uropathic,  
 CC neuroprotective, antiparkinsonian, tranquilizer, antidiabetic, anabolic,  
 CC hypertensive, and vulnary. The albumin fusion protein nucleic acid may  
 CC be used in gene therapy to treat disorders. The albumin fusion protein is  
 CC useful for diagnosing, treating, preventing or ameliorating diseases or

disorders comprising indication: Y. The diseases or disorders include:  
 CC cancer (e.g. leukaemia, colon, bone, breast, liver or lung cancer),  
 CC immune or haematopoietic diseases (e.g. anaemia, Hodgkin's disease, acute  
 CC lymphocytic anaemia, multiple myeloma, arthritis, asthma, AIDS,  
 CC autoimmune disease, inflammatory bowel disease, psoriasis or Lyme  
 CC disease), reproductive system disorders (e.g. prostatitis, inguinal  
 CC hernia, varicocele, penile carcinoma, ovarian adenocarcinoma or Sertoli-  
 CC leydig tumours), musculoskeletal diseases (e.g. giant cell tumours,  
 CC Paget's disease, systemic lupus erythematosus, gout, muscular dystrophy  
 CC or cachexia), cardiovascular disease (e.g. rhabdomyomas, heart disease,  
 CC arrhythmia, cardiac arrest, heat valve disease, hypernatraemia or  
 CC hyponatraemia), mixed foetal diseases (e.g. foetal alcohol syndrome,  
 CC Down's syndrome, Patau syndrome, Turner's syndrome, Apert syndrome or Tay  
 CC -Sachs disease), excretory diseases (e.g. urinary incontinence, urinary  
 CC tract infections or renal disorders), neural or sensory disease (e.g.  
 CC Alzheimer's disease, Parkinson's disease, cerebral malaria, meningitis,  
 CC cerebellar ataxia, attention deficit disorder, autism or obsessive  
 CC compulsive disorder), respiratory disease (e.g. emphysema, lung cancer or  
 CC occupational lung disease), endocrine diseases (e.g. diabetes, Addison's  
 CC disease or glomerulonephritis), digestive diseases (e.g. portal  
 CC or connective tissue or epithelial diseases (e.g. Crohn's disease,  
 CC scleroderma, wound healing or epidermolysis bullosa). This sequence  
 CC represents a therapeutic protein X relating to the albumin fusion protein  
 CC of the invention. The sequence listing data for this specification was  
 CC downloaded from the USPTO website.  
 XX  
 SQ Sequence 380 AA;  
 Query Match 68.5%; Score 37; DB 8; Length 380;  
 Best Local Similarity 87.5%; Pred. No. 1.8e+02;  
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 LGTYVDFS 10  
 DB 183 LGTYVDFS 190

RESULT 33  
 ADS10470  
 ID ADS10470 standard; protein; 380 AA.  
 XX  
 AC ADS10470;  
 XX  
 DT 16-DEC-2004 (first entry)  
 XX  
 DE Human therapeutic protein - SEQ ID 707.  
 XX  
 KW antiinflammatory; neuroprotective; antianaemic; cytostatic; vulnary;  
 KW inflammatory; haematopoiesis; immunity; neurodegenerative; stem cell;  
 KW aplastic anaemia; cancer; wound healing; gene therapy.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2004080148-A2.  
 XX  
 PD 23-SEP-2004.  
 XX  
 PF 30-SEP-2003; 2003WO-US030720.  
 XX  
 PR 02-OCT-2002; 2002US-0416186P.  
 XX  
 PA (NUVE-) NUVELO INC.  
 XX  
 PI Tang YT, Asundi V, Ren F, Zhang J, Zhang J, Wehrman T, Wang Z, Ma Y; Zhou P;  
 PI Wang D, Chen R, Zhao QA, Wang J, Ghosh M, Xue AJ, Weng G, Zhou P;  
 XX WPI; 2004-668857/65.  
 DR N-PSDB; ADS09786.  
 XX  
 XX New polynucleotide, useful in preparing a composition for diagnosing or  
 PT treating inflammatory, neurodegenerative or stem cell disorders, e.g.,  
 PT aplastic anemia or cancer for promoting wound healing.

XX PS Claim 20; SEQ ID NO 707; 718pp; English.

XX CC The invention relates to a novel isolated polynucleotide and the encoded

XX CC polypeptide. The molecules of the invention demonstrate antiinflammatory,

XX CC neuroprotective, antianaemic, cytostatic and vulnerary activities and may

XX CC be useful in preparing a composition for diagnosing or treating

XX CC inflammatory, haematopoietic, immune, neurodegenerative or stem cell

XX CC disorders, such as aplastic anaemia or cancer, as well as for promoting

XX CC wound healing. The molecules may also be utilised during gene therapy

XX CC procedures. The current sequence is that of a human therapeutic protein

XX CC of the invention. The current sequence is not shown explicitly within the

XX CC specification but can be accessed from the WIPO web-site.

XX SQ Sequence 380 AA;

Query Match 68.5%; Score 37; DB 8; Length 380;

Best Local Similarity 87.5%; Pred. No. 1.8e+02;

Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 LGTYYPDS 10

DB 183 LGTYYSDS 190

RESULT 34

ABP40106

ID ABP40106 standard; protein; 388 AA.

AC ABP40106;

XX DT 24-JUL-2002 (first entry)

XX DE Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:4951.

XX KW Staphylococcus epidermidis; open reading frame; ORF; bacterial infection;

XX KW antibacterial; gene therapy.

XX OS Staphylococcus epidermidis.

XX PN US6380370-B1.

XX PD 30-APR-2002.

XX PF 13-AUG-1998; 98US-00134001.

XX PR 14-AUG-1997; 97US-0055779P.

XX PR 08-NOV-1997; 97US-0064964P.

XX PA (GENO-) GENOME THERAPEUTICS CORP.

XX PI Doucette-Stamm LA, Bush D;

XX DR WPI; 2002-381255/41.

XX DR N-PSDB; ABN92851.

XX PT Novel isolated nucleic acid encoding a Staphylococcus epidermis

XX PT polypeptide, useful for diagnosing and treating bacterial infections.

XX PS Disclosure; SEQ ID NO 4951; 267pp; English.

XX CC ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading

XX CC frame (ORF) nucleic acid sequences which encode the amino acid sequences

XX CC given in ABP35124 to ABP37960. The S. epidermidis sequences have

XX CC antibacterial activity and can be used in gene therapy. The sequences can

XX CC also be used in the diagnosis and treatment of bacterial infections,

XX CC particularly S. epidermidis infections. The sequences can be used to

XX CC screen for compounds able to interfere with the S. epidermidis life cycle

XX CC or inhibit S. epidermidis infection. N.B. The sequence data for this

XX CC patent did not form part of the printed specification, but was obtained

XX CC in electronic format directly from the USPTO web site

XX SQ Sequence 388 AA;

Query Match 68.5%; Score 37; DB 5; Length 388;

Best Local Similarity 66.7%; Pred. No. 1.8e+02;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 KLGTYYFDS 10

DB 250 RVGTYYFGS 258

RESULT 35

ADS05035

ID ADS05035 standard; protein; 388 AA.

XX AC ADS05035;

XX DT 04-NOV-2004 (first entry)

XX DE Staphylococcus epidermis polypeptide seqid 4330.

XX KW antibacterial; vaccine; antisense therapy; Staphylococcus epidermidis;

XX KW recombinant expression vector; infection; computer readable medium;

XX KW computer based system.

XX OS Staphylococcus epidermidis.

XX PN US2004147734-A1.

XX PD 29-JUL-2004.

XX PF 01-DEC-2003; 2003US-00724972.

XX PR 08-NOV-1997; 97US-0064964P.

XX PR 13-AUG-1998; 98US-00134001.

XX PR 29-NOV-1999; 99US-00450969.

XX PA (DOUC/) DOUCETTE-STAMM L.

XX PA (BUSH/) BUSH D.

XX PI Doucette-Stamm L, Bush D;

XX DR WPI; 2004-580138/56.

XX DR N-PSDB; ADS01263.

XX PT New isolated polypeptide and encoding nucleic acid derived from

XX PT Staphylococcus epidermidis, useful for diagnosing, preventing and/or

XX PT treating an S. epidermidis bacterial infection.

XX PS Claim 17; SEQ ID NO 4330; 741pp; English.

XX CC The invention describes an isolated nucleic acid comprising a nucleotide

XX CC sequence with any of 3772 fully defined nucleotide sequences (SEQ ID NO:

XX CC 1-3772) and encoding an Staphylococcus epidermidis polypeptide with any

XX CC of 3772 fully defined amino acid sequences (SEQ ID NO: 3772-7544) as

XX CC given in the specification. Also described are: a recombinant expression

XX CC vector; a cell comprising a recombinant expression vector of (1);

XX CC producing an S. epidermidis polypeptide; an isolated nucleic acid

XX CC comprising a nucleotide sequence of at least 8 nucleotides in length; a

XX CC vaccine composition for prevention or treatment of an S. epidermidis

XX CC infection, comprising a nucleic acid cited above and a carrier; treating

XX CC a subject for S. epidermidis infection; a recombinant or substantially

XX CC pure preparation of an S. epidermidis polypeptide or its fragment; a

XX CC vaccine composition for prevention or treatment of an S. epidermidis

XX CC infection; detecting the presence of a Staphylococcus nucleic acid in a

XX CC sample; a computer readable medium having recorded in it the nucleotide

XX CC sequences with SEQ ID NO: 1-3772 or its fragments; a computer based

XX CC system for identifying fragments of the Staphylococcus genome of

XX CC commercial importance; a computer based system for identifying fragments

XX CC of the Staphylococcus plasmids of commercial importance; identifying

XX CC commercially important nucleic acid fragments of the Staphylococcus

XX CC genome and/or plasmids; and identifying an expression modulating fragment

XX CC of the Staphylococcus genome and/or plasmids. The methods and

XX CC compositions of the present invention are useful for the diagnosis,

CC prevention and/or treatment of an Staphylococcal epidermidis bacterial  
CC infection. This is the amino acid sequence of a S. epidermis protein of  
CC the invention.

XX  
SQ Sequence 388 AA;

Query Match 68.5%; Score 37; DB 8; Length 388;  
Best Local Similarity 66.7%; Pred. No. 1.8e+02;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 KLGYTFDS 10  
:::|||||  
DB 250 RVGYTFGS 258

## RESULT 36

AB88481  
ID AAB88481 standard; protein; 393 AA.

XX  
AC AAB88481;

XX 23-MAY-2001 (first entry)

XX Human membrane or secretory protein clone PSEC0251.

XX Human; secretory protein; membrane protein; vaccine; gene therapy;  
KW rheumatoid arthritis; diabetes.

XX Homo sapiens.

XX EP1067182-A2.

XX 10-JAN-2001.

XX 07-JUL-2000; 2000EP-00114090.

XX 08-JUL-1999; 99JP-00194179.

PR 11-JAN-2000; 2000JP-00118775.

PR 02-MAY-2000; 2000JP-001183766.

XX (HELI-) HELIX RES INST.

XX Ota T, Isogai T, Nishikawa T, Kawai Y, Sugiyama T, Hayashi K;

XX WPI; 2001-093989/11.

DR N-PSDB; AAF93308.

XX Nucleic acids encoding secretory proteins/membrane proteins, useful in  
PT gene therapy or as candidate target molecules in drug development.

XX Claim 1; SEQ ID NO 330; 609pp + Sequence Listing; English.

XX This invention relates to nucleic acid sequences AAF93744 - AAF93916  
CC which encode human secretory or membrane proteins represented by AAB88317  
CC - AAB88419. Included in the invention are primers AAF93917 - AAF94295 and  
CC AAF62232 - AAF62235 which are used to isolate the cDNA sequences of the  
CC invention. The invention also includes methods for the production of  
CC antibodies directed against the proteins, and cDNA sequences, which can  
CC be used in vaccines. The polynucleotide sequences can be used in gene  
CC therapy. The polynucleotide sequences and the proteins they encode may be  
CC used in the prevention, treatment and diagnosis of diseases associated  
CC with inappropriate secretory protein/membrane protein expression. The  
CC nucleic acids and complementary sequences may also be used as DNA probes  
CC in diagnostic assays (e.g. polymerase chain reactions (PCR)) to detect  
CC and quantitate the presence of similar nucleic acid sequences in samples.  
CC They may also be used to study the expression and function of secretory  
CC proteins/membrane polypeptides and their role in metabolism. The  
CC polypeptides may be used as antigens in the production of antibodies  
CC against them and in assays to identify modulators (agonists and  
CC antagonists) of expression and activity. The antibodies and antagonists  
CC may also be used as therapeutic agents to down regulate expression and  
CC activity. The antibodies may also be used as diagnostic agents for  
CC detecting the presence of the polypeptides in samples (e.g. by enzyme

CC linked immunosorbant assay (ELISA). Examples of diseases which may be  
CC treated include rheumatoid arthritis and diabetes

XX Sequence 393 AA;

Query Match 68.5%; Score 37; DB 4; Length 393;  
Best Local Similarity 87.5%; Pred. No. 1.8e+02;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 LGTYTFDS 10  
|||||  
DB 196 LGTYFSDS 203

## RESULT 37

ADY63323  
ID ADY63323 standard; protein; 393 AA.

XX  
AC ADY63323;

XX 02-JUN-2005 (first entry)

XX Human clone PSEC0251 protein, SEQ ID 330.

XX Gene therapy.

XX Homo sapiens.

XX EP1514933-A1.

XX 16-MAR-2005.

XX 07-JUL-2000; 2004EP-00027228.

XX 08-JUL-1999; 99JP-00194179.

PR 11-JAN-2000; 2000JP-00118775.

PR 02-MAY-2000; 2000JP-001183766.

PR 07-JUL-2000; 2000EP-00114090.

XX (REAS-) RES ASSOC BIOTECHNOLOGY.

XX Ota T, Isogai T, Nishikawa T, Kawai Y, Sugiyama T, Hayashi K;

XX WPI; 2005-203865/22.

DR N-PSDB; ADY63322.

XX Novel isolated polynucleotide encoding human secretory proteins or  
PT membrane proteins, useful for examination and diagnosis of abnormality of  
PT human secretory proteins.

XX Disclosure; SEQ ID NO 330; 1240pp; English.

XX The present invention relates to novel human secretory proteins or  
CC membrane proteins, and their coding sequences. The present sequence is  
CC one such protein sequence. The coding sequences of the invention are  
CC useful for examination and diagnosis of abnormality of the human  
CC secretory proteins and in gene therapy methods. The coding sequences and  
CC proteins are useful as candidates for medicines or as target molecules  
CC for developing medicines. Antibodies against the proteins of the  
CC invention are useful for treating diseases that are associated with the  
CC proteins. Note: The sequence data for this patent did not form part of  
CC the printed specification, but was obtained from sequence information  
CC supplied by the European Patent Office.

XX Sequence 393 AA;

Query Match 68.5%; Score 37; DB 9; Length 393;  
Best Local Similarity 87.5%; Pred. No. 1.8e+02;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 LGTYTFDS 10  
|||||  
DB 196 LGTYFSDS 203

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RESULT 38
ABO64573
ID ABO64573 standard; protein; 685 AA.
XX AC
XX ABO64573;
XX AC
DT 29-JUL-2004 (first entry)
XX DE
XX Klebsiella pneumoniae polypeptide seqid 11090.
XX DE
XX Recombinant expression vector; transcription regulatory element;
XX KW
XX Klebsiella pneumoniae protein; antibacterial; Vaccine.
XX KW
XX Klebsiella pneumoniae.
XX OS
XX US6610836-B1.
XX PN
XX 26-AUG-2003.
XX PD
XX 27-JAN-2000; 2000US-00489039.
XX PF
XX 29-JAN-1999; 99US-0117747P.
XX PR
XX (GENO-) GENOME THERAPEUTICS CORP.
XX PA
XX Breton GL, Osborne M;
XX PI
XX WPI; 2003-895346/82.
XX DR
XX N-PSDB; ACH98124.
XX DR
XX New nucleic acid encoding a Klebsiella pneumoniae polypeptide, useful for
PT preparing a vaccine composition against Klebsiella pneumoniae.
XX PT
XX Disclosure; SEQ ID NO 11090; 932pp; English.
XX PS
XX The invention describes a new isolated nucleic acid encoding a Klebsiella
CC pneumoniae polypeptide. Also described are: a recombinant expression
CC vector comprising the nucleic acid, operably linked to a transcription
CC regulatory element; and a cell comprising the recombinant expression
CC vector. The nucleic acid is useful for preparing a vaccine composition
CC against Klebsiella pneumoniae. This is the amino acid sequence of a
CC Klebsiella pneumoniae polypeptide of the invention
XX CC
XX Sequence 685 AA;
SQ
Query Match 68.5%; Score 37; DB 7; Length 685;
Best Local Similarity 85.7%; Pred. No. 3.4e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 4 GTYYFDS 10
Db 577 GTYYFDS 583
||:|||||
||:|||||

RESULT 39
ABR63232
ID ABR63232 standard; protein; 2022 AA.
XX ID
XX ABR63232;
XX AC
XX 27-AUG-2003 (first entry)
XX DT
XX Glucansucrase sequence from strain MLL.
XX DE
XX Glucan; glucosyltransferase activity; thickener; prebiotic;
XX KW
XX bioactive agent; anti-corrosion agent; foodstuff; gastrointestinal tract.
XX KW
XX Lactobacillus reuteri.
XX OS
XX WO2003008618-A2.
XX PN
XX
XX

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PD 30-JAN-2003.
XX 22-JUL-2002; 2002WO-NL000495.
XX PF
XX 20-JUL-2001; 2001EP-00202752.
XX PR
XX 25-JUL-2001; 2001EP-00202841.
XX PR
XX (NEDE ) NEDERLANDSE ORG TOEGEPAST.
XX PA
XX Van Geel- Schutten GH;
XX PI
XX WPI; 2003-289780/28.
XX DR
XX N-PSDB; ACC84448.
XX DR
XX Novel glucan produced by glucosyltransferase activity of lactic acid
PT bacterium on sucrose substrate, and having backbone consisting of alpha
PT (1,3)- and alpha (1,6)-linked anhydroglucose units, useful as thickener.
XX PT
XX Claim 11; Fig 1; 51pp; English.
XX PS
XX The present invention relates to glucan capable of being produced by
CC glucosyltransferase activity of a lactic acid bacterium on a sucrose
CC substrate. The method is useful as a thickener, as a prebiotic and as a
CC bioactive agent and as an anti-corrosion agent. The glucan can be
CC incorporated in foodstuffs such as beverages, sauces, dressings, dairy
CC products. The glucan is useful as anticorrosion agent, e.g. for the
CC protection of ship hulls. It can also be incorporated in nutritional or
CC pharmaceutical compositions intended for improving the condition of the
CC gastrointestinal tract. The present sequence represents a sequence of the
CC glucansucrase gene
XX CC
XX Sequence 2022 AA;
SQ
Query Match 68.5%; Score 37; DB 6; Length 2022;
Best Local Similarity 72.7%; Pred. No. 1.1e+03;
Matches 8; Conservative 1; Mismatches 0; Indels 2; Gaps 1;
QY 1 VKLG--TYFFD 9
Db 1724 VKIGNDTYFFD 1734
||:|||||
||:|||||

RESULT 40
ABP30519
ID ABP30519 standard; protein; 160 AA.
XX ID
XX ABP30519;
XX AC
XX 02-JUL-2002 (first entry)
XX DT
XX Streptococcus polypeptide SEQ ID NO 10214.
XX DE
XX Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae;
KW group A streptococcus; Streptococcus pyogenes; antibacterial;
KW antiinflammatory; infection; vaccine; meningitis; gene therapy.
XX KW
XX Streptococcus agalactiae.
XX OS
XX WO200234771-A2.
XX PN
XX 02-MAY-2002.
XX PD
XX 29-OCT-2001; 2001WO-GB004789.
XX PF
XX 27-OCT-2000; 2000GB-00026333.
XX PR
XX 24-NOV-2000; 2000GB-00028727.
XX PR
XX 07-MAR-2001; 2001GB-00005640.
XX PR
XX (CHIR-) CHIRON SPA.
XX PA
XX (GENO-) INST GENOMIC RES.
XX PA
XX Telford J, Massignani V, Margarit Y Rosl, Grandi G, Fraser C;
XX PI Tettelin H;

```



XX WPI; 2002-352536/38.  
 DR N-PSDB; ABN71150.  
 XX  
 PT New Streptococcus protein for the treatment or prevention of infection or  
 PT disease caused by Streptococcus bacteria, such as meningitis, and for  
 PT detecting a compound that binds to the protein.  
 XX  
 PS Claim 1; Page 4151; 4525pp; English.  
 XX  
 CC The invention relates to a protein (ABP25413-ABP30895) from group B  
 CC streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS  
 CC (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in  
 CC the specification. The proteins have antibacterial and antiinflammatory  
 CC activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and  
 CC antibodies that bind (I) are used in the manufacture of medicaments for  
 CC the treatment or prevention of infection or disease caused by  
 CC Streptococcus bacteria, particularly S. agalactiae and S. pyogenes.  
 CC Nucleic acids encoding (I) are used to detect Streptococcus in a  
 CC biological sample. (I) is used to determine whether a compound binds to  
 CC Streptococcus bacteria, particularly S. agalactiae and S. pyogenes.  
 CC (I). A composition comprising (I) or a nucleic acid encoding (I), may be  
 CC used as a vaccine or diagnostic composition. The disease caused by  
 CC Streptococcus that is prevented or treated may be meningitis. Nucleic  
 CC acid encoding (I) may be used to recombinantly produce (I) and may be  
 CC used in gene therapy. Antibodies to (I) are used for affinity  
 CC chromatography, immunoassays, and distinguishing/identifying  
 CC Streptococcus proteins  
 XX  
 SQ Sequence 160 AA;  
 Query Match 66.7%; Score 36; DB 5; Length 160;  
 Best Local Similarity 75.0%; Pred. No. 1.1e+02;  
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 KLGTYYFD 9  
 Db :|||  
 110 ELGEYYFD 117  
 RESULT 41  
 ID ABP26309  
 AC ABP26309 standard; protein; 163 AA.  
 AC ABP26309;  
 XX  
 XX 02-JUL-2002 (first entry)  
 DT  
 DE Streptococcus polypeptide SEQ ID NO 1794.  
 XX  
 XX Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae;  
 KW group A streptococcus; Streptococcus pyogenes; antibacterial;  
 KW antiinflammatory; infection; vaccine; meningitis; gene therapy.  
 XX  
 OS Streptococcus agalactiae.  
 XX  
 XX WO200234771-A2.  
 PN  
 XX 02-MAY-2002.  
 PD  
 XX 29-OCT-2001; 2001WO-GB004789.  
 XX  
 XX 27-OCT-2000; 2000GB-00026333.  
 PR  
 PR 24-NOV-2000; 2000GB-00028727.  
 PR  
 PR 07-MAR-2001; 2001GB-00005640.  
 XX  
 XX (CHIR-) CHIRON SPA.  
 PA (GENO-) INST GENOMIC RES.  
 PA  
 XX Telford J, Massignani V, Margarit Y Rosl, Grandi G, Fraser C;  
 PI Tettelein H;  
 XX  
 XX WPI; 2002-352536/38.  
 DR N-PSDB; ABN66940.

XX New Streptococcus protein for the treatment or prevention of infection or  
 PT disease caused by Streptococcus bacteria, such as meningitis, and for  
 PT detecting a compound that binds to the protein.  
 XX  
 PS Claim 1; Page 3329; 4525pp; English.  
 XX  
 CC The invention relates to a protein (ABP25413-ABP30895) from group B  
 CC streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS  
 CC (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in  
 CC the specification. The proteins have antibacterial and antiinflammatory  
 CC activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and  
 CC antibodies that bind (I) are used in the manufacture of medicaments for  
 CC the treatment or prevention of infection or disease caused by  
 CC Streptococcus bacteria, particularly S. agalactiae and S. pyogenes.  
 CC Nucleic acids encoding (I) are used to detect Streptococcus in a  
 CC biological sample. (I) is used to determine whether a compound binds to  
 CC Streptococcus bacteria, particularly S. agalactiae and S. pyogenes.  
 CC (I). A composition comprising (I) or a nucleic acid encoding (I), may be  
 CC used as a vaccine or diagnostic composition. The disease caused by  
 CC Streptococcus that is prevented or treated may be meningitis. Nucleic  
 CC acid encoding (I) may be used to recombinantly produce (I) and may be  
 CC used in gene therapy. Antibodies to (I) are used for affinity  
 CC chromatography, immunoassays, and distinguishing/identifying  
 CC Streptococcus proteins  
 XX  
 SQ Sequence 163 AA;  
 Query Match 66.7%; Score 36; DB 5; Length 163;  
 Best Local Similarity 75.0%; Pred. No. 1.1e+02;  
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 KLGTYYFD 9  
 Db :|||  
 113 ELGEYYFD 120  
 RESULT 42  
 ID AAG09510  
 AC AAG09510 standard; protein; 257 AA.  
 AC AAG09510;  
 XX  
 XX 17-OCT-2000 (first entry)  
 DT  
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 7473.  
 XX  
 XX Protein identification; signal transduction pathway; metabolic pathway;  
 KW hybridisation assay; genetic mapping; gene expression control; promoter;  
 KW termination sequence.  
 XX  
 OS Arabidopsis thaliana.  
 XX  
 XX EP1033405-A2.  
 PN  
 XX 06-SEP-2000.  
 PD  
 XX 25-FEB-2000; 2000EP-00301439.  
 PF  
 XX 25-FEB-1999; 99US-0121825P.  
 PR 05-MAR-1999; 99US-0123180P.  
 PR 09-MAR-1999; 99US-0123548P.  
 PR 23-MAR-1999; 99US-0125788P.  
 PR 25-MAR-1999; 99US-0126264P.  
 PR 29-MAR-1999; 99US-0126785P.  
 PR 01-APR-1999; 99US-0127462P.  
 PR 06-APR-1999; 99US-0128234P.  
 PR 18-APR-1999; 99US-0128714P.  
 PR 19-APR-1999; 99US-0129845P.  
 PR 21-APR-1999; 99US-0130077P.  
 PR 23-APR-1999; 99US-0130449P.  
 PR 23-APR-1999; 99US-0130510P.  
 PR 28-APR-1999; 99US-0130891P.  
 PR 28-APR-1999; 99US-0131449P.



PR	30-APR-1999;	99US-0132048P.	PR	21-JUL-1999;	99US-0145086P.
PR	30-APR-1999;	99US-0132407P.	PR	21-JUL-1999;	99US-0145088P.
PR	04-MAY-1999;	99US-0132484P.	PR	22-JUL-1999;	99US-0145085P.
PR	05-MAY-1999;	99US-0132485P.	PR	22-JUL-1999;	99US-0145087P.
PR	06-MAY-1999;	99US-0132486P.	PR	22-JUL-1999;	99US-0145089P.
PR	06-MAY-1999;	99US-0132487P.	PR	22-JUL-1999;	99US-0145192P.
PR	07-MAY-1999;	99US-0132863P.	PR	23-JUL-1999;	99US-0145145P.
PR	11-MAY-1999;	99US-0134256P.	PR	23-JUL-1999;	99US-0145218P.
PR	14-MAY-1999;	99US-0134218P.	PR	23-JUL-1999;	99US-0145224P.
PR	14-MAY-1999;	99US-0134219P.	PR	26-JUL-1999;	99US-0145276P.
PR	14-MAY-1999;	99US-0134221P.	PR	27-JUL-1999;	99US-0145913P.
PR	14-MAY-1999;	99US-0134370P.	PR	27-JUL-1999;	99US-0145918P.
PR	18-MAY-1999;	99US-0134768P.	PR	27-JUL-1999;	99US-0145919P.
PR	19-MAY-1999;	99US-0134941P.	PR	28-JUL-1999;	99US-0145951P.
PR	20-MAY-1999;	99US-0135124P.	PR	02-AUG-1999;	99US-0146386P.
PR	21-MAY-1999;	99US-0135353P.	PR	02-AUG-1999;	99US-0146388P.
PR	24-MAY-1999;	99US-0135629P.	PR	02-AUG-1999;	99US-0146389P.
PR	25-MAY-1999;	99US-0136021P.	PR	03-AUG-1999;	99US-0147038P.
PR	27-MAY-1999;	99US-0136392P.	PR	04-AUG-1999;	99US-0147204P.
PR	28-MAY-1999;	99US-0136782P.	PR	04-AUG-1999;	99US-0147302P.
PR	01-JUN-1999;	99US-0137222P.	PR	05-AUG-1999;	99US-0147192P.
PR	03-JUN-1999;	99US-0137528P.	PR	05-AUG-1999;	99US-0147260P.
PR	04-JUN-1999;	99US-0137502P.	PR	06-AUG-1999;	99US-0147303P.
PR	07-JUN-1999;	99US-0137724P.	PR	06-AUG-1999;	99US-0147416P.
PR	08-JUN-1999;	99US-0138094P.	PR	09-AUG-1999;	99US-0147493P.
PR	10-JUN-1999;	99US-0138540P.	PR	09-AUG-1999;	99US-0147935P.
PR	10-JUN-1999;	99US-0138847P.	PR	10-AUG-1999;	99US-0148171P.
PR	14-JUN-1999;	99US-0139119P.	PR	11-AUG-1999;	99US-0148319P.
PR	16-JUN-1999;	99US-0139452P.	PR	12-AUG-1999;	99US-0148341P.
PR	16-JUN-1999;	99US-0139453P.	PR	13-AUG-1999;	99US-0148565P.
PR	17-JUN-1999;	99US-0139492P.	PR	13-AUG-1999;	99US-0148684P.
PR	18-JUN-1999;	99US-0139454P.	PR	16-AUG-1999;	99US-0149368P.
PR	18-JUN-1999;	99US-0139455P.	PR	17-AUG-1999;	99US-0149175P.
PR	18-JUN-1999;	99US-0139456P.	PR	18-AUG-1999;	99US-0149426P.
PR	18-JUN-1999;	99US-0139457P.	PR	20-AUG-1999;	99US-0149722P.
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PR	19-JUL-1999;	99US-0144325P.	PR	12-OCT-1999;	99US-0158369P.
PR	19-JUL-1999;	99US-0144331P.	PR	13-OCT-1999;	99US-0159293P.
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Query Match 66.7%; Score 36; DB 3; Length 257;

Best Local Similarity 75.0%; Pred. No. 1.8e+02; Mismatches 1; Indels 0; Gaps 0;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 LGTYFDS 10  
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Db 10 LGLYFDT 17

#### RESULT 43

AAG48547  
ID AAG48547 standard; protein; 257 AA.

XX AC AAG48547;

XX DT 18-OCT-2000 (first entry)

XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 61317.

XX KW Protein identification; signal transduction pathway; metabolic pathway;  
KW hybridisation assay; genetic mapping; gene expression control; promoter;  
KW termination sequence.

XX OS Arabidopsis thaliana.

XX PN EP1033405-A2.

XX PD 06-SEP-2000.

XX PF 25-FEB-2000; 2000EP-00301439.

XX PR 25-FEB-1999; 99US-0121825P.

PR 05-MAR-1999; 99US-0123180P.

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 PR 29-OCT-1999; 99US-0162142P.

Query Match 66.7%; Score 36; DB 3; Length 257;  
 Best Local Similarity 75.0%; Pred. No. 1.8e+02;  
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 LGTYTFDS 10  
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 Db 10 LGLYYFDT 17

RESULT 44  
 ADN46472  
 ID ADN46472 standard; protein; 258 AA.  
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 AC ADN46472;  
 XX  
 DT 01-JUL-2004 (first entry)  
 XX  
 DE Thermococcus kodakaraensis KOD1 protein sequence SeqID350.  
 XX  
 KW gene disruption; gene targeting; marker gene; transformation;  
 KW homologous recombination; hyperthermostable archaeobacterium; KOD1;  
 KW gene structure; gene function; enzyme activity; medicine;  
 KW forensic science; food; drug inspection; molecular biology; immunology.  
 XX  
 OS Thermococcus kodakaraensis.  
 XX  
 FN WO2004022736-A1.  
 XX  
 PD 18-MAR-2004.  
 XX  
 PF 29-AUG-2003; 2003WO-IB003597.  
 XX  
 PR 30-AUG-2002; 2002JP-00319011.  
 XX  
 XX (NISC-) JAPAN SCI & TECHNOLOGY CORP.  
 XX  
 PI Imanaka T, Atomi H;  
 XX  
 XX WPI; 2004-257583/24.  
 XX  
 PT Method for disrupting targeted gene in genome of organism particularly  
 PT thermostable bacterium and with genome chips for analysis, applicable in  
 PT studying gene structure and functions.  
 XX  
 PS Claim 9; SEQ ID NO 350; 598pp; Japanese.  
 XX  
 CC This invention relates to a novel method for targeting disruption of an  
 CC arbitrary gene in a genome of an organism which comprises providing the  
 CC whole sequential data of the genome of such organism, selecting at least  
 CC 1 arbitrary region in the sequence, providing a vector that contains a  
 CC sequence homologous with the selected region and a marker gene,  
 CC transformation, and homologous recombination. The genome is preferably  
 CC the genome of a hyperthermostable archaeobacterium, particularly  
 CC Thermococcus kodakaraensis KOD1. The method is for targeting the  
 CC disruption of a gene in the genome of an organism, which is applicable in  
 CC studying gene structure and functions as well as enzyme activities of  
 CC encoded proteins and useful in medicine, forensic science, food or drug  
 CC inspection, molecular biology and immunology. With this method, the  
 CC disruption of a gene at an arbitrary position in a genome can be achieved  
 CC efficiently and reliably. The present sequence is that of a protein

CC encoded by the genome of *Thermococcus kodakaraensis* which was derived  
CC using the method of the invention. Note: The sequence data for this  
CC patent did not form part of the printed specification, but was obtained  
CC in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences

XX  
SQ Sequence 258 AA;

Query Match 66.7%; Score 36; DB 8; Length 258;  
Best Local Similarity 60.0%; Pred. No. 1.8e+02;  
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 VKLGYTFYDS 10  
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Db 194 VRVGNYYVDS 203

## RESULT 45

AAG48546  
ID AAG48546 standard; protein; 260 AA.

XX AAG48546;

XX 18-OCT-2000 (first entry)

XX Arabidopsis thaliana protein fragment SEQ ID NO: 61316.

KW Protein identification; signal transduction pathway; metabolic pathway;  
KW hybridisation assay; genetic mapping; gene expression control; promoter;  
KW termination sequence.

OS Arabidopsis thaliana.

XX EP1033405-A2.

XX 06-SEP-2000.

XX 25-FEB-2000; 2000EP-00301439.

XX 25-FEB-1999; 99US-0121825P.

PR 05-MAR-1999; 99US-0123180P.

PR 09-MAR-1999; 99US-0123548P.

PR 23-MAR-1999; 99US-0125788P.

PR 25-MAR-1999; 99US-0126264P.

PR 29-MAR-1999; 99US-0126785P.

PR 01-APR-1999; 99US-0127462P.

PR 06-APR-1999; 99US-0128234P.

PR 08-APR-1999; 99US-0128714P.

PR 16-APR-1999; 99US-0129845P.

PR 19-APR-1999; 99US-0130077P.

PR 21-APR-1999; 99US-0130449P.

PR 23-APR-1999; 99US-0130510P.

PR 23-APR-1999; 99US-0130891P.

PR 28-APR-1999; 99US-0131449P.

PR 30-APR-1999; 99US-0132048P.

PR 30-APR-1999; 99US-0132407P.

PR 04-MAY-1999; 99US-0132484P.

PR 05-MAY-1999; 99US-0132485P.

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KW termination sequence.  
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PR 07-MAY-1999;	99US-0132863P.	PR	27-JUL-1999;	99US-0145913P.
PR 11-MAY-1999;	99US-0134256P.	PR	27-JUL-1999;	99US-0145918P.
PR 14-MAY-1999;	99US-0134218P.	PR	28-JUL-1999;	99US-0145951P.
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PR 21-MAY-1999;	99US-0135353P.	PR	05-AUG-1999;	99US-0147260P.
PR 24-MAY-1999;	99US-0135629P.	PR	06-AUG-1999;	99US-0147303P.
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PR 01-JUN-1999;	99US-0137222P.	PR	10-AUG-1999;	99US-0148171P.
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PR 16-JUN-1999;	99US-0139453P.	PR		
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PR 18-JUN-1999;	99US-0139454P.	PR		
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 PR 23-AUG-1999; 99US-0149902P.  
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 PR 31-AUG-1999; 99US-0151438P.  
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 PR 10-SEP-1999; 99US-0153070P.  
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 PR 15-SEP-1999; 99US-0154018P.  
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 PR 28-OCT-1999; 99US-0161920P.  
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 PR 29-OCT-1999; 99US-0162142P.

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 Best Local Similarity 75.0%; Pred. No. 2.5e+02;  
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 LGTYFYFDS 10  
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 Db 107 LGLYFYFDT 114

RESULT 48  
 ABB67540  
 ID ABB67540 standard; protein; 361 AA.  
 XX

AC ABB67540;  
 XX  
 DT 26-MAR-2002 (first entry)  
 XX  
 DE Drosophila melanogaster polypeptide SEQ ID NO 29412.  
 XX  
 KW Drosophila; developmental biology; cell signalling; insecticide;  
 KW pharmaceutical.  
 OS Drosophila melanogaster.  
 XX  
 PN WO200171042-A2.  
 XX  
 PD 27-SEP-2001.  
 XX  
 PF 23-MAR-2001; 2001WO-US009231.  
 XX  
 PR 23-MAR-2000; 2000US-0191637P.  
 PR 11-JUL-2000; 2000US-00614150.  
 XX  
 PA (PEKE ) PE CORP NY.  
 XX  
 PI Venter JC, Adams M, Li PWD, Myers EW;  
 XX  
 DR WPI; 2001-656860/75.  
 DR N-PSDB; ABL11643.  
 XX  
 PT New isolated nucleic acid detection reagent for detecting 1000 or more  
 PT genes from Drosophila and for elucidating cell signaling and cell-cell  
 PT interactions.  
 XX  
 PS Disclosure; SEQ ID NO 29412; 21pp + Sequence Listing; English.  
 XX  
 CC The invention relates to an isolated nucleic acid detection reagent  
 CC capable of detecting 1000 or more genes from Drosophila. The invention is  
 CC useful in developmental biology and in elucidating cell signaling and  
 CC cell-cell interactions in higher eukaryotes for the development of  
 CC insecticides, therapeutics and pharmaceutical drugs. The invention  
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA  
 CC sequences (ABL01840-ABL16175) and the encoded proteins (ABBS7737-  
 CC ABB72072). The sequence data for this patent did not form part of the  
 CC printed specification, but was obtained in electronic format directly  
 CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 361 AA;  
 Query Match 66.7%; Score 36; DB 4; Length 361;  
 Best Local Similarity 75.0%; Pred. No. 2.6e+02;  
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 3 LGTYFYFDS 10  
 |||||  
 Db 21 LNTYFYFDT 28  
 RESULT 49  
 AAB75213  
 ID AAB75213 standard; protein; 361 AA.  
 XX  
 AC AAB75213;  
 XX  
 DT 03-APR-2001 (first entry)  
 XX  
 DE Drosophila gustatory receptor GR47A.1 protein sequence.  
 XX  
 KW Gustatory receptor; fruit fly; taste; pheromone; semiochemical;  
 KW crop damage; pest control.  
 XX  
 OS Drosophila melanogaster.  
 XX  
 PN WO200077208-A2.  
 XX  
 PD 21-DEC-2000.



XX 14-JUN-2000; 2000WO-US016211.  
 PF 14-JUN-1999; 99US-0138668P.  
 PR 10-FEB-2000; 2000US-0181704P.  
 XX (UYVA ) UNIV YALE.  
 PA Carlson PJ, Clyne PJ, Warr CG;  
 XX WPI; 2001-061873/07.  
 PI DR N-PSDB; AAF63752.  
 XX DR N-PSDB; AAF63752.  
 XX New isolated nucleic acid molecule encoding Drosophila Gustatory Receptor  
 PT protein useful for e.g. identification of compounds which may be used for  
 PT pest management.  
 XX  
 XX Claim 12; Page 146-147; 227pp; English.  
 PS  
 XX This invention relates to polynucleotide sequences AAF63732 - AAF63777  
 CC which encode Drosophila gustatory receptor proteins represented by  
 CC sequences AAB75193 - AAB75238. The invention includes methods for  
 CC determining gustatory receptor ligands. Also included is a method for  
 CC modulating the expression of the DNA encoding the receptors. The DNA and  
 CC protein sequences may be used for the identification of compounds, e.g.  
 CC pheromones and other semiochemicals, which may be used for pest  
 CC management. The DNA sequences may also be used for behavioural studies  
 CC involving gustatory systems in various organisms. Also, the DNA sequences  
 CC may also be used to track down gustatory receptor genes in insects that  
 CC damage crops or transmit diseases  
 XX  
 SQ Sequence 361 AA;  
 Query Match 66.7%; Score 36; DB 4; Length 361;  
 Best Local Similarity 75.0%; Pred. No. 2.6e+02;  
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 3 LGTYFYFDS 10  
 Db | | | | | |  
 21 LNTYFYFDT 28  
 RESULT 50  
 AAE30515  
 ID AAE30515 standard; protein; 361 AA.  
 AC AAE30515;  
 XX 24-FEB-2003 (first entry)  
 XX Fruit fly gustatory receptor protein, Gr47A1.  
 XX Fruit fly; gustatory receptor; Gr; odorant receptor; Or; pesticide;  
 KW Gr47A1.  
 XX Drosophila melanogaster.  
 OS WO200268593-A2.  
 PN WO200268593-A2.  
 XX 06-SEP-2002.  
 PD 22-FEB-2002; 2002WO-US005414.  
 XX 23-FEB-2001; 2001US-0271319P.  
 PR (UYCO ) UNIV COLUMBIA NEW YORK.  
 XX Axel R, Scott K;  
 XX WPI; 2002-698668/75.  
 DR Novel nucleic acid encoding insect gustatory or odorant receptor protein  
 PT useful for identifying a compound which specifically binds to the

PT receptor for controlling a pest population in an area.  
 XX Disclosure; Page 203-205; 264pp; English.  
 XX The invention relates to an isolated nucleic acid encoding an insect  
 CC gustatory receptor (Gr) or odorant receptor (Or) protein which comprises  
 CC seven transmembrane domains and a C-terminal domain comprising  
 CC consecutive amino acids. The invention is useful for identifying a  
 CC compound which activates the insect receptor or inhibits the activity of  
 CC the insect receptor. The purified insect receptor protein is embedded in  
 CC a lipid bilayer. The invention is sprayed for combating ingestion of  
 CC crops by pest insects, combating disease-carrying insects in an area and  
 CC controlling a pest population in an area. The invention is useful for  
 CC detecting the presence of insect gustatory or odorant receptor and for  
 CC inhibiting the function of the receptor in humans or animals or in  
 CC biological fluids isolated from them. The invention is also useful for  
 CC identifying or isolating other insect receptors and for combating pest  
 CC nuisances. The present sequence is fruit fly gustatory receptor (Gr)  
 CC protein  
 XX Sequence 361 AA;  
 SQ  
 Query Match 66.7%; Score 36; DB 5; Length 361;  
 Best Local Similarity 75.0%; Pred. No. 2.6e+02;  
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 3 LGTYFYFDS 10  
 Db | | | | | |  
 21 LNTYFYFDT 28  
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OM protein - protein search, using sw model

Run on: April 6, 2006, 08:56:41 ; Search time 10 Seconds  
(without alignments)  
96.217 Million cell updates/sec

Title: US-10-089-500-5  
Perfect score: 54  
Sequence: 1 VKLGTGVFDS 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database :

1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	43	79.6	456	2 D97168	uncharacterized prote
2	40	74.1	144	2 E41287	Ig heavy chain pr
3	39	72.2	2817	2 B97033	uncharacterized pr
4	38	70.4	587	1 B4276	coat protein vp1 -
5	38	70.4	716	1 VCPV2M	coat protein vp1 -
6	38	70.4	718	1 VCPVIM	coat protein vp1 -
7	38	70.4	847	2 S75975	hypothetical prote
8	38	70.4	907	2 A86460	99.9K hypothetical
9	38	70.4	921	2 S49965	probable membrane
10	37	68.5	814	2 T02130	hypothetical prote
11	36	66.7	203	2 C69872	hypothetical prote
12	36	66.7	361	2 T48029	hypothetical prote
13	36	66.7	637	2 F90257	hypothetical prote
14	35	64.8	222	2 T31541	hypothetical prote
15	35	64.8	228	2 S09772	hypothetical prote
16	35	64.8	271	2 E72331	hypothetical prote
17	35	64.8	339	2 T21476	hypothetical prote
18	35	64.8	372	2 C86660	endo-1,4-beta-xyla
19	35	64.8	669	2 T28028	hypothetical prote
20	35	64.8	685	2 T22223	sel-1 protein - Ca
21	35	64.8	696	2 G88851	protein ZK829.10 (
22	35	64.8	837	2 B89583	protein K07E3.2 (i
23	35	64.8	1113	2 T20140	hypothetical prote
24	34	63.0	84	2 A46158	nicotinic acetylch
25	34	63.0	110	2 A32189	Ig heavy chain v r
26	34	63.0	110	2 S09831	hypothetical prote
27	34	63.0	140	2 PH1486	Ig heavy chain v r
28	34	63.0	140	2 PH1499	Ig heavy chain v r
29	34	63.0	204	2 E90868	hypothetical prote

30	34	63.0	209	2 C70424	hypothetical prote
31	34	63.0	230	2 D85750	hypothetical prote
32	34	63.0	258	2 B81307	chitin bio synthet
33	34	63.0	277	2 A64659	outer membrane pr
34	34	63.0	277	2 B71856	probable outer mem
35	34	63.0	309	2 T08150	chitinase (EC 3.2.
36	34	63.0	357	2 T48055	hypothetical prote
37	34	63.0	510	2 C64883	membrane protein y
38	34	63.0	524	2 A45472	protein kinase (EC
39	34	63.0	586	2 F64186	ABC-type transport
40	34	63.0	627	2 AD1818	N-acetylglucosyl-L
41	34	63.0	692	2 G90284	hypothetical prote
42	34	63.0	705	2 A48144	protein kinase CDC
43	34	63.0	784	2 AI0513	organic solvent to
44	34	63.0	1411	2 A84460	probable retrovira
45	34	63.0	1943	2 B64596	toxin-like outer m
46	34	63.0	2176	2 T39188	probable U5 snRNP-
47	34	63.0	4767	2 T31345	hypothetical prote
48	33	61.1	67	2 T11144	H+-transporting tw
49	33	61.1	90	2 PH1485	Ig heavy chain v r
50	33	61.1	97	2 S26885	Ig heavy chain v r
51	33	61.1	97	2 S26886	Ig heavy chain v r
52	33	61.1	102	2 PH1490	Ig heavy chain v r
53	33	61.1	114	2 PH1523	Ig heavy chain v r
54	33	61.1	114	2 PH1522	Ig heavy chain v r
55	33	61.1	116	2 S12557	Ig heavy chain - h
56	33	61.1	118	2 S38565	Ig heavy chain v r
57	33	61.1	119	2 PH1510	Ig heavy chain v r
58	33	61.1	119	2 PH1505	Ig heavy chain v r
59	33	61.1	119	2 PH1518	Ig heavy chain v r
60	33	61.1	119	2 PH1517	Ig heavy chain v r
61	33	61.1	119	2 PH1502	Ig heavy chain v r
62	33	61.1	119	2 PH1521	Ig heavy chain v r
63	33	61.1	119	2 PH1500	Ig heavy chain v r
64	33	61.1	119	2 PH1516	Ig heavy chain v r
65	33	61.1	119	2 PH1503	Ig heavy chain v r
66	33	61.1	119	2 PH1504	Ig heavy chain v r
67	33	61.1	119	2 PH1520	Ig heavy chain v r
68	33	61.1	119	2 PH1519	Ig heavy chain v r
69	33	61.1	119	2 PH1512	Ig heavy chain v r
70	33	61.1	120	2 S44111	Ig heavy chain V-D
71	33	61.1	123	2 S24693	Ig heavy chain V6
72	33	61.1	127	2 H90091	hypothetical prote
73	33	61.1	135	2 PH1494	Ig heavy chain v r
74	33	61.1	135	2 PH1493	Ig heavy chain v r
75	33	61.1	137	2 I47193	Ig heavy chain var
76	33	61.1	140	2 PH1498	Ig heavy chain v r
77	33	61.1	140	2 PH1483	Ig heavy chain v r
78	33	61.1	140	2 PH1488	Ig heavy chain v r
79	33	61.1	140	2 PH1482	Ig heavy chain v r
80	33	61.1	140	2 PH1484	Ig heavy chain v r
81	33	61.1	140	2 PH1489	Ig heavy chain v r
82	33	61.1	164	2 C89854	hypothetical prote
83	33	61.1	204	2 D86396	hypothetical prote
84	33	61.1	254	2 H96660	protein F2k11.6 (i
85	33	61.1	256	2 S58743	H+-transporting tw
86	33	61.1	271	2 JC6553	transcription fact
87	33	61.1	272	2 E64163	hypothetical prote
88	33	61.1	360	2 AE0172	probable outer mem
89	33	61.1	369	2 S70847	outer membrane por
90	33	61.1	375	2 A83788	spore germination
91	33	61.1	390	2 G88022	protein T27A1.4 (i
92	33	61.1	400	2 AI1211	integrases homolog
93	33	61.1	473	2 S04113	nitrogenase (EC 1.
94	33	61.1	474	2 C35405	nitrogenase (EC 1.
95	33	61.1	537	2 AB0660	periplasmic murein
96	33	61.1	537	2 AB0660	probable periplasm
97	33	61.1	548	2 AD0285	periplasmic oligop
98	33	61.1	544	2 D64882	probable transport
99	33	61.1	544	2 G90867	probable transport
100	33	61.1	550	2 B85751	oligopeptide ABC t
101	33	61.1	609	2 B97346	hypothetical prote
102	33	61.1	639	2 A10055	probable soluble 1

103	33	61.1	679	2	T40219	hypothetical prote	176	32	59.3	932	2	S76501	preprotein translo
104	33	61.1	731	2	AE1945	hypothetical prote	177	32	59.3	948	2	JC2190	preprotein translo
105	33	61.1	826	2	AC0086	outer membrane u	178	32	59.3	970	2	S48485	transcription acti
106	33	61.1	959	2	H69344	hypothetical prote	179	32	59.3	1373	2	J50095	gastric mucin MUC5
107	33	61.1	2163	2	S50675	pre-mRNA splicing	180	32	59.3	1440	2	J27942	lin-15B protein -
108	33	61.1	2971	2	T08026	hypothetical prote	181	32	59.3	1518	2	A44811	glucosyltransferas
109	33	61.1	3194	2	D71917	toxin-like outer m	182	32	59.3	1628	2	E90538	hypothetical prote
110	33	61.1	3871	2	T22812	hypothetical prote	183	32	59.3	3110	2	AC0116	probable virulence
111	33	61.1	8243	2	T31307	type I fatty acid	184	31.5	58.3	676	2	H96970	endo-arabinase rel
112	32	59.3	10	2	PT0291	Ig heavy chain CRD	185	31	57.4	25	2	PH1686	Ig heavy chain v r
113	32	59.3	14	2	PT0252	Ig heavy chain CRD	186	31	57.4	63	2	T16936	hypothetical prote
114	32	59.3	113	2	JT0518	Ig heavy chain V-I	187	31	57.4	82	2	G89987	hypothetical prote
115	32	59.3	47	2	H97009	hypothetical prote	188	31	57.4	105	2	S24249	Ig heavy chain v r
116	32	59.3	50	2	H81815	hypothetical prote	189	31	57.4	110	2	PH1014	Ig heavy chain v r
117	32	59.3	52	2	H81815	hypothetical prote	190	31	57.4	111	2	PH1007	Ig heavy chain v r
118	32	59.3	114	2	AH2217	hypothetical prote	191	31	57.4	117	2	PH0988	Ig heavy chain v r
119	32	59.3	117	2	S01822	Ig heavy chain V-D	192	31	57.4	111	2	S31109	Ig heavy chain - h
120	32	59.3	119	2	S24683	Ig heavy chain V6	193	31	57.4	119	2	C90351	hypothetical prote
121	32	59.3	120	2	S36273	Ig heavy chain v r	194	31	57.4	121	2	T27677	hypothetical prote
122	32	59.3	122	2	PC2398	anti-tetanus toxin	195	31	57.4	125	1	Z7BPT9	gene 50 protein -
123	32	59.3	129	2	B87775	protein C24A11.5 (	196	31	57.4	134	2	A30563	T-cell receptor be
124	32	59.3	170	2	D70158	probable signal pe	197	31	57.4	149	2	G59107	hypothetical prote
125	32	59.3	176	2	A71009	hypothetical prote	198	31	57.4	154	2	AG0967	probable exported
126	32	59.3	209	2	G75181	hypothetical prote	199	31	57.4	165	2	D83698	hypothetical prote
127	32	59.3	219	2	AF2658	conserved hypotet	200	31	57.4	174	2	F96917	N-terminal Zn-ribb
128	32	59.3	219	2	C97440	hypothetical prote	201	31	57.4	186	2	T48092	hypothetical prote
129	32	59.3	228	2	D69169	conserved hypotet	202	31	57.4	211	2	E82055	sodium-type flagel
130	32	59.3	230	2	T15861	hypothetical prote	203	31	57.4	230	2	JC5724	CpsC protein - Str
131	32	59.3	284	2	C90339	conserved hypotet	204	31	57.4	231	2	AB1038	hypothetical prote
132	32	59.3	281	2	T22670	hypothetical prote	205	31	57.4	235	2	S48924	hypothetical prote
133	32	59.3	287	2	S77309	hypothetical prote	206	31	57.4	257	2	C87550	polysaccharide dea
134	32	59.3	288	2	C70303	3-hydroxyisobutyr	207	31	57.4	258	2	H70487	cytochrome-c oxida
135	32	59.3	305	2	H90406	succinate dehydrog	208	31	57.4	259	2	D91130	hypothetical prote
136	32	59.3	311	2	T43221	serine/threonine-S	209	31	57.4	259	2	D85975	hypothetical prote
137	32	59.3	312	2	H96002	probable sugar kin	210	31	57.4	263	2	S73719	MG313 homolog H08
138	32	59.3	324	2	E64487	hypothetical prote	211	31	57.4	267	2	S38044	hypothetical prote
139	32	59.3	328	2	E72347	flagellar motor sw	212	31	57.4	267	2	S52347	hypothetical prote
140	32	59.3	329	2	B87790	protein B0207.4 (l	213	31	57.4	271	2	F64349	fatty acid metabol
141	32	59.3	331	2	T27906	hypothetical prote	214	31	57.4	279	2	B82144	hypothetical prote
142	32	59.3	337	2	S46010	hypothetical prote	215	31	57.4	287	2	T35587	hypothetical prote
143	32	59.3	338	2	A97914	choline-binding pr	216	31	57.4	287	2	I39689	hypothetical prote
144	32	59.3	340	2	G95043	hypothetical prote	217	31	57.4	293	2	T32892	probable methionyl
145	32	59.3	343	2	T26784	hypothetical prote	218	31	57.4	318	2	H86977	hypothetical prote
146	32	59.3	348	2	AG2043	RNA 3'-terminal ph	219	31	57.4	325	2	T31989	ubiquitin fusion d
147	32	59.3	348	2	C86619	D-amino acid dehydr	220	31	57.4	340	2	T32891	conserved hypotet
148	32	59.3	348	2	H72005	probable d-amino a	221	31	57.4	342	2	T33667	hypothetical prote
149	32	59.3	374	2	AH1284	cystathionine gamm	222	31	57.4	343	2	D70188	hypothetical prote
150	32	59.3	394	2	A71963	probable lipopolys	223	31	57.4	343	2	T05221	oligopeptide ABC t
151	32	59.3	416	2	A27810	tubulin beta-2 cha	224	31	57.4	344	2	AB1349	oligopeptide ABC t
152	32	59.3	455	2	A83658	UDP-N-acetylglucos	225	31	57.4	344	2	AF1719	hypothetical prote
153	32	59.3	458	2	C86860	hypothetical prote	226	31	57.4	349	2	T33263	hypothetical prote
154	32	59.3	459	2	B95114	UDP-N-acetylglucos	227	31	57.4	353	2	T19522	hypothetical prote
155	32	59.3	479	2	C97983	UDP-N-acetylglucos	228	31	57.4	359	2	H86555	hypothetical prote
156	32	59.3	484	1	ERAD12	early E2A DNA-bind	229	31	57.4	359	2	D81598	hypothetical prote
157	32	59.3	496	2	B45868	glycerol kinase (E	230	31	57.4	363	2	F97899	hypothetical prote
158	32	59.3	496	2	J05390	glycerol kinase (E	231	31	57.4	369	2	E71194	probable N2,N2-dim
159	32	59.3	497	2	E83786	glycerol kinase gl	232	31	57.4	381	2	JC7507	45K WW domain-cont
160	32	59.3	498	2	G89904	glycerol kinase [i	233	31	57.4	382	2	JC7508	45K WW domain-cont
161	32	59.3	498	2	A83635	conserved hypotet	234	31	57.4	386	2	JC7508	serine proteinase
162	32	59.3	499	2	D97000	methyl-accepting c	235	31	57.4	392	1	A30100	nitrogen fixation
163	32	59.3	500	2	G70104	hypothetical prote	236	31	57.4	393	2	D90533	alanine racemase (
164	32	59.3	521	2	E64181	probable cytochrom	237	31	57.4	399	2	AE3556	conserved hypotet
165	32	59.3	551	2	T09647	beta-glucosidase (	238	31	57.4	411	2	B96035	probable sugar upt
166	32	59.3	585	2	A84919	auxin-regulated pr	239	31	57.4	420	2	F90345	probable oxidoredu
167	32	59.3	625	2	D64107	transferrin-bindin	240	31	57.4	431	2	F64072	probable glycosylc
168	32	59.3	629	2	A30001	ribosomal protein	241	31	57.4	449	2	G97167	UDP-N-acetylglucos
169	32	59.3	630	2	S70909	transferrin-bindin	242	31	57.4	456	2	S66080	UDP-N-acetylglucos
170	32	59.3	733	1	B30001	ribosomal protein	243	31	57.4	457	2	AG1099	UDP-N-acetylglucos
171	32	59.3	735	1	FC4225	replication licens	244	31	57.4	462	2	AF1462	avrRpt2-induced pr
172	32	59.3	757	2	T33749	bacteriophage prot	245	31	57.4	463	2	T02653	rad22 protein - fi
173	32	59.3	909	2	T33749	hypothetical prote	246	31	57.4	469	2	S41496	N-acetylmuramoyl-L
174	32	59.3	926	1	A35905	endopeptidase Clp	247	31	57.4	481	2	JQ1147	hypothetical prote
175	32	59.3	930	2	AC2412	preprotein translo	248	31	57.4	493	2	T25357	hypothetical prote

249	31	57.4	495	1	S16447	NADH2 dehydrogenas	322	30.5	56.5	311	2	S66468	catechol 1,2-dioxy
250	31	57.4	495	1	S25942	NADH2 dehydrogenas	323	30.5	56.5	318	2	D95226	autolysin [impor
251	31	57.4	495	2	S43882	NADH2 dehydrogenas	324	30.5	56.5	318	2	A25634	N-acetylmuramoyl-L
252	31	57.4	510	2	D96741	hypothetical prote	325	30.5	56.5	318	2	H98090	N-acetylramamoyl-L
253	31	57.4	516	2	C82946	hypothetical prote	326	30.5	56.5	449	2	H69862	Na+-transporting A
254	31	57.4	523	1	T11916	NADH2 dehydrogenas	327	30.5	56.5	449	2	F84036	Na+-transporting A
255	31	57.4	533	1	GRBYCP	cytosine/purine tr	328	30	55.6	65	2	C41384	nicotinic acetylch
256	31	57.4	548	2	S20806	swallow protein -	329	30	55.6	81	2	AD2080	hypothetical prote
257	31	57.4	559	2	G86238	protein T10024.13	330	30	55.6	92	2	H82598	hypothetical prote
258	31	57.4	561	2	T46845	Ki-transporting Ar	331	30	55.6	104	2	A41384	hypothetical prote
259	31	57.4	565	2	E86582	efflux protein [im	332	30	55.6	105	2	PH1020	nicotinic acetylch
260	31	57.4	565	2	F72041	efflux protein - C	333	30	55.6	108	2	H96930	ig heavy chain V r
261	31	57.4	568	2	S74481	probable phosphoe	334	30	55.6	111	2	PH1659	nitrogen regulator
262	31	57.4	569	2	E81624	conserved hypotet	335	30	55.6	114	2	E95195	ig heavy chain V r
263	31	57.4	583	2	G95214	ABC transporter, A	336	30	55.6	114	2	B98062	hypothetical prote
264	31	57.4	583	2	F98078	hypothetical prote	337	30	55.6	115	1	H3HUTL	ig heavy chain V -
265	31	57.4	591	2	G97531	feruloyl-CoA synth	338	30	55.6	115	2	E27889	ig heavy chain V r
266	31	57.4	591	2	JQ2036	hypothetical 68K p	339	30	55.6	118	2	G97857	hypothetical prote
267	31	57.4	611	2	AH2750	long-chain-fatty-a	340	30	55.6	122	2	AI1234	B. subtilis Ynep p
268	31	57.4	626	2	T18733	hypothetical prote	341	30	55.6	124	2	S20784	ig heavy chain V r
269	31	57.4	631	2	S70908	transferrin-bindin	342	30	55.6	138	2	D70160	ribosomal protein
270	31	57.4	631	2	T70910	transferrin-bindin	343	30	55.6	150	2	H89931	arginine repressor
271	31	57.4	633	2	A75069	dipeptide transpor	344	30	55.6	152	2	H64243	galactoside O-acet
272	31	57.4	641	2	A71163	hypothetical prote	345	30	55.6	154	2	E69870	hypothetical prote
273	31	57.4	646	2	G70032	ABC transporter (p	346	30	55.6	158	2	H82688	hypothetical prote
274	31	57.4	654	2	S70905	transferrin-bindin	347	30	55.6	159	2	AI0772	probable exported
275	31	57.4	660	2	S70904	transferrin-bindin	348	30	55.6	175	2	G70157	hypothetical prote
276	31	57.4	686	2	T14203	NADH2 dehydrogenas	349	30	55.6	181	2	T51663	myb-related transc
277	31	57.4	700	2	T38028	hypothetical prote	350	30	55.6	183	1	TLBP84	tail fiber assembl
278	31	57.4	700	2	T32205	hypothetical prote	351	30	55.6	183	1	S13240	tail fiber assembl
279	31	57.4	703	2	AD0772	hypothetical prote	352	30	55.6	185	1	PTWBD	H+-transporting tw
280	31	57.4	709	2	G96610	probable disease r	353	30	55.6	186	1	IVBOB1	interferon beta-1
281	31	57.4	717	2	A96780	hypothetical prote	354	30	55.6	191	2	H72767	hypothetical prote
282	31	57.4	749	2	A45046	basic juvenile hor	355	30	55.6	196	2	S25784	hypothetical prote
283	31	57.4	754	2	T16182	hypothetical prote	356	30	55.6	202	2	AD3007	probable glutathio
284	31	57.4	780	2	AE0061	organic solvent to	357	30	55.6	209	2	AD3004	conserved hypotet
285	31	57.4	784	1	F64726	organic solvent to	358	30	55.6	219	2	T07931	probable GTP-bind
286	31	57.4	784	2	C85487	organic solvent to	359	30	55.6	227	2	D90512	conserved hypotet
287	31	57.4	784	2	C90836	organic solvent to	360	30	55.6	227	2	E84381	hypothetical prote
288	31	57.4	797	2	H84919	hypothetical prote	361	30	55.6	229	2	F69670	glycine betaine/ca
289	31	57.4	824	2	I49564	polycystic kidney	362	30	55.6	231	2	S26035	cytochrome-c oxida
290	31	57.4	849	2	S37350	luxN protein - Vib	363	30	55.6	245	2	S72289	ribosomal protein
291	31	57.4	857	2	E71377	probable ATP-depen	364	30	55.6	245	2	A64232	ATP-binding protei
292	31	57.4	889	2	F96637	hypothetical prote	365	30	55.6	261	2	D90562	hypothetical prote
293	31	57.4	912	2	D72644	hypothetical prote	366	30	55.6	284	2	T37996	probable aldose re
294	31	57.4	928	2	C81265	probable lipoprote	367	30	55.6	289	2	S74632	hypothetical prote
295	31	57.4	967	2	AH2660	isoleucyl-tRNA syn	368	30	55.6	292	2	B86692	hypothetical prote
296	31	57.4	967	2	F97442	isoleucyl-tRNA syn	369	30	55.6	293	2	A97396	hypothetical prote
297	31	57.4	972	2	AB3640	isoleucine-tRNA li	370	30	55.6	293	2	AB3614	hypothetical prote
298	31	57.4	978	2	D81411	probable lipoprote	371	30	55.6	294	2	F89897	conserved hypotet
299	31	57.4	984	1	DJNVCP	DNA-directed DNA p	372	30	55.6	295	2	C97357	uncharacterized co
300	31	57.4	986	2	T41809	DNA polymerase orf	373	30	55.6	307	2	F83339	probable transcrip
301	31	57.4	1045	2	B30239	hydroxymethylgluta	374	30	55.6	309	2	T33259	hypothetical prote
302	31	57.4	1132	2	AF2481	hypothetical prote	375	30	55.6	312	2	F86876	hypothetical prote
303	31	57.4	1173	2	T30308	rexa protein - Lac	376	30	55.6	312	2	G71146	hypothetical prote
304	31	57.4	1190	2	T00842	probable histidine	377	30	55.6	313	2	T04776	hypothetical prote
305	31	57.4	1203	2	D86625	subunit A of Arp-d	378	30	55.6	314	2	T21971	hypothetical prote
306	31	57.4	1207	2	T52459	sensory transducti	379	30	55.6	317	2	D75296	signal recognition
307	31	57.4	1230	2	T19999	hypothetical prote	380	30	55.6	325	2	D83366	probable transcrip
308	31	57.4	1327	2	T21268	hypothetical prote	381	30	55.6	330	2	T25940	hypothetical prote
309	31	57.4	1337	2	T30291	dextranase - Strep	382	30	55.6	330	2	T25939	hypothetical prote
310	31	57.4	1365	2	A41483	glucosyltransferas	383	30	55.6	332	2	H95043	hypothetical prote
311	31	57.4	1484	2	C97196	probable membrane	384	30	55.6	335	2	D86410	choleone binding pr
312	31	57.4	1508	2	T31098	probable dextranase	385	30	55.6	339	1	MUBPCP	protein F3M18.16 [
313	31	57.4	1553	2	T18502	hypothetical prote	386	30	55.6	339	1	MUBPCP	N-acetylmuramoyl-L
314	31	57.4	1658	2	D75489	hypothetical prote	387	30	55.6	339	2	T50263	probable arginine
315	31	57.4	1770	2	A71517	hypothetical prote	388	30	55.6	343	1	A57014	proctasin [EC 3.4.
316	31	57.4	2364	2	T40884	cytotoxin L - Clo	389	30	55.6	348	2	T26447	hypothetical prote
317	31	57.4	2399	2	H71879	toxin-like outer m	390	30	55.6	352	2	C71521	probable (G-amino
318	31	57.4	4688	2	F82885	hypothetical prote	391	30	55.6	353	2	S71965	GTP-binding regula
319	30.5	56.5	217	2	T31990	hypothetical prote	392	30	55.6	354	2	AG0617	probable bacteriop
320	30.5	56.5	310	2	B83331	catechol 1,2-dioxy	393	30	55.6	356	2	AD2945	GTP-binding protei
321	30.5	56.5	311	2	S66469	catechol 1,2-dioxy	394	30	55.6	361	2	D72384	conserved hypotet

395	30	55.6	362	2	T05167	hypothetical prote	468	30	55.6	535	2	E95929	probable methylcro
396	30	55.6	366	2	F84579	probable arginine	469	30	55.6	535	2	AF3492	methylecrotonoyl-Co
397	30	55.6	366	2	AB2893	dehydrogenase Atuo	470	30	55.6	537	2	B98299	probable acyl-CoA
398	30	55.6	366	2	F97474	hypothetical prote	471	30	55.6	538	2	B81376	probable membrane
399	30	55.6	371	2	T46421	hypothetical prote	472	30	55.6	544	2	A13266	integral membrane
400	30	55.6	373	2	E64486	ATP-dependent 26S	473	30	55.6	545	2	F64579	site-specific DNA-
401	30	55.6	374	2	E98279	hypothetical prote	474	30	55.6	549	2	AB0987	alpha,alpha-trehal
402	30	55.6	376	2	T52248	protein-arginine N	475	30	55.6	549	2	G91178	cytoplasmic trehal
403	30	55.6	379	2	D96506	hypothetical prote	476	30	55.6	549	2	H86024	cytoplasmic trehal
404	30	55.6	390	2	A88066	protein R52.3 [imp	477	30	55.6	549	2	S47739	probable alpha,alp
405	30	55.6	390	2	AE2576	hypothetical prote	478	30	55.6	556	2	T46842	K+-transporting AT
406	30	55.6	390	2	T09914	protein-arginine N	479	30	55.6	557	2	H97351	K+-transporting AT
407	30	55.6	390	2	T18640	hypothetical prote	480	30	55.6	557	2	B83962	hypothetical prote
408	30	55.6	391	2	A10524	probable fibribial	481	30	55.6	560	2	T02404	probable beta-gluc
409	30	55.6	400	2	T33073	hypothetical prote	482	30	55.6	561	2	AG2336	potassium-dependen
410	30	55.6	402	2	T25001	hypothetical prote	483	30	55.6	562	2	T34319	hypothetical prote
411	30	55.6	411	2	T26506	hypothetical prote	484	30	55.6	570	2	T28495	hypothetical prote
412	30	55.6	416	2	T20448	hypothetical prote	485	30	55.6	572	2	T28514	hypothetical prote
413	30	55.6	421	2	T25383	hypothetical prote	486	30	55.6	572	2	S73730	MG307 homolog H08
414	30	55.6	425	2	AC2092	hypothetical prote	487	30	55.6	585	2	S46034	conserved hypoteth
415	30	55.6	428	2	B82248	long-chain fatty a	488	30	55.6	602	2	E70067	hypothetical prote
416	30	55.6	429	2	AC3303	isocitrate lyase (	489	30	55.6	608	1	S28313	hypothetical prote
417	30	55.6	430	2	T35676	probable ABC-type	490	30	55.6	613	2	T15905	probable beta-gluc
418	30	55.6	434	2	AB2651	isocitrate lyase (	491	30	55.6	614	2	T01121	hypothetical prote
419	30	55.6	434	2	AB7433	ici containing pro	492	30	55.6	614	2	T30973	ABC transporter (p
420	30	55.6	434	2	F81920	hypothetical integ	493	30	55.6	622	2	B70074	hypothetical prote
421	30	55.6	440	2	D69596	branched-chain ami	494	30	55.6	622	2	T27155	hypothetical prote
422	30	55.6	443	2	C71904	anaerobic c4-dicar	495	30	55.6	626	2	B72281	hypothetical prote
423	30	55.6	443	2	D64610	dicarboxylate memb	496	30	55.6	630	2	T05433	glucan 1,6-alpha-1
424	30	55.6	443	2	T17868	hypothetical prote	497	30	55.6	641	2	A55549	ABC transporter (p
425	30	55.6	445	2	I49458	acetylcholine rece	498	30	55.6	648	2	B84139	hypothetical prote
426	30	55.6	446	2	T26039	hypothetical prote	499	30	55.6	678	2	F70451	hypothetical prote
427	30	55.6	453	2	F75206	maltose-binding pe	500	30	55.6	692	2	T32980	hypothetical prote
428	30	55.6	456	1	ACCHAN	nicotinic acetylch	501	30	55.6	710	2	T21339	hypothetical prote
429	30	55.6	457	1	ACBOA1	nicotinic acetylch	502	30	55.6	731	2	T18524	hypothetical prote
430	30	55.6	457	1	ACHUA1	nicotinic acetylch	503	30	55.6	738	2	T45916	copper-transportin
431	30	55.6	457	1	A24383	nicotinic acetylch	504	30	55.6	745	1	H64653	copper-transportin
432	30	55.6	457	2	S08162	nicotinic acetylch	505	30	55.6	745	2	A71941	vacu protein (impo
433	30	55.6	457	2	S13872	nicotinic acetylch	506	30	55.6	745	2	G84995	probable cation-tr
434	30	55.6	464	2	T24011	hypothetical prote	507	30	55.6	785	2	E81320	probable TonB-depe
435	30	55.6	464	2	B86079	probable glycopori	508	30	55.6	789	2	H83354	probable integral
436	30	55.6	464	2	C91232	probable glycoprot	509	30	55.6	823	2	B81282	large hellicase-rel
437	30	55.6	472	2	B82492	tryptophanase VCA0	510	30	55.6	847	2	T52436	protein F7G19.9 [i
438	30	55.6	472	2	B86730	dipeptidase [impor	511	30	55.6	912	2	B75127	protein F7G19.8 [i
439	30	55.6	472	2	C86387	hypothetical prote	512	30	55.6	936	2	D86222	isooleucine-tRNA l1
440	30	55.6	477	2	G70427	biotin carboxylase	513	30	55.6	938	1	SYECIT	isooleucine-tRNA l1
441	30	55.6	478	2	S61192	hypothetical prote	514	30	55.6	938	2	D85483	isooleucine tRNA sy
442	30	55.6	480	2	F84454	hypothetical prote	515	30	55.6	938	2	E90632	isooleucine-tRNA l1
443	30	55.6	482	2	S15748	nitrogenase (EC 1.	516	30	55.6	938	2	AH0058	isooleucine-tRNA l1
444	30	55.6	483	2	F84454	hypothetical prote	517	30	55.6	941	2	S78633	isooleucyl-cRNA syn
445	30	55.6	484	2	G86475	unknown protein, 1	518	30	55.6	944	2	AI0507	probable membrane
446	30	55.6	489	2	F83109	probable phosphate	519	30	55.6	949	2	S54020	probable DNA-direc
447	30	55.6	495	2	T31944	hypothetical prote	520	30	55.6	992	2	T28421	tetratricopeptide
448	30	55.6	496	2	B64591	aminopeptidase a/i	521	30	55.6	1039	2	T43678	tetratricopeptide
449	30	55.6	496	2	F71920	aminopeptidase - H	522	30	55.6	1039	2	T38447	dotA protein - Leg
450	30	55.6	498	2	AG0988	probable low-affin	523	30	55.6	1048	1	S61388	hypothetical prote
451	30	55.6	498	2	AI0482	phosphate transpor	524	30	55.6	1277	2	E97580	synaptic scaffold
452	30	55.6	499	2	E91174	low-affinity phosph	525	30	55.6	1277	2	T14152	probable membrane
453	30	55.6	499	2	E86020	low-affinity phosph	526	30	55.6	1308	2	E71622	protoporphyrin IX
454	30	55.6	499	2	S47713	pitA protein - Eec	527	30	55.6	1321	2	E69129	hypothetical prote
455	30	55.6	503	2	H81056	PgiA family protei	528	30	55.6	1465	2	A70199	surface layer prot
456	30	55.6	503	2	G95251	conserved hypoteth	529	30	55.6	1465	2	S68553	probable GTPase-ac
457	30	55.6	503	2	D98116	hypothetical prote	530	30	55.6	1524	2	T14106	hypothetical prote
458	30	55.6	506	2	F88954	protein K04Fl.14 [	531	30	55.6	1822	2	S64604	hypothetical prote
459	30	55.6	508	2	T32847	phosphate transpor	532	30	55.6	1967	2	T33162	hypothetical prote
460	30	55.6	513	2	T43867	hypothetical prote	533	30	55.6	2030	2	E86342	hypothetical prote
461	30	55.6	525	2	A59259	sensory neuron mem	534	30	55.6	2178	2	S55805	alpha-toxin - Clos
462	30	55.6	526	2	E88940	protein C05P4.9 [i	535	30	55.6	2178	2	AE2136	peptide synthetase
463	30	55.6	526	2	AH0820	conserved hypoteth	536	30	55.6	2617	2	S52136	hypothetical prote
464	30	55.6	529	2	F70550	probable accu1 pro	537	30	55.6	3165	2	E71086	hypothetical prote
465	30	55.6	532	2	T52442	hypothetical prote	538	30	55.6	4436	2	S71086	hypothetical prote
466	30	55.6	533	2	AE2984	3-methylcrotonoyl-	539	30	55.6	4868	2	S54161	ryanodine-binding
467	30	55.6	535	2	C83395	probable acyl-CoA	540	30	55.6	4967	2	S72269	ryanodine receptor

541	30	55.6	4969	2	A37113	ryanodine receptor	614	29	53.7	252	2	D86075	hypothetical prote
542	30	55.6	5369	2	T44807	myosubtilin synth	615	29	53.7	254	2	S02066	transcription regu
543	29.5	54.6	338	2	T28779	hypothetical prote	616	29	53.7	256	2	S54803	mezozoite surface
544	29.5	54.6	423	2	AH0334	probable long-chain	617	29	53.7	256	2	G97031	TPK-repeat contain
545	29.5	54.6	437	2	AB0805	long-chain fatty a	618	29	53.7	258	2	T50676	bacteriorhodopsin
546	29.5	54.6	448	2	F65007	long-chain fatty a	619	29	53.7	259	2	S14731	bacteriorhodopsin
547	29.5	54.6	448	2	D85876	long-chain fatty a	620	29	53.7	260	2	A34178	bacteriorhodopsin
548	29.5	54.6	448	2	C91032	long-chain fatty a	621	29	53.7	261	2	D71508	probable glutamine
549	29.5	54.6	509	2	T31797	hypothetical prote	622	29	53.7	263	2	C81667	amino acid ABC tra
550	29.5	54.6	714	2	T31819	hypothetical prote	623	29	53.7	264	2	AE2134	hypothetical prote
551	29	53.7	35	2	E70243	hypothetical prote	624	29	53.7	266	2	AB1404	B. subtilis ybaF p
552	29	53.7	63	2	F95059	hypothetical prote	625	29	53.7	266	2	A11779	B. subtilis ybaF p
553	29	53.7	70	2	T11209	isocitrate lyase (	626	29	53.7	270	2	S51269	inosine kinase (SC
554	29	53.7	78	2	G64333	hypothetical prote	627	29	53.7	270	2	C86794	hypothetical prote
555	29	53.7	89	2	T18817	hypothetical prote	628	29	53.7	272	2	E84379	prephenate dehydra
556	29	53.7	92	2	S56009	Ig heavy chain var	629	29	53.7	275	2	T26235	hypothetical prote
557	29	53.7	96	2	A88086	protein T11F1.3 (I	630	29	53.7	275	2	D96926	prephenate dehydro
558	29	53.7	99	2	S62029	hypothetical prote	631	29	53.7	275	2	T43119	hypothetical prote
559	29	53.7	102	2	PH1491	Ig heavy chain v r	632	29	53.7	278	2	B82388	probable maltose o
560	29	53.7	103	2	F75010	hypothetical prote	633	29	53.7	278	2	D86277	F14L17.8 protein -
561	29	53.7	103	2	G71141	hypothetical prote	634	29	53.7	281	2	AF2090	hypothetical prote
562	29	53.7	108	2	PH1006	Ig heavy chain v r	635	29	53.7	281	2	S54804	mezozoite surface
563	29	53.7	111	2	S13687	Ig heavy chain v r	636	29	53.7	282	2	AB1266	prephenate dehydra
564	29	53.7	117	2	B34964	Ig heavy chain pre	637	29	53.7	282	2	AB1629	prephenate dehydra
565	29	53.7	118	2	A49026	Ig heavy chain v r	638	29	53.7	282	2	B38771	reaction center pr
566	29	53.7	119	2	S24655	Ig heavy chain v r	639	29	53.7	282	2	G98066	hypothetical prote
567	29	53.7	121	2	C90510	hypothetical prote	640	29	53.7	284	2	AB1141	hypothetical prote
568	29	53.7	124	2	B87345	hypothetical prote	641	29	53.7	284	2	AG1499	hypothetical prote
569	29	53.7	133	2	F64700	biopolymer transpo	642	29	53.7	289	2	T40596	probable DNA repa
570	29	53.7	148	2	S75431	hypothetical prote	643	29	53.7	289	2	A70475	H+-transporting tw
571	29	53.7	150	2	I47200	Ig heavy chain var	644	29	53.7	291	2	T47475	hypothetical prote
572	29	53.7	152	2	B84409	hypothetical prote	645	29	53.7	291	2	T23595	hypothetical prote
573	29	53.7	162	2	F95165	hypothetical prote	646	29	53.7	293	2	T00099	glycosyltransferas
574	29	53.7	162	2	E98031	hypothetical prote	647	29	53.7	294	2	AC3642	2,5-diketo-D-gluco
575	29	53.7	168	2	JC1383	hypothetical 19.1K	648	29	53.7	294	2	D64175	glycosyltransferas
576	29	53.7	170	2	C83481	hypothetical prote	649	29	53.7	304	2	A84811	hypothetical prote
577	29	53.7	173	2	G90351	hypothetical prote	650	29	53.7	305	2	S77033	hypothetical prote
578	29	53.7	175	2	S42095	capsid protein - o	651	29	53.7	307	2	G75280	homoserine kinase
579	29	53.7	179	2	F75392	hypothetical prote	652	29	53.7	307	2	G69501	UDP-glucose 4-epim
580	29	53.7	184	2	A13539	hypothetical prote	653	29	53.7	316	2	S63385	hypothetical prote
581	29	53.7	186	2	S76659	hypothetical prote	654	29	53.7	318	2	AB1792	transcription regu
582	29	53.7	187	2	E86478	protein F15O4.9 (i	655	29	53.7	321	2	T21248	hypothetical prote
583	29	53.7	194	2	T24491	hypothetical prote	656	29	53.7	325	2	C71040	hypothetical prote
584	29	53.7	195	2	C83076	type 4 fibrinall bi	657	29	53.7	326	2	H96623	probable Aldo/keto
585	29	53.7	198	2	JQ0864	hypothetical 21.9K	658	29	53.7	327	2	G96623	probable Aldo/keto
586	29	53.7	201	2	F69988	hypothetical prote	659	29	53.7	328	1	Q9BEF6	probable HVI44 prote
587	29	53.7	203	2	B84859	hypothetical prote	660	29	53.7	328	2	AF2469	hypothetical prote
588	29	53.7	204	2	C47686	bacteriorhodopsin-	661	29	53.7	332	2	S19835	probable serine-ap
589	29	53.7	207	2	AE0434	probable exported	662	29	53.7	333	2	AD2608	aldo-keto reductas
590	29	53.7	207	2	B70708	hypothetical prote	663	29	53.7	333	2	H87620	oxidoreductase, al
591	29	53.7	213	1	EP80	phosphatidylcholin	664	29	53.7	337	2	T31711	hypothetical prote
592	29	53.7	214	1	KABQSB	alpha-s1-casein pr	665	29	53.7	339	2	AF0329	probable membrane
593	29	53.7	215	2	H86737	conserved hypotet	666	29	53.7	347	2	A84516	probable replicat1
594	29	53.7	220	2	F64332	hypothetical prote	667	29	53.7	348	2	C26720	CAMP-regulated D2
595	29	53.7	223	2	D82556	cytidylate kinase	668	29	53.7	353	2	T24616	hypothetical prote
596	29	53.7	228	2	AH1841	ribonuclease III (	669	29	53.7	356	2	H72395	probable aldose 1-
597	29	53.7	230	2	F65192	yshA protein - Es	670	29	53.7	356	2	F89977	hypothetical prote
598	29	53.7	231	2	B82820	two-component syst	671	29	53.7	358	2	T26231	hypothetical prote
599	29	53.7	231	2	C69104	hypothetical prote	672	29	53.7	362	2	S12933	killer toxin K2 pr
600	29	53.7	231	2	B84124	hypothetical prote	673	29	53.7	362	2	T22204	hypothetical prote
601	29	53.7	235	2	S25759	Ig lambda chain -	674	29	53.7	369	2	C97390	aldo/keto reductas
602	29	53.7	238	2	I64038	fatty acid metabol	675	29	53.7	374	2	A70361	acri flavin reasista
603	29	53.7	239	2	AF0261	hypothetical prote	676	29	53.7	375	2	H96633	RNA polymerase sub
604	29	53.7	243	2	G99867	hypothetical prote	677	29	53.7	381	2	S74777	hypothetical prote
605	29	53.7	244	2	H84853	hypothetical prote	678	29	53.7	382	2	A13406	permease (imported
606	29	53.7	249	2	S62709	H+-transporting tw	679	29	53.7	383	2	G89902	competence-damage
607	29	53.7	250	2	A86566	glutamine binding	680	29	53.7	386	2	S64614	probable membrane
608	29	53.7	250	2	F72057	amino acid ABC tra	681	29	53.7	386	2	T28176	hypothetical prote
609	29	53.7	250	2	A10258	probable phage pro	682	29	53.7	389	2	S73942	oligopeptide trans
610	29	53.7	250	2	D70242	conserved hypotet	683	29	53.7	392	2	E86799	prophage p13 prote
611	29	53.7	251	2	JQ2299	coat protein - pep	684	29	53.7	401	2	T52250	probable alanine-g
612	29	53.7	251	2	S31874	AR1 protein - pepp	685	29	53.7	401	2	D30962	probable transport
613	29	53.7	252	2	E91228	hypothetical prote	686	29	53.7	401	2	D85810	probable transport

687	29	53.7	401	2	F64956	membrane protein y	760	29	53.7	617	2	AB1167	phosphotransferase
688	29	53.7	404	2	AF0034	probable integral	761	29	53.7	620	2	T32966	hypothetical prote
689	29	53.7	407	2	A41106	GTP-binding protei	762	29	53.7	627	2	A81818	N-acetylmuramoyl-L
690	29	53.7	407	2	T39970	guanine nucleotide	763	29	53.7	631	2	T15370	hypothetical prote
691	29	53.7	408	1	VCWVSR	env polyprotein -	764	29	53.7	641	2	F81408	ABC-type transmemb
692	29	53.7	408	2	A86008	hypothetical prote	765	29	53.7	648	2	T37581	probable serine-th
693	29	53.7	408	2	H91161	hypothetical prote	766	29	53.7	651	2	G71697	probable soluble l
694	29	53.7	408	2	H65137	hypothetical 45.1	767	29	53.7	655	2	T32472	hypothetical prote
695	29	53.7	409	2	AF3271	probable allantoin	768	29	53.7	657	2	E96949	serine/threonine p
696	29	53.7	421	2	AF0751	probable membrane	769	29	53.7	661	2	F96665	protein F22C12.14
697	29	53.7	421	2	AB2189	hypothetical prote	770	29	53.7	665	2	F86181	protein F13M7.17 [
698	29	53.7	422	2	T01197	pectin acetyl ester	771	29	53.7	666	2	H99581	protein dim-1 [imp
699	29	53.7	422	2	E83984	isocitrate lyase B	772	29	53.7	667	2	T20799	hypothetical prote
700	29	53.7	427	2	AC1627	N-acetylmuramoyl-L	773	29	53.7	680	2	T23813	hypothetical prote
701	29	53.7	427	2	A11264	isocitrate lyase (	774	29	53.7	692	2	AB0124	probable TonB-depe
702	29	53.7	434	1	WZECIC	isocitrate lyase (	775	29	53.7	707	2	D86565	oligopeptide bindi
703	29	53.7	434	2	AE1011	isocitrate lyase (	776	29	53.7	707	2	E72059	peptide ABC transp
704	29	53.7	434	2	E91245	isocitrate lyase (	777	29	53.7	712	2	T33231	hypothetical prote
705	29	53.7	434	2	B97018	xre family DNA-bin	778	29	53.7	715	2	B43943	ATP-dependent memb
706	29	53.7	435	2	AE0453	isocitrate lyase (	779	29	53.7	715	2	G86634	hypothetical prote
707	29	53.7	435	2	C95975	probable polysacch	780	29	53.7	715	2	AF1829	two-component hybr
708	29	53.7	437	2	D90289	isocitrate lyase (	781	29	53.7	721	2	B83820	hypothetical prote
709	29	53.7	437	2	B82288	isocitrate lyase v	782	29	53.7	722	1	VCPVCN	coat protein VP1 -
710	29	53.7	439	2	C86093	isocitrate lyase (	783	29	53.7	722	1	VCPVME	coat protein VP1 -
711	29	53.7	442	2	D49757	polyglycerol phosp	784	29	53.7	727	1	VCPVIF	coat protein VP1 -
712	29	53.7	442	2	G90388	thermopsine precu	785	29	53.7	727	1	VCPVFP	coat protein VP1 -
713	29	53.7	446	2	H97091	chitinase family p	786	29	53.7	731	2	B70770	probable glgB prot
714	29	53.7	448	2	H70320	transcription regu	787	29	53.7	737	1	VCPVCD	hypothetical prote
715	29	53.7	453	2	G89045	protein B0238.2 [i	788	29	53.7	737	2	T41730	enhancer-of-reste
716	29	53.7	454	2	D91141	probable C4-dicarb	789	29	53.7	746	2	G02838	coat protein VP1 -
717	29	53.7	454	2	G85986	probable transport	790	29	53.7	748	1	VCPVCP	two-component hybr
718	29	53.7	455	2	E65114	Putative cryptic C	791	29	53.7	759	2	AB2052	hypothetical prote
719	29	53.7	458	2	E72244	conserved hypothet	792	29	53.7	760	2	T25769	hypothetical prote
720	29	53.7	459	2	S70702	maackiain detoxifi	793	29	53.7	768	2	A29066	DNA ligase (ATP) (
721	29	53.7	461	2	T47782	hypothetical prote	794	29	53.7	781	2	E87493	TonB-dependent rec
722	29	53.7	464	2	C75470	isocitrate lyase -	795	29	53.7	787	2	D82323	organic solvent to
723	29	53.7	466	2	G87612	cytosol aminopepti	796	29	53.7	790	2	D83064	hypothetical prote
724	29	53.7	466	2	T02324	hypothetical prote	797	29	53.7	805	2	S50277	ubiquitin-specific
725	29	53.7	466	2	F95041	hypothetical prote	798	29	53.7	819	2	E70105	PI15 protein homol
726	29	53.7	472	2	B90100	SNF-related kinase	799	29	53.7	835	2	T47521	respiratory burst
727	29	53.7	475	2	S54511	hypothetical prote	800	29	53.7	869	2	C56617	cfac protein precu
728	29	53.7	476	2	B67664	protein integral m	801	29	53.7	905	1	A27410	nucleotide diphosp
729	29	53.7	478	1	S60754	transcription fact	802	29	53.7	913	2	G64110	hypothetical prote
730	29	53.7	478	1	T03134	helicase-primase c	803	29	53.7	919	2	B72263	isoleucine-tRNA li
731	29	53.7	486	1	TVHUEG	transforming prote	804	29	53.7	934	1	A34372	complement C6 prec
732	29	53.7	488	2	AF1557	phytoene dehydroge	805	29	53.7	939	2	AB0032	two-component sens
733	29	53.7	491	2	B70414	NADH2 dehydrogenas	806	29	53.7	940	2	C84947	isoleucine-tRNA li
734	29	53.7	492	2	H95199	ABC transporter, A	807	29	53.7	949	2	D82293	isoleucyl-tRNA syn
735	29	53.7	505	2	F82075	conserved hypothet	808	29	53.7	952	2	AG1209	B. subtilis YfhO p
736	29	53.7	513	2	F85095	hypothetical prote	809	29	53.7	988	2	A40628	probable transposa
737	29	53.7	513	2	T21887	hypothetical prote	810	29	53.7	993	2	C82687	glycine decarboxyl
738	29	53.7	515	2	JC7533	inulinase (EC 3.2.	811	29	53.7	1004	2	A39611	probable GTP-bindi
739	29	53.7	517	2	D86804	sensor protein kin	812	29	53.7	1021	2	E64576	hypothetical prote
740	29	53.7	520	2	B75332	extracellular solu	813	29	53.7	1034	2	F71460	probable outer mem
741	29	53.7	531	1	JS0723	cytochrome P450 AL	814	29	53.7	1036	2	T23845	hypothetical prote
742	29	53.7	534	2	H71069	probable nodulatio	815	29	53.7	1036	2	B69368	hypothetical prote
743	29	53.7	534	2	T26079	hypothetical prote	816	29	53.7	1041	2	T31437	middle wall protei
744	29	53.7	563	2	F95076	sensor histidine k	817	29	53.7	1084	2	A28555	integrin alpha cha
745	29	53.7	563	2	C97944	histidine kinase (	818	29	53.7	1144	2	A36968	PI-like adhesin pr
746	29	53.7	567	2	B89900	proline-tRNA ligas	819	29	53.7	1156	2	I38005	M130 antigen precu
747	29	53.7	571	2	T02213	NBS-LRR type resis	820	29	53.7	1161	2	S72645	pi1y1 protein - Pa
748	29	53.7	572	1	B43675	64K protein - infe	821	29	53.7	1291	2	T21267	hypothetical prote
749	29	53.7	577	2	T40380	major facilitator	822	29	53.7	1307	2	T17453	ERG-associated pro
750	29	53.7	584	2	F49594	capsid protein VP2	823	29	53.7	1320	2	E59092	hypothetical prote
751	29	53.7	588	2	S70900	ABC-type transport	824	29	53.7	1324	1	VGIH59	E2 glycoprotein pr
752	29	53.7	593	2	S75352	ABC-type transport	825	29	53.7	1353	1	JQ2168	E2 glycoprotein pr
753	29	53.7	595	2	B82231	transport ATP-bind	826	29	53.7	1360	2	F96596	hypothetical prote
754	29	53.7	599	2	B83241	hypothetical prote	827	29	53.7	1361	2	S29998	surface protein -
755	29	53.7	609	1	FFGO	alpha-fetoprotein	828	29	53.7	1362	2	A37474	surface glycoprote
756	29	53.7	609	1	FFHU	alpha-fetoprotein	829	29	53.7	1363	1	VGIHQU	E2 glycoprotein pr
757	29	53.7	609	2	JC4258	alpha-fetoprotein	830	29	53.7	1363	1	VGIHVA	E2 glycoprotein pr
758	29	53.7	609	2	JC7819	metalloproteinase	831	29	53.7	1363	1	VGIHFI	E2 glycoprotein pr
759	29	53.7	611	1	FPRT	alpha-fetoprotein	832	29	53.7	1363	1	VGIHL9	E2 glycoprotein pr



833	29	53.7	1363	1	VG1HLY	E2 glycoprotein pr	906	28	51.9	150	2	S39980	hemoglobin II alph
834	29	53.7	1363	1	VG1HNM	E2 glycoprotein pr	907	28	51.9	151	2	S68222	M-caveolin - mouse
835	29	53.7	1363	2	S44241	surface protein -	908	28	51.9	152	2	S72685	hypothetical prote
836	29	53.7	1363	2	J40240	dextranucrase (EC	909	28	51.9	152	2	T16760	hypothetical prote
837	29	53.7	1375	2	JT0345	E2 glycoprotein pr	910	28	51.9	153	2	S48998	hypothetical prote
838	29	53.7	1376	1	JQ1534	E2 glycoprotein pr	911	28	51.9	154	2	S17149	rusicicvanin - Thio
839	29	53.7	1376	1	VG1HJ2	polyprotein - Arab	912	28	51.9	155	1	CUBCRT	rusicicvanin - Thio
840	29	53.7	1390	2	T31353	polymorphic membra	913	28	51.9	155	2	S29825	rusicicvanin - Thio
841	29	53.7	1460	2	D81675	hypothetical prote	914	28	51.9	158	2	E90198	multidrug resistan
842	29	53.7	1573	2	T21219	DNA-directed RNA p	915	28	51.9	164	2	C69842	hypothetical prote
843	29	53.7	1574	2	G70466	S-layer protein -	916	28	51.9	166	2	T29641	neurotensin precu
844	29	53.7	1664	2	T18262	serine/threonine k	917	28	51.9	170	1	UNDG	hypothetical prote
845	29	53.7	1808	2	AB1847	SEC7 protein - yea	918	28	51.9	185	2	T08543	conserved hypotet
846	29	53.7	2009	2	S49764	probable ATP-depen	919	28	51.9	189	2	E90157	hypothetical prote
847	29	53.7	2172	2	T00936	hypothetical prote	920	28	51.9	189	2	T31864	hypothetical prote
848	29	53.7	2245	2	T21087	hypothetical prote	921	28	51.9	190	2	AD2332	hypothetical prote
849	29	53.7	2245	2	T21086	genome polyprotein	922	28	51.9	191	2	E90305	hypothetical prote
850	29	53.7	2264	1	GNVVTB	Notch homolog prot	923	28	51.9	193	2	H71881	hypothetical prote
851	29	53.7	2352	2	T30201	hyperplastic discs	924	28	51.9	194	2	E97220	transcription regu
852	29	53.7	2657	2	T18497	polyprotein - marm	925	28	51.9	196	2	D75137	hypothetical prote
853	29	53.7	2895	2	T08437	probable polyketid	926	28	51.9	201	2	T47113	procatenulate 3,
854	29	53.7	2970	2	T08839	ryanodine receptor	927	28	51.9	201	2	E64633	hypothetical prote
855	29	53.7	4151	2	G70944	ryanodine-binding	928	28	51.9	202	2	B61090	hypothetical prote
856	29	53.7	4869	2	S66572	rifamycin polyketi	929	28	51.9	202	2	B86447	hypothetical prote
857	29	53.7	5037	1	A54161	1,4-dihydroxy-2-na	930	28	51.9	204	2	S30539	proteaseome endope
858	29	53.7	5069	2	T17464	hypothetical prote	931	28	51.9	205	2	S54040	hypothetical prote
859	28.5	52.8	305	2	AG0013	hypothetical prote	932	28	51.9	206	2	B71821	hypothetical prote
860	28.5	52.8	347	2	T25586	GTP-binding protei	933	28	51.9	206	2	H64697	hypothetical prote
861	28.5	52.8	426	2	T48424	glutamyl-tRNAGln a	934	28	51.9	206	2	B28439	maturase-related h
862	28.5	52.8	438	2	B75563	amidase slr0877 -	935	28	51.9	208	2	A54589	proteaseome endope
863	28.5	52.8	478	2	D97266	glutamyl-tRNA(Gln)	936	28	51.9	214	2	D82839	hemolysin III prot
864	28.5	52.8	483	1	S77264	glu-trNAGln amidot	937	28	51.9	215	2	I52906	proteaseome subunit
865	28.5	52.8	483	2	AC1294	probable Glu-tRNA(	938	28	51.9	219	2	T18797	hypothetical prote
866	28.5	52.8	483	2	AI1665	Ig H chain V-D-J r	939	28	51.9	219	2	AD2202	hypothetical prote
867	28.5	52.8	485	2	F97228	Ig lambda chain V	940	28	51.9	220	2	B64681	hypothetical prote
868	28.5	52.8	497	2	T35815	hypothetical prote	941	28	51.9	220	2	B71832	nicotinamide monon
869	28	51.9	14	2	PH1601	hypothetical prote	942	28	51.9	221	2	C97253	fof1-type ATP synt
870	28	51.9	25	2	A49038	Ig heavy chain V-I	943	28	51.9	224	2	AH0599	hypothetical tetr-
871	28	51.9	25	2	A83679	Ig heavy chain V-I	944	28	51.9	227	2	S70883	hypothetical prote
872	28	51.9	60	2	JT0512	ferredoxin 2(4Fe-4	945	28	51.9	227	2	AB1593	B. subtilis PBSX p
873	28	51.9	63	1	FERF1P	hypothetical prote	946	28	51.9	227	2	B90738	probable transcrip
874	28	51.9	65	2	G81292	hypothetical prote	947	28	51.9	227	2	C85588	probable transcrip
875	28	51.9	95	2	A86801	hypothetical prote	948	28	51.9	227	2	D64816	probable transcrip
876	28	51.9	97	2	T18173	hypothetical prote	949	28	51.9	228	2	H69399	hypothetical prote
877	28	51.9	101	2	S37929	hypothetical prote	950	28	51.9	229	2	S44217	coat protein - tom
878	28	51.9	101	2	T17954	hypothetical prote	951	28	51.9	229	2	H75205	hypothetical prote
879	28	51.9	105	2	S57104	probable membrane	952	28	51.9	229	2	E90271	hypothetical prote
880	28	51.9	106	1	L4HJML	Ig lambda chain V-	953	28	51.9	229	2	C90285	hypothetical prote
881	28	51.9	106	1	S30697	Cyay protein - Esc	954	28	51.9	229	2	C90298	hypothetical prote
882	28	51.9	106	2	AG0919	Cyay protein limpo	955	28	51.9	231	2	D81283	hypothetical prote
883	28	51.9	106	2	A91221	hypothetical prote	956	28	51.9	231	2	AF2536	hypothetical prote
884	28	51.9	107	2	C86067	hypothetical prote	957	28	51.9	232	2	A97748	hypothetical prote
885	28	51.9	107	2	C86127	hypothetical prote	958	28	51.9	232	2	A86344	protein T2211.8 [
886	28	51.9	108	2	G91285	hypothetical prote	959	28	51.9	233	2	S66732	probable membrane
887	28	51.9	109	2	C30515	Ig heavy chain V r	960	28	51.9	234	2	A82280	hypothetical prote
888	28	51.9	109	2	G71077	hypothetical prote	961	28	51.9	235	2	S39736	ywfC protein - Bac
889	28	51.9	109	2	S33836	hypothetical prote	962	28	51.9	235	2	H85564	hypothetical prote
890	28	51.9	110	2	T00142	hypothetical prote	963	28	51.9	235	2	C90714	hypothetical prote
891	28	51.9	111	2	AH1833	hypothetical prote	964	28	51.9	235	2	C64799	hypothetical prote
892	28	51.9	117	2	C59092	hypothetical prote	965	28	51.9	238	2	A46130	fiber protein E6 (
893	28	51.9	118	2	S38717	Ig heavy chain V r	966	28	51.9	239	2	E71343	hypothetical prote
894	28	51.9	119	2	PL0086	Ig heavy chain V r	967	28	51.9	241	1	QOCW2	coat protein - abu
895	28	51.9	119	2	PL0085	Ig heavy chain V r	968	28	51.9	241	2	C64006	probable S-adenosy
896	28	51.9	122	2	T28977	hypothetical prote	969	28	51.9	241	2	S65062	fiber protein E6 (
897	28	51.9	122	2	F75316	conserved hypotet	970	28	51.9	242	2	S06942	hypothetical prote
898	28	51.9	132	2	B69889	hypothetical prote	971	28	51.9	242	2	S14154	ribosomal protein
899	28	51.9	133	2	A91192	hypothetical prote	972	28	51.9	243	2	G90186	conserved hypotet
900	28	51.9	135	2	I37778	Ig variable region	973	28	51.9	243	2	T12734	structural protein
901	28	51.9	140	2	E95094	MutT/nudix family	974	28	51.9	245	2	A69148	hypothetical prote
902	28	51.9	140	2	A97962	conserved hypotet	975	28	51.9	246	2	S65063	fiber protein E6 (
903	28	51.9	143	2	AG0418	conserved hypotet	976	28	51.9	247	1	QOCVR1	coat protein - tom
904	28	51.9	147	2	AF0799	probable sugar pho	977	28	51.9	247	2	B71684	virb8 protein (vir
905	28	51.9	147	2	F70216	hypothetical prote	978	28	51.9	249	2	T11932	H+-transporting tw

979 28 51.9 250 2 A61153 spectinomycin aden  
980 28 51.9 250 2 A56572 homeotic protein H  
981 28 51.9 251 1 JQ1869 coat protein - tom  
982 28 51.9 251 1 QQCVP2 coat protein - pot  
983 28 51.9 251 1 QQCVS2 coat protein - squ  
984 28 51.9 251 2 T21104 minor tail protein  
985 28 51.9 251 2 T21114 hypothetical prote  
986 28 51.9 252 2 S08054 hypothetical prote  
987 28 51.9 252 2 P89869 conserved hypothet  
988 28 51.9 253 2 S12059 DNA-3-methyladenin  
989 28 51.9 254 2 A69187 hypothetical prote  
990 28 51.9 255 2 E71967 hypothetical prote  
991 28 51.9 256 1 JQ1886 coat protein - tom  
992 28 51.9 256 2 JQ2326 coat protein - Ind  
993 28 51.9 256 2 S58346 coat protein VI -  
994 28 51.9 257 2 S58108 26S proteasome reg  
995 28 51.9 258 1 QQOMC1 coat protein - cas  
996 28 51.9 258 1 VCOMCN coat protein - cas  
997 28 51.9 258 2 S25624 coat protein - cas  
998 28 51.9 258 2 S25622 coat protein - cas  
999 28 51.9 258 2 S25623 coat protein - cas  
1000 28 51.9 258 2 P47116 trifoletoxin synth

## ALIGNMENTS

RESULT 1  
D97168  
uncharacterized protein, CGEB homolog [imported] - Clostridium acetobutylicum  
C:Species: Clostridium acetobutylicum  
C:Date: 14-Sep-2001 #sequence\_revision 14-Sep-2001 #text\_change 09-Jul-2004  
C:Accession: D97168  
R:Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,  
J. Bacteriol. 183, 4823-4838, 2001  
A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo  
A:Reference number: A96900; MUID:21359325; PMID:21359325  
A:Accession: D97168  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-456 <KUR>  
A:Cross-references: UNIPROT:Q97H36; UNIPARC:UPI00000CA438; GB:AE001437; PIDN:AAK80135.1;  
A:Experimental source: Clostridium acetobutylicum ATCC824  
C:Genetics:  
A:Gene: CAC2177

Query Match 79.6%; Score 43; DB 2; Length 456;  
Best Local Similarity 70.0%; Pred. No. 3.1;  
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 VKLGTYFDS 10  
:  
Db 380 IKFNTYFDS 389

RESULT 2  
E41287  
Ig heavy chain precursor V-V region (257-D) (anti-HIV-1) - human  
C:Species: Homo sapiens (man)  
C:Date: 21-Apr-1992 #sequence\_revision 21-Apr-1992 #text\_change 21-Jan-2000  
C:Accession: E41287  
R:Andris, J.S.; Johnson, S.; Zolla-Pazner, S.; Capra, J.D.  
Proc. Natl. Acad. Sci. U.S.A. 88, 7783-7787, 1991  
A:Title: Molecular characterization of five human anti-human immunodeficiency virus type  
A:Reference number: A41287; MUID:91352074; PMID:1909030  
A:Accession: E41287  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-144 <AND>  
A:Cross-references: UNIPARC:UPI0000113A7E; GB:M67504; NID:g185413; PIDN:AAAS2946.1; PID:  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotrimer; immunoglobulin

F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 74.1%; Score 40; DB 2; Length 144;  
Best Local Similarity 75.0%; Pred. No. 3.5;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 KLGTYYFD 9  
:  
Db 117 RLGTYYFD 124

RESULT 3  
B97033  
uncharacterized protein, related to enterotoxins of other Clostridiales [imported] - Clo  
C:Species: Clostridium acetobutylicum  
C:Date: 14-Sep-2001 #sequence\_revision 14-Sep-2001 #text\_change 09-Jul-2004  
C:Accession: B97033  
R:Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,  
J. Bacteriol. 183, 4823-4838, 2001  
A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo  
A:Reference number: A96900; MUID:21359325; PMID:21359325  
A:Accession: B97033  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-2817 <KUR>  
A:Cross-references: UNIPROT:Q97K42; UNIPARC:UPI00000CA0A0; GB:AE001437; PIDN:AAK79053.1;  
A:Experimental source: Clostridium acetobutylicum ATCC824  
C:Genetics:  
A:Gene: CAC1079

Query Match 72.2%; Score 39; DB 2; Length 2817;  
Best Local Similarity 70.0%; Pred. No. 1.1e+02;  
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 VKLGTYFDS 10  
:  
Db 612 IKGNTYFDS 621

RESULT 4  
B44276  
coat protein VP1 - parvovirus LuIII  
C:Species: parvovirus LuIII  
C:Date: 17-Feb-1994 #sequence\_revision 17-Feb-1994 #text\_change 09-Jul-2004  
C:Accession: B44276  
R:Diffoot, N.; Chen, K.C.; Bates, R.C.; Lederma, M.  
Virology 192, 339-345, 1993  
A:Title: The complete nucleotide sequence of parvovirus LuIII and localization of a unit,  
A:Reference number: A44276; MUID:93297126; PMID:8517025  
A:Accession: B44276  
A:Status: translation not shown  
A:Molecule type: DNA  
A:Residues: 1-587 <DIF>  
A:Cross-references: UNIPROT:P36310; UNIPARC:UPI0000127D7E; GB:M81888  
C:Superfamily: parvovirus coat protein  
C:Keywords: coat protein; glycoprotein  
F:49,90,220,304,371,503,511,514,539,571/Binding site: carbohydrate (Asn) (covalent) #sta

Query Match 70.4%; Score 38; DB 1; Length 587;  
Best Local Similarity 85.7%; Pred. No. 34;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 GTYYFDS 10  
:  
Db 267 GTYFDT 273

RESULT 5  
VCPV2M  
coat protein VP1 - minute virus of mice  
C:Species: minute virus of mice, murine parvovirus  
C:Date: 14-Nov-1983 #sequence\_revision 14-Nov-1983 #text\_change 09-Jul-2004

C;Accession: A03700  
R;Astell, C.R.; Thomson, M.; Merchlineky, M.; Ward, D.C.  
Nucleic Acids Res. 11, 999-1018, 1983  
A;Title: The complete DNA sequence of minute virus of mice, an autonomous parvovirus.  
A;Reference number: A03696; MUID:83143341; PMID:6298737  
A;Accession: A03700  
A;Molecule type: DNA  
A;Residues: 1-716 <AST>  
A;Cross-references: UNIPROT:P03137; UNIPARC:UPI00000127D6D; EMBL:V01115  
C;Superfamily: parvovirus coat protein  
C;Keywords: coat protein

Query Match 70.4%; Score 38; DB 1; Length 716;  
Best Local Similarity 85.7%; Pred. No. 41;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 GTTYFDS 10  
|||||:  
Db 397 GTTYFDT 403

RESULT 6  
VCPVIM  
C;Species: minute virus of mice (strain MVMI)  
C;Date: 28-Dec-1987 #sequence\_revision 28-Dec-1987 #text\_change 09-Jul-2004  
C;Accession: B23008; B29510  
R;Sahl, R.; McMaster, G.K.; Hirt, B.  
Nucleic Acids Res. 13, 3617-3633, 1985  
A;Title: DNA sequence comparison between two tissue-specific variants of the autonomous  
A;Reference number: A23008; MUID:85242059; PMID:3855242  
A;Accession: B23008  
A;Molecule type: DNA  
A;Residues: 1-718 <SAH>  
A;Cross-references: UNIPROT:P07302; UNIPARC:UPI00000174963; EMBL:X02481; NID:G60918; PIDN  
R;Astell, C.R.; Gardiner, E.M.; Tattersall, P.  
J. Virol. 57, 656-669, 1986  
A;Title: DNA sequence of the lymphotropic variant of minute virus of mice, MVMI(1), and C  
A;Reference number: A29510; MUID:86115415; PMID:3502703  
A;Accession: B29510  
A;Molecule type: DNA  
A;Residues: 1-143, 'A', 145-718 <AST>  
A;Cross-references: UNIPARC:UPI00000127D6C; EMBL:M12032  
C;Superfamily: parvovirus coat protein  
C;Keywords: coat protein

Query Match 70.4%; Score 38; DB 1; Length 718;  
Best Local Similarity 85.7%; Pred. No. 41;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 GTTYFDS 10  
|||||:  
Db 399 GTTYFDT 405

RESULT 7  
S75975  
hypothetical protein - Synchocystis sp. (strain PCC 6803)  
C;Species: Synchocystis sp.  
A;Variety: PCC 6803  
C;Date: 25-Apr-1997 #sequence\_revision 25-Apr-1997 #text\_change 09-Jul-2004  
C;Accession: S75975  
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;  
O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda  
DNA Res. 3, 109-136, 1996  
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synchocystis  
s.  
A;Reference number: S74322; MUID:97061201; PMID:8905231  
A;Accession: S75975  
A;Status: nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-847 <KAN>  
A;Cross-references: UNIPROT:Q55476; UNIPARC:UPI00000034332; EMBL:D64006; GB:AB001339; NID

A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996  
C;Genetics:  
A;Start codon: GTG

Query Match 70.4%; Score 38; DB 2; Length 847;  
Best Local Similarity 66.7%; Pred. No. 49;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 VKLGTYYFD 9  
|:|:|:|:  
Db 759 VNMGTWYFD 767

RESULT 8  
A86460  
99.9K hypothetical protein T1B4.10 - Arabidopsis thaliana  
C;Species: Arabidopsis thaliana (mouse-ear cross)  
C;Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004  
C;Accession: A86460  
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso  
Chin, C.W.; Hughes, B.; Huizar, L.  
Nature 408, 816-820, 2000  
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.  
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziani,  
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,  
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A;Reference number: A86141; MUID:21016719; PMID:11130712  
A;Accession: A86460  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-907 <STO>  
A;Cross-references: UNIPROT:Q9FW49; UNIPARC:UPI000009C8C3; GB:AE005172; NID:G10998940;  
C;Genetics:  
A;Map position: 1

Query Match 70.4%; Score 38; DB 2; Length 907;  
Best Local Similarity 85.7%; Pred. No. 52;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 GTTYFDS 10  
|||||:  
Db 795 GTTYFDS 801

RESULT 9  
S49965  
probable membrane protein Y1L017c - yeast (Saccharomyces cerevisiae)  
N;Alternate names: hypothetical protein Y13299.14c  
C;Species: Saccharomyces cerevisiae  
C;Date: 28-May-1993 #sequence\_revision 24-Feb-1995 #text\_change 09-Jul-2004  
C;Accession: S49965  
R;Skellton, J.; Churcher, C.  
submitted to the EMBL Data Library, December 1994  
A;Reference number: S49965  
A;Accession: S49965  
A;Molecule type: DNA  
A;Residues: 1-921 <SKE>  
A;Cross-references: UNIPROT:P40547; UNIPARC:UPI000013B37D; EMBL:Z46881; NID:G599967; PI  
C;Genetics:  
A;Gene: SGD:Y1L017c  
A;Cross-references: SGD:S0001279  
A;Map position: 9L  
C;Superfamily: Saccharomyces cerevisiae probable membrane protein Y1L017c  
C;Keywords: transmembrane protein  
F;145-161/Domain: transmembrane #status predicted <TM1>  
F;532-548/Domain: transmembrane #status predicted <TM2>

Query Match 70.4%; Score 38; DB 2; Length 921;  
Best Local Similarity 85.7%; Pred. No. 53;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 LGTYFYD 9  
:|||||  
Db 72 VGTYFYD 78

RESULT 10  
T02130  
hypothetical protein F8K4.5 - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C>Date: 05-Mar-1999 #sequence\_revision 05-Mar-1999 #text\_change 09-Jul-2004  
C:Accession: T02130  
R;Vysotskaia, V.S.; Schwartz, J.R.; Toriumi, M.; Kwan, A.; Yu, G.; Oji, O.; Liu, S.; Li, R.; Vysotskaia, V.S.; Palm, C.J.; Shinn, P.; Sun, H.; Davis, R.W.; Ecker, J.R.; Federspiel, N.  
submitted to the EMBL Data Library, August 1998  
A:Description: Arabidopsis thaliana chromosome 1 BAC F8K4 sequence.  
A:Reference number: Z14574  
A:Accession: T02130  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-814 <VYS>  
A:Cross-references: UNIPROT:O80692; UNIPARC:UPI000000AAA62; EMBL:AC004392; NID:G3282170;  
C:Genetics:  
A:Gene: ATSP:F8K4.5  
A:Map position: 1

Query Match 68.5%; Score 37; DB 2; Length 814;  
Best Local Similarity 70.0%; Pred. No. 72;  
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 VKLGTYFYD 10  
:|||||  
Db 758 LKLGKIFYD 767

RESULT 11  
C69872  
hypothetical protein ylaE - Bacillus subtilis  
C:Species: Bacillus subtilis  
C>Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 09-Jul-2004  
C:Accession: C69872  
R;Kunet, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berton  
C.; Bron, S.; Broutlet, S.; Bruchi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho  
A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.  
Nature 390, 249-256, 1997  
A:Authors: Foulger, D.; Frittz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallen  
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.  
Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,  
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Maguda, S.; Maueel  
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle  
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,  
A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seron  
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpetra, P.; Tognoni, A.; Tosato, V.; Uchiyama,  
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K  
A:Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.  
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.  
A:Reference number: A69580; MUID:38044033; PMID:9384377  
A:Accession: C69872  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-203 <KUN>  
A:Cross-references: UNIPROT:O07629; UNIPARC:UPI0000060350; GB:Z99111; GB:AL009126; NID:9  
A:Experimental source: strain 168  
C:Genetics:  
A:Gene: ylaE  
C:Superfamily: Bacillus subtilis hypothetical protein ylaE

Query Match 66.7%; Score 36; DB 2; Length 203;  
Best Local Similarity 85.7%; Pred. No. 28;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GTTYFYD 10  
:|||||

Db 68 GVIYFDS 74

RESULT 12  
T48029  
hypothetical protein T12C14.70 - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C>Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 09-Jul-2004  
C:Accession: T48029  
R;Barques, M.; Perez-Perez, A.; Terol, J.; Torres, A.; Perez-Alonso, M.; Mewes, H.W.; R.  
submitted to the Protein Sequence Database, March 2000  
A:Reference number: Z24493  
A:Accession: T48029  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-361 <BAR>  
A:Cross-references: UNIPROT:O9LZQ3; UNIPARC:UPI000000AABQF; EMBL:AL162507  
A:Experimental source: cultivar Columbia; BAC clone T12C14  
C:Genetics:  
A:Map position: 3  
A:Introns: 85/3; 108/2; 130/3; 182/2; 206/1; 229/1; 262/3  
A:Note: T12C14.70  
C:Superfamily: Arabidopsis thaliana hypothetical protein T12C14.70

Query Match 66.7%; Score 36; DB 2; Length 361;  
Best Local Similarity 75.0%; Pred. No. 49;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 KLGTYFYD 9  
:|||||  
Db 242 KKGTYFYD 249

RESULT 13  
F90257  
hypothetical protein SSO1053 [imported] - Sulfolobus solfataricus  
C:Species: Sulfolobus solfataricus  
C>Date: 24-May-2001 #sequence\_revision 24-May-2001 #text\_change 09-Jul-2004  
C:Accession: F90257  
R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-  
arrett, R.A.; Ragan, M.A.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P.  
submitted to GenBank, April 2001  
A:Description: Sulfolobus solfataricus complete genome.  
A:Reference number: A99139  
A:Accession: F90257  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-637 <KUR>  
A:Cross-references: UNIPROT:Q97276; UNIPARC:UPI0000064333; GB:AE006641; NID:gl3814241; F  
C:Genetics:  
A:Gene: SSO1053

Query Match 66.7%; Score 36; DB 2; Length 637;  
Best Local Similarity 66.7%; Pred. No. 87;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 VKLGTYYFD 9  
:|||||  
Db 360 VKVGNYYID 368

RESULT 14  
T31541  
hypothetical protein Y47D3A.9 - Caenorhabditis elegans (fragment)  
C:Species: Caenorhabditis elegans  
C>Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 29-Oct-1999  
C:Accession: T31541  
R;Matthews, L.  
submitted to the EMBL Data Library, October 1999  
A:Reference number: Z21043  
A:Accession: T31541  
A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA  
A:Residues: 1-222 <WIL>  
A:CROSS-references: UNIPARC:UPI000017BC86; EMBL:AL117202; PIDN:CAB57890.1; CESP:Y47D3A.9  
A:Experimental source: Clone Y47D3A  
C:Genetics:  
A:Note: Intron positions not resolved (incomplete sequence)

Query Match 64.8%; Score 35; DB 2; Length 222;  
Best Local Similarity 55.6%; Pred. No. 46;  
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 VKLGTYYFD 9  
:|:||||:  
Db 110 IKIHTYTF 118

RESULT 15  
S09772  
hypothetical protein UL9 precursor - human cytomegalovirus (strain AD169)  
C:Species: human cytomegalovirus, human herpesvirus 5  
A:Note: host Homo sapiens (man)  
C:Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 09-Jul-2004  
C:Accession: S09772  
R:Chee, M.S.; Bankier, A.T.; Beck, S.; Bohni, R.; Brown, C.M.; Cerny, R.; Horsnell, T.; M.; Barrell, B.G.  
Curr. Top. Microbiol. Immunol. 154, 125-169, 1990  
A:Title: Analysis of the protein-coding content of the sequence of human cytomegalovirus  
A:Reference number: S09749; MUID:90269039; PMID:2161319  
A:Accession: S09772  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-228 <CHE>  
A:CROSS-references: UNIPROT:P16745; UNIPARC:UPI0000137B47; EMBL:X17403; NID:G59591; PIDN  
A:Note: this sequence was submitted to the EMBL Data Library, December 1989  
C:Keywords: glycoprotein; transmembrane protein  
F:1-25/Domain: signal sequence #status predicted <SIG>  
F:1-25/Domain: signal sequence #status predicted  
F:26-228/Product: hypothetical protein UL9 #status predicted <MAT>  
F:187-207/Domain: transmembrane #status predicted <TM>  
F:41,93,100,128,164/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 64.8%; Score 35; DB 2; Length 228;  
Best Local Similarity 85.7%; Pred. No. 48;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GTYYFDS 10  
:|:||||:  
Db 107 GIYYFDS 113

RESULT 16  
E72331  
hypothetical protein TM0812 - Thermotoga maritima (strain MSB8)  
C:Species: Thermotoga maritima  
C:Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 09-Jul-2004  
C:Accession: E72331  
R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey  
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.; C.M.  
Nature 399, 323-329, 1999  
A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq  
A:Reference number: A72200; MUID:99287316; PMID:10360571  
A:Accession: E72331  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-271 <ARN>  
A:CROSS-references: UNIPROT:Q9WZR9; UNIPARC:UPI000000D3988; GB:AE001748; GB:AE000512; NID  
A:Experimental source: strain MSB8  
C:Genetics:  
A:Gene: TM0812  
C:Superfamily: maltose transport protein malG

Query Match 64.8%; Score 35; DB 2; Length 271;

Best Local Similarity 60.0%; Pred. No. 57;  
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 VKLGTYYFDS 10  
:|:||||:  
Db 62 VKLGNYYLNT 71

RESULT 17  
T21476  
hypothetical protein F28C12.4 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C:Accession: T21476  
R:Kershaw, J.  
submitted to the EMBL Data Library, March 1997  
A:Reference number: Z19428  
A:Accession: T21476  
A:Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 1-339 <WIL>  
A:CROSS-references: UNIPROT:O17844; UNIPARC:UPI0000060FED; EMBL:Z93380; PIDN:CAB07600.1  
A:Experimental source: clone F28C12  
C:Genetics:  
A:Gene: CESP:F28C12.4  
A:Map position: 1  
A:Introns: 85/3; 134/2; 224/2; 289/3  
C:Superfamily: Caenorhabditis elegans hypothetical protein F18C5.1

Query Match 64.8%; Score 35; DB 2; Length 339;  
Best Local Similarity 100.0%; Pred. No. 71;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LGTYTF 8  
:|:||||:  
Db 164 LGTYTF 169

RESULT 18  
C86660  
endo-1,4-beta-xylanase D [imported] - Lactococcus lactis subsp. lactis (strain IL1403)  
C:Species: Lactococcus lactis subsp. lactis  
C:Date: 23-Mar-2001 #sequence\_revision 23-Mar-2001 #text\_change 09-Jul-2004  
C:Accession: C86660  
R:Bohotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarma, K.; Weissenbach, J.; Ehrh  
Genome Res. 11, 731-753, 2001  
A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis s  
A:Reference number: A86625; MUID:21235196; PMID:11337471  
A:Accession: C86660  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-372 <STO>  
A:CROSS-references: UNIPROT:O9CIS3; UNIPARC:UPI00000C67CC; GB:AE005176; PID:G12723145;  
A:Experimental source: strain IL1403  
C:Genetics:  
A:Gene: xynD

Query Match 64.8%; Score 35; DB 2; Length 372;  
Best Local Similarity 71.4%; Pred. No. 78;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 LGTYTFD 9  
:|:||||:  
Db 32 VGTYTFD 38

RESULT 19  
T28028  
hypothetical protein ZK829.10 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C:Accession: T28028  
R:Harris, B.

submitted to the EMBL Data Library, May 1996

A:Reference number: Z20458  
A:Accession: T22028  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-669 <WIL>  
A:Cross-references: UNIPROT:O18300; UNIPARC:UPI0000075BB9; EMBL:Z73899; PIDN:CAA98079.2;  
A:Experimental source: clone ZK829  
C:Genetics:  
A:Gene: CESP:ZK829.10  
A:Map position: 4  
A:Introns: 20/3; 146/1; 175/2; 222/3; 299/3; 344/1; 384/1; 427/3; 526/3; 561/3; 595/3; 6

Query Match 64.8%; Score 35; DB 2; Length 669;  
Best Local Similarity 55.6%; Pred. No. 1.4e+02;  
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 VKLGTYYFD 9  
:|:|:|  
Db 399 IKMKTYYFD 407

## RESULT 20

T22223  
sel-1 protein - Caenorhabditis elegans  
N:Alternate names: regulator of lin-12  
C:Species: Caenorhabditis elegans  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C:Accession: T22223; S68303; S68304  
R:White, S.

submitted to the EMBL Data Library, August 1996

A:Reference number: Z19532  
A:Accession: T22223  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-685 <WIL>  
A:Cross-references: UNIPROT:Q20423; UNIPARC:UPI000007DE30; EMBL:Z78063; PIDN:CAB01505.1;  
A:Experimental source: clone F45D3  
R:Grant, B.; Greenwald, I.  
Genetics 143, 237-247, 1996

A:Title: The Caenorhabditis elegans sel-1 gene, a negative regulator of lin-12 and glp-1

A:Reference number: S68303; MUID:96304591; PMID:8722778

A:Accession: S68303

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-685 <GRA>

A:Cross-references: UNIPARC:UPI000007DE30; GB:U50828; NID:g1255198; PIDN:AAC47112.1; PID

A:Accession: S68304

A:Molecule type: mRNA

A:Residues: 1-685 <GR2>

A:Cross-references: UNIPARC:UPI000007DE30; EMBL:U50829; NID:g1255200; PID:g1255201

C:Genetics:

A:Gene: sel-1

A:Map position: 5

A:Introns: 41/1; 90/2; 210/3; 411/1; 548/1

Query Match 64.8%; Score 35; DB 2; Length 685;

Best Local Similarity 75.0%; Pred. No. 1.4e+02;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VKLGTYYF 8  
|||:|:|  
Db 554 VKLGDYYY 561

## RESULT 21

G88851  
protein ZK829.10 [imported] - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 09-Jul-2004  
C:Accession: G88851  
R:anonymous, The C. elegans Sequencing Consortium.

Science 282, 2012-2018, 1998

A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biology

A:Reference number: A75000; MUID:99069613; PMID:9851916

A:Notes: see websites genome.wustl.edu/gsc/C\_elegans/ and www.sanger.ac.uk/Projects/C\_ele

A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and

A:Accession: G88851

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-696 <STO>

A:Cross-references: UNIPROT:O18300; UNIPARC:UPI000017A62B; GB:chr\_IV; PIDN:CAA98079.1; P

C:Genetics:

A:Gene: ZK829.10

A:Map position: 4

Query Match 64.8%; Score 35; DB 2; Length 696;

Best Local Similarity 55.6%; Pred. No. 1.5e+02;

Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 VKLGTYYFD 9  
:|:|:|  
Db 415 IKMKTYYFD 423

## RESULT 22

B89583  
protein K07E3.2 [imported] - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 09-Jul-2004  
C:Accession: B89583  
R:anonymous, The C. elegans Sequencing Consortium.

Science 282, 2012-2018, 1998

A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biology

A:Reference number: A75000; MUID:99069613; PMID:9851916

A:Note: see websites genome.wustl.edu/gsc/C\_elegans/ and www.sanger.ac.uk/Projects/C\_ele

A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and

A:Accession: B89583

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-837 <STO>

A:Cross-references: UNIPROT:Q21287; UNIPARC:UPI000007D805; GB:chr\_X; PIDN:AAC69099.1; PI

C:Genetics:

A:Gene: K07E3.2

A:Map position: X

Query Match 64.8%; Score 35; DB 2; Length 837;

Best Local Similarity 55.6%; Pred. No. 1.7e+02;

Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 VKLGTYYFD 9  
:|:|:|  
Db 374 IKLGMFFFD 382

## RESULT 23

T20140  
hypothetical protein C51F7.1 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C:Accession: T20140  
R:White, S.

submitted to the EMBL Data Library, June 1998

A:Reference number: Z19228

A:Accession: T20140

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-1113 <WIL>

A:Cross-references: UNIPROT:Q9XXK4; UNIPARC:UPI0000079E99; EMBL:AL023811; PIDN:CAA19422

A:Experimental source: clone C51F7

C:Genetics:

A:Gene: CESP:C51F7.1

A:Map position: 5

A:Introns: 61/3; 127/3; 155/2; 204/2; 393/1; 434/1; 676/3; 845/1; 929/2; 944/2

```
Query Match      64.8%; Score 35; DB 2; Length 1113;
Best Local Similarity 85.7%; Pred. No. 2.3e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      4 GTYTFFDS 10
      | | | | |
Db      852 GDVYFFDS 858

RESULT 24
A46158
nicotinic acetylcholine receptor alpha subunit (cholinergic binding site) - African mong
C;Species: Herpestes ichneumon (African mongoose)
C;Date: 21-Sep-1993 #sequence_revision 10-Nov-1994 #text_change 09-Jul-2004
C;Accession: A46158
R;Barchan, D.; Kachalsky, S.; Neumann, D.; Vogel, Z.; Ovadia, M.; Kochva, E.; Fuchs, S.
Proc. Natl. Acad. Sci. U.S.A. 89, 7717-7721, 1992
A;Title: How the mongoose can fight the snake: the binding site of the mongoose acetylch
A;Reference number: A46158; MUID:92366533; PMID:1380164
A;Accession: A46158
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-84 <BAR>
A;Cross-references: UNIPROT:P54251; UNIPARC:UPI000012524D; GB:M93639; NID:G164173; PIDN:
A;Note: sequence extracted from NCBI backbone (NCBIN:110811, NCBIP:110812)
C;Superfamily: acetylcholine receptor
C;Keywords: neurotransmitter receptor

Query Match      63.0%; Score 34; DB 2; Length 84;
Best Local Similarity 60.0%; Pred. No. 27;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy      1 VKLGTYYFDS 10
      : | | | | :
Db      23 MKLGTWTYDS 32

RESULT 25
A32189
Ig heavy chain V region (anti-arsonate antibody) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 12-Oct-1989 #sequence_revision 12-Oct-1989 #text_change 16-Aug-1996
C;Accession: A32189
R;Jascombe, M.B.; Alzari, P.M.; Boulot, G.; Saludjian, P.; Tougard, P.; Berek, C.; Haba,
Proc. Natl. Acad. Sci. U.S.A. 86, 607-611, 1989
A;Title: Three-dimensional structure of Fab R19.9, a monoclonal murine antibody specific
A;Reference number: A32189; MUID:89098979; PMID:2911596
A;Accession: A32189
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-110 <LAS>
A;Cross-references: UNIPARC:UPI0000176B3D
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotrimer; immunoglobulin

Query Match      63.0%; Score 34; DB 2; Length 110;
Best Local Similarity 75.0%; Pred. No. 35;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      3 LGTYTFFDS 10
      | | | | |
Db      92 LAVYFFDS 99

RESULT 26
S09831
hypothetical protein UL68 - human cytomegalovirus (strain AD169)
C;Species: human cytomegalovirus, human herpesvirus 5
A;Note: host Homo sapiens (man)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C;Accession: S09831
R;Chee, M.S.; Bankier, A.T.; Beck, S.; Bohni, R.; Brown, C.M.; Cerny, R.; Horsnell, T.;
M.; Barrell, B.G.
```

```
Curr. Top. Microbiol. Immunol. 154, 125-169, 1990
A;Title: Analysis of the protein-coding content of the sequence of human cytomegaloviru
A;Reference number: S09749; MUID:90269039; PMID:2161319
A;Accession: S09831
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-110 <CHE>
A;Cross-references: UNIPROT:P16748; UNIPARC:UPI0000137BDD; EMBL:X17403; NID:G59591; PID:
A;Note: this sequence was submitted to the EMBL Data Library, December 1989
C;Superfamily: human cytomegalovirus hypothetical protein UL68

Query Match      63.0%; Score 34; DB 2; Length 110;
Best Local Similarity 50.0%; Pred. No. 35;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy      1 VKLGTYYFDS 10
      : | | | | :
Db      63 IELGVYFFSS 72

RESULT 27
PHI486
Ig heavy chain V region (clone X7-3D12) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C;Accession: PHI486
R;Giusti, A.M.; Manser, T.
J. Exp. Med. 177, 797-809, 1993
A;Title: Hypermutation is observed only in antibody H chain V region transgenes that ha
d for somatic mutation.
A;Reference number: PHI482; MUID:93171820; PMID:8436910
A;Accession: PHI486
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-140 <GIU>
A;Cross-references: UNIPARC:UPI0000176BA6
A;Experimental source: hybridoma cell
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotrimer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match      63.0%; Score 34; DB 2; Length 140;
Best Local Similarity 71.4%; Pred. No. 45;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      4 GTTYFDS 10
      | | | | :
Db      123 GSYTFDN 129

RESULT 28
PHI499
Ig heavy chain V region (clone X7-3D12H) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C;Accession: PHI499
R;Giusti, A.M.; Manser, T.
J. Exp. Med. 177, 797-809, 1993
A;Title: Hypermutation is observed only in antibody H chain V region transgenes that ha
d for somatic mutation.
A;Reference number: PHI482; MUID:93171820; PMID:8436910
A;Accession: PHI499
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-140 <GIU>
A;Cross-references: UNIPARC:UPI0000176BAC
A;Experimental source: hybridoma cell
C;Genetics:
A;Intons: 16/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotrimer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>
```



Query Match 63.0%; Score 34; DB 2; Length 140;  
 Best Local Similarity 71.4%; Pred. No. 45;  
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 GTYYFDS 10  
 |:|:|:|:  
 DB 123 GSYFFDN 129

RESULT 29  
 E90868  
 hypothetical protein EC61917 [imported] - Escherichia coli (strain O157:H7, substrain R157:H7)  
 C;Species: Escherichia coli  
 C;Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 09-Jul-2004  
 C;Accession: E90868  
 R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.;  
 gaeawara, N.; Yagunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.  
 DNA Res. 8, 11-22, 2001  
 A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gen  
 A;Reference number: A99629; MUID:21156231; PMID:11258796  
 A;Accession: E90868  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-204 <HAY>  
 A;Cross-references: UNIPROT:Q8X8N7; UNIPARC:UPI0000165444; GB:BA000007; PIDN:BA035340.1;  
 A;Experimental source: strain O157:H7, substrain R157:H7, substrain R157:H7, substrain R157:H7  
 C;Genetics:  
 A;Gene: EC61917

Query Match 63.0%; Score 34; DB 2; Length 204;  
 Best Local Similarity 100.0%; Pred. No. 65;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KLGTYY 7  
 :|:|:|:|:  
 DB 162 KLGTYY 167

RESULT 30  
 C70424  
 hypothetical protein aq\_1428 - Aquifex aeolicus  
 C;Species: Aquifex aeolicus  
 C;Date: 08-May-1998 #sequence\_revision 08-May-1998 #text\_change 09-Jul-2004  
 C;Accession: C70424  
 R;Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; O  
 V.  
 Nature 392, 353-358, 1998  
 A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.  
 A;Reference number: A70300; MUID:98196666; PMID:9537320  
 A;Accession: C70424  
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A;Molecule type: DNA  
 A;Residues: 1-209 <AQF>  
 A;Cross-references: UNIPROT:O67421; UNIPARC:UPI0000056606; GB:AE000740; NID:g2983826; PI  
 A;Experimental source: strain VF5  
 C;Genetics:  
 A;Gene: aq\_1428  
 C;Superfamily: Aquifex aeolicus hypothetical protein aq\_1428

Query Match 63.0%; Score 34; DB 2; Length 209;  
 Best Local Similarity 63.6%; Pred. No. 67;  
 Matches 7; Conservative 2; Mismatches 0; Indels 2; Gaps 1;

QY 2 KLG--TYFFDS 10  
 |:|:|:|:|:  
 DB 121 KIGNTYFFDT 131

RESULT 31  
 D85750  
 hypothetical protein Z2431 [imported] - Escherichia coli (strain O157:H7, substrain EDJ5  
 C;Species: Escherichia coli  
 C;Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 09-Jul-2004

C;Accession: D85750  
 R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew  
 iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,  
 Nature 409, 529-533, 2001  
 A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.  
 A;Reference number: A85480; MUID:21074935; PMID:11206551  
 A;Accession: D85750  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-230 <STO>  
 A;Cross-references: UNIPROT:Q8X8N7; UNIPARC:UPI00000008F9; GB:AE005174; NID:g12515422; F  
 A;Experimental source: strain O157:H7, substrain EDJ933  
 C;Genetics:  
 A;Gene: Z2431

Query Match 63.0%; Score 34; DB 2; Length 230;  
 Best Local Similarity 100.0%; Pred. No. 74;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KLGTYY 7  
 :|:|:|:|:  
 DB 188 KLGTYY 193

RESULT 32  
 B81307  
 thiamin biosynthesis protein thiG Cj1045c (similarity) - Campylobacter jejuni (strain NC  
 C;Species: Campylobacter jejuni  
 C;Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 09-Jul-2004  
 C;Accession: B81307  
 R;Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chillin  
 C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrel  
 Nature 403, 665-668, 2000  
 A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp  
 A;Reference number: A81250; MUID:20150912; PMID:10688204  
 A;Accession: B81307  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-258 <PAR>  
 A;Cross-references: UNIPROT:Q9PNP6; UNIPARC:UPI0000136DEC; GB:AL1139077; GB:AL111168; NID  
 A;Experimental source: serotype O2, strain NCTC 11168  
 C;Genetics:  
 A;Gene: thiG; Cj1045c  
 C;Superfamily: thiamin biosynthesis protein thiG

Query Match 63.0%; Score 34; DB 2; Length 258;  
 Best Local Similarity 60.0%; Pred. No. 83;  
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 VKLGTYYFDS 10  
 :|:|:|:|:  
 DB 10 LKIGKYEFD 19

RESULT 33  
 A64659  
 outer membrane protein - Helicobacter pylori (strain 26695)  
 C;Species: Helicobacter pylori  
 C;Date: 09-Aug-1997 #sequence\_revision 09-Aug-1997 #text\_change 09-Jul-2004  
 C;Accession: A64659  
 R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.  
 Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenn  
 son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Matthey, L  
 Nature 388, 539-547, 1997  
 A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.  
 A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.  
 A;Reference number: A64520; MUID:97394467; PMID:9252185  
 A;Accession: A64659  
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A;Molecule type: DNA  
 A;Residues: 1-277 <YOM>  
 A;Cross-references: UNIPROT:O25740; UNIPARC:UPI00000D304C; GB:AE000617; GB:AE000511; NID  
 C;Genetics:



A;Start codon: TTG

Query Match 63.0%; Score 34; DB 2; Length 277;  
Best Local Similarity 55.6%; Pred. No. 89;  
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 VKLGTYYFD 9  
: : |||||  
Db 220 IKIPTYFVN 228

#### RESULT 34

B71856  
probable outer membrane protein - Helicobacter pylori (strain J99)  
C;Species: Helicobacter pylori  
A;Variety: strain J99  
C;Date: 12-Feb-1999 #sequence\_revision 12-Feb-1999 #text\_change 09-Jul-2004  
C;Accession: B71856  
R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.;  
Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.;  
Nature 397, 176-180, 1999  
A;Title: Genomic sequence comparison of two unrelated isolates of the human gastric path  
A;Reference number: A71800; MUID:99120557; PMID:9923682  
A;Accession: B71856  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-277 <ARN>  
A;Cross-references: UNIPROT:Q9ZKA1; UNIPARC:UPI00000036E0; GB:AE001532; GB:AE001439; NID  
A;Experimental source: strain J99  
C;Genetics:  
A;Gene: jhp1040

Query Match 63.0%; Score 34; DB 2; Length 277;  
Best Local Similarity 55.6%; Pred. No. 89;  
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 VKLGTYYFD 9  
: : |||||  
Db 220 IKIPTYFVN 228

#### RESULT 35

T08150  
Chitinase (EC 3.2.1.14) - Volvox carteri f. nagariensis  
C;Species: Volvox carteri f. nagariensis  
C;Date: 21-May-1999 #sequence\_revision 21-May-1999 #text\_change 09-Jul-2004  
C;Accession: T08150  
R;Amon, P.; Haas, E.; Sumper, M.  
Plant Cell 10, 781-789, 1998  
A;Title: The sex-inducing pheromone and wounding trigger the same set of genes in the mu  
A;Reference number: Z16381; MUID:98259000; PMID:9596636  
A;Accession: T08150  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-309 <AMO>  
A;Cross-references: UNIPROT:O65213; UNIPARC:UPI0000005C934; EMBL:AF058716; NID:G3047412;  
C;Keywords: glycosidase; hydrolase

Query Match 63.0%; Score 34; DB 2; Length 309;  
Best Local Similarity 83.3%; Pred. No. 99;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 GTYYFD 9  
: : |||||  
Db 172 GTYYFD 177

#### RESULT 36

T48055  
hypothetical protein F26K9.90 - Arabidopsis thaliana  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 09-Jul-2004  
C;Accession: T48055

R;Bloeker, H.; Mewes, H.W.; Rudd, S.; Lemcke, K.; Mayer, K.F.X.; Quetier, F.; Salanoub  
submitted to the Protein Sequence Database, March 2000  
A;Reference number: Z24465  
A;Accession: T48055  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-357 <BLO>  
A;Cross-references: UNIPROT:Q9LZJ9; UNIPARC:UPI00000488BC; EMBL:AL162651  
A;Experimental source: cultivar Columbia; BAC clone F26K9  
C;Genetics:  
A;Map position: 3  
A;Note: F26K9.90

Query Match 63.0%; Score 34; DB 2; Length 357;  
Best Local Similarity 66.7%; Pred. No. 11e+02;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 VKLGTYYFD 9  
: : |||||  
Db 132 LKLKYYFD 140

#### RESULT 37

C64883  
membrane protein ydaH - Escherichia coli (strain K-12)  
C;Species: Escherichia coli  
C;Date: 12-Sep-1997 #sequence\_revision 17-Sep-1997 #text\_change 09-Jul-2004  
C;Accession: C64883  
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; C;  
A.; Rose, D.J.; Mau, B.; Shao, Y.  
Science 277, 1453-1462, 1997

A;Title: The complete genome sequence of Escherichia coli K-12.  
A;Reference number: A64720; MUID:97426617; PMID:9278503  
A;Accession: C64883  
A;Status: nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-510 <BLAT>  
A;Cross-references: UNIPROT:P46133; UNIPARC:UPI000012513A; GB:AE000231; GB:U00096; NID:  
A;Experimental source: strain K-12, substrain MG1655  
C;Genetics:

A;Gene: ydaH  
F;33-49/Domain: transmembrane #status predicted <TM01>  
F;90-106/Domain: transmembrane #status predicted <TM02>  
F;145-161/Domain: transmembrane #status predicted <TM03>  
F;166-182/Domain: transmembrane #status predicted <TM04>  
F;218-234/Domain: transmembrane #status predicted <TM05>  
F;267-283/Domain: transmembrane #status predicted <TM06>  
F;303-319/Domain: transmembrane #status predicted <TM07>  
F;346-362/Domain: transmembrane #status predicted <TM08>  
F;389-405/Domain: transmembrane #status predicted <TM09>  
F;409-425/Domain: transmembrane #status predicted <TM10>  
F;443-459/Domain: transmembrane #status predicted <TM11>  
F;481-497/Domain: transmembrane #status predicted <TM12>

Query Match 63.0%; Score 34; DB 2; Length 510;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KLGTYY 7  
: : |||||  
Db 468 KLGTYY 473

#### RESULT 38

A45472  
protein kinase (EC 2.7.1.37) - malaria parasite (Plasmodium falciparum)  
N;Alternate names: calcium-dependant protein kinase  
C;Species: Plasmodium falciparum  
C;Date: 17-Feb-1994 #sequence\_revision 17-Feb-1994 #text\_change 09-Jul-2004  
C;Accession: A45472; E71605; S28590  
R;Zhao, Y.; Kappe, B.; Franklin, R.M.  
J. Biol. Chem. 268, 4347-4354, 1993  
A;Title: Gene structure and expression of an unusual protein kinase from Plasmodium fal.

A;Reference number: A45472; MUID:93179444; PMID:8440720  
A;Contents: K1  
A;Accession: A45472  
A;Molecule type: DNA  
A;Residues: 1-524 <SHA>  
A;Cross-references: UNIPROT:Q27731; UNIPARC:UPI00000818F2; EMBL:X67286; NID:g9877; PIDN:  
A;Note: sequence extracted from NCBI backbone (NCBIN:125849, NCBIIP:125850)  
R;Gardner, M.J.; Tetzelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.V.;  
; Petrea, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.O.  
Science 282, 1126-1132, 1998  
A;Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.  
A;Reference number: A71600; MUID:99021743; PMID:9804551  
A;Accession: E71605  
A;Status: nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-524 <GAR>  
A;Cross-references: UNIPARC:UPI00000818F2; GB:AE001419; GB:AE001362; NID:g3845281; PIDN:  
A;Experimental source: clone 3D7  
C;Genetics:  
A;Gene: cpk; PF08015W  
A;Introns: 406/3; 440/1; 479/3; 505/3  
C;Superfamily: calcium-dependent protein kinase; calmodulin repeat homology; protein kin  
C;Keywords: ATP; calcium binding; EF hand; phosphotransferase; serine/threonine-specific  
F;54-325/Domain: protein kinase homology <KIN>  
F;62-70/Region: protein kinase ATP-binding motif  
F;416-448/Domain: calmodulin repeat homology <EF4>  
  
Query Match 63.0%; Score 34; DB 2; Length 524;  
Best Local Similarity 66.7%; Pred. No. 1.7e+02;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
  
Qy 1 VKLGYTFD 9  
| : | |||  
Db 279 VEKGYTFD 287  
  
RESULT 39  
F64186  
ABC-type transport protein cydd - Haemophilus influenzae (strain Rd KW20)  
C;Species: Haemophilus influenzae  
C;Date: 18-Aug-1995 #sequence\_revision 18-Aug-1995 #text\_change 05-Oct-2004  
C;Accession: F64186  
R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A  
; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J  
; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.  
Science 269, 496-512, 1995  
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,  
A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.  
A;Reference number: A64000; MUID:95350630; PMID:7542800  
A;Accession: F64186  
A;Status: nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-586 <TIGR>  
A;Cross-references: UNIPROT:P45082; UNIPARC:UPI0000128BED; GB:U32795; GB:L42023; NID:g15  
C;Genetics:  
A;Gene: cydd  
C;Keywords: ATP; nucleotide binding; P-loop; transmembrane protein; transport protein  
F;23-39/Domain: transmembrane #status predicted <TM1>  
F;66-82/Domain: transmembrane #status predicted <TM2>  
F;145-161/Domain: transmembrane #status predicted <TM3>  
F;167-183/Domain: transmembrane #status predicted <TM4>  
F;252-268/Domain: transmembrane #status predicted <TM5>  
F;285-301/Domain: transmembrane #status predicted <TM6>  
F;366-557/Domain: ATP-binding cassette homology <ABC>  
F;383-390/Region: nucleotide-binding motif A (P-loop)  
  
Query Match 63.0%; Score 34; DB 2; Length 586;  
Best Local Similarity 85.7%; Pred. No. 1.9e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 3 LGTYTFD 9  
| |||||  
Db 307 LGTYTFD 313

RESULT 40  
AD1818  
N-acetylmuramoyl-L-alanine amidase [imported] - Nostoc sp. (strain PCC 7120)  
C;Species: Nostoc sp. PCC 7120  
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120  
C;Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 09-Jul-2004  
C;Accession: AD1818  
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriquch  
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata,;  
DNA Res. 8, 205-213, 2001  
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium An  
A;Reference number: AB1807; MUID:21595285; PMID:11759840  
A;Accession: AD1818  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-627 <KUR>  
A;Cross-references: UNIPROT:Q82039; UNIPARC:UPI00000C0CD1D; GB:BA000019; PIDN:BA077616.1  
A;Experimental source: strain PCC 7120  
C;Genetics:  
A;Gene: alr0092  
  
Query Match 63.0%; Score 34; DB 2; Length 627;  
Best Local Similarity 75.0%; Pred. No. 2e+02;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 3 LGTYTFDS 10  
| |||||  
Db 542 LETYYTDS 549  
  
RESULT 41  
G90284  
hypothetical protein SSO1297 [imported] - Sulfolobus solfataricus  
C;Species: Sulfolobus solfataricus  
C;Date: 24-May-2001 #sequence\_revision 24-May-2001 #text\_change 09-Jul-2004  
C;Accession: G90284  
R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan  
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder,  
arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.  
submitted to GenBank, April 2001  
A;Description: Sulfolobus solfataricus complete genome.  
A;Reference number: A99139  
A;Accession: G90284  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-692 <KUR>  
A;Cross-references: UNIPROT:Q97YM6; UNIPARC:UPI00000643ED; GB:AE006641; NID:g13814498;  
C;Genetics:  
A;Gene: SSO1297  
  
Query Match 63.0%; Score 34; DB 2; Length 692;  
Best Local Similarity 75.0%; Pred. No. 2.2e+02;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 1 VKLGYTF 8  
| |||||  
Db 335 VTILGYTF 342  
  
RESULT 42  
A48144  
protein kinase CDC5 (EC 2.7.1.1-) - yeast (Saccharomyces cerevisiae)  
N;Alternate names: protein kinase PKX2; protein YM8270.03c; protein YMR001c  
C;Species: Saccharomyces cerevisiae  
C;Date: 30-Jun-1995 #sequence\_revision 30-Jun-1995 #text\_change 31-Dec-2004  
C;Accession: A48144; S53030; S27445  
R;Kitada, K.; Johnson, A.L.; Johnston, L.H.; Sugino, A.  
Mol. Cell. Biol. 13, 4445-4457, 1993  
A;Title: A multicopy suppressor gene of the Saccharomyces cerevisiae G-1 cell cycle mut  
A;Reference number: A48144; MUID:93309479; PMID:8321244  
A;Accession: A48144

A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-705 <KLT>  
A;Cross-references: UNIPROT:P32562; UNIPARC:UPI0000127258; EMBL:M84220; NID:g172186; PID:172186  
R;Devlin, K.; Churcher, C.M.  
submitted to the EMBL Data Library, March 1995  
A;Reference number: S53028  
A;Accession: S53030  
A;Molecule type: DNA  
A;Residues: 1-705 <DEV>  
A;Cross-references: UNIPARC:UPI0000127258; EMBL:Z48613; NID:g728645; PIDN:CAA88516.1; PIDN:CAA88516.1  
A;Experimental source: strain AB972  
C;Genetics:  
A;Gene: SGD:CD5; PKX2  
A;Cross-references: SGD:S0004603; MIPS:YMR001c  
A;Map position: 13R  
C;Keywords: ATP; cell cycle control; phosphotransferase; protein kinase  
F;80-337/Domain: protein kinase homology <KIN>

Query Match 63.0%; Score 34; DB 2; Length 705;  
Best Local Similarity 60.0%; Pred. No. 2.3e+02;  
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 VKLGTYYFDS 10  
:|||||  
Db 205 LKLGNIFFDS 214

RESULT 43  
AI0513  
Organic solvent tolerance protein precursor [imported] - Salmonella enterica subsp. enterica  
C;Species: Salmonella enterica subsp. enterica serovar Typhi  
A;Title: This species has also been called Salmonella typhi  
C;Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 18-Nov-2002  
C;Accession: AI0513  
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moulé, S.; O'Gaora, P.  
Nature 413, 848-852, 2001  
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi  
A;Reference number: AB0502; MUID:21534947; PMID:11677608  
A;Accession: AI0513  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-784 <PAR>  
A;Cross-references: UNIPARC:UPI00000599C0; GB:AL513382; PIDN:CAD01249.1; PID:g16501378;  
C;Genetics:  
A;Gene: STY0108  
C;Superfamily: organic solvent tolerance protein

Query Match 63.0%; Score 34; DB 2; Length 784;  
Best Local Similarity 62.5%; Pred. No. 2.5e+02;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 LGTYVYFDS 10  
:|||||  
Db 700 VGAYYFD 707

RESULT 44  
AB4460  
Probable retroelement pol polyprotein [imported] - Arabidopsis thaliana  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 09-Jul-2004  
C;Accession: AB4460  
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.; eus, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999  
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
A;Reference number: AB4420; MUID:20083487; PMID:10617197  
A;Accession: AB4460

A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-1411 <STO>  
A;Cross-references: UNIPROT:Q9SJ92; UNIPARC:UPI000009D8DC; GB:AE002093; NID:g4544430; P  
C;Genetics:  
A;Gene: At2g04670  
A;Map position: 2

Query Match 63.0%; Score 34; DB 2; Length 1411;  
Best Local Similarity 55.6%; Pred. No. 4.5e+02;  
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 KLGTYYFDS 10  
:|||||  
Db 132 RIGTWYFSS 140

RESULT 45  
B64596  
toxin-like outer membrane protein HP0610 - Helicobacter pylori (strain 26695)  
C;Species: Helicobacter pylori  
C;Date: 09-Aug-1997 #sequence\_revision 09-Aug-1997 #text\_change 09-Jul-2004  
C;Accession: B64596  
R;Tomb, J.P.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D. Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKen son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L. Nature 388, 539-547, 1997  
A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C. A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.  
A;Reference number: A64520; MUID:97394467; PMID:9252185  
A;Accession: B64596  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-1943 <TOM>  
A;Cross-references: UNIPROT:Q25331; UNIPARC:UPI000003D30AD; GB:AE000575; GB:AE000511; NI  
C;Genetics:  
A;Start codon: GTG

Query Match 63.0%; Score 34; DB 2; Length 1943;  
Best Local Similarity 66.7%; Pred. No. 6.2e+02;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 KLGTYYFDS 10  
:|||||  
Db 651 KVGTYLTS 659

RESULT 46  
T39188  
Probable U5 snRNP-specific 200kd protein - fission yeast (Schizosaccharomyces pombe)  
C;Species: Schizosaccharomyces pombe  
C;Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004  
C;Accession: T39188  
R;Redler, H.; Duesterhoeft, A.; Lyne, M.H.; Rajandream, M.A.; Barrell, B.G.  
submitted to the EMBL Data Library, October 1999  
A;Reference number: Z21834  
A;Accession: T39188  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-2176 <WED>  
A;Cross-references: UNIPROT:Q9UT24; UNIPARC:UPI0000068CA7; EMBL:AL121764; PIDN:CAB57421  
A;Experimental source: strain 972h; cosmid c9  
C;Genetics:  
A;Gene: SPDB:SPAC9.03c  
A;Map position: 1

Query Match 63.0%; Score 34; DB 2; Length 2176;  
Best Local Similarity 66.7%; Pred. No. 7e+02;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 KLGTYYFDS 10  
:|||||  
Db 709 KKGLFYFDS 717

```

RESULT 47
T31345
hypothetical protein G01D9.5 - Caenorhabditis briggsae
C:Species: Caenorhabditis briggsae
C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C:Accession: T31345
R:Waterston, R.
submitted to the EMBL Data Library, April 1996
A:Description: The C. briggsae genome sequencing project.
A:Accession: T31345
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-4767 <WAT>
A:Cross-references: UNIPROT:Q17301; UNIPARC:UPI000011013B; EMBL:US6248; NID:g1293789; PI
C:Genetics:
A:Introns: 269/3; 341/3; 853/1; 920/2; 4452/3; 4534/3; 4592/3; 4654/3; 4670/3; 4707/2; 4
A>Note: G01D9.5
C:Keywords: carrier protein; phosphopantetheine; phosphoprotein
F:3472-3541/Domain: acyl carrier protein homology <ACPL>
F:4039-4427/Domain: acetate-CoA ligase homology <ACL>
F:4447-4514/Domain: acyl carrier protein homology <ACP2>
F:2210,3505/Binding site: phosphopantetheine (Ser) (covalent) #status predicted

Query Match 63.0%; Score 34; DB 2; Length 4767;
Best Local Similarity 66.7%; Pred. No. 1.5e+03;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 KLGTYYFDS 10
|||:|
DB 2050 KLGGFYFSS 2058

RESULT 48
T11144
H+-transporting two-sector ATPase (EC 3.6.3.14) protein 8 - fruit bat (Artibeus jamaicensis)
C:Species: mitochondrion Artibeus jamaicensis
C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 31-Dec-2004
C:Accession: T11144
R:Pumo, D.E.; Finamore, P.S.; Franek, W.R.; Phillips, C.J.; Tarzami, S.; Balzarano, D.
J. Mol. Evol. 47, 709-717, 1998
A:Title: Complete mitochondrial genome of a neotropical fruit bat, Artibeus jamaicensis,
A:Reference number: Z17251; MUID:99065764; PMID:9847413
A:Accession: T11144
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-67 <PUM>
A:Cross-references: UNIPROT:O99598; UNIPARC:UPI000012635F; EMBL:AF061340; NID:g4164474;
C:Genetics:
A:Genome: mitochondrion
A>Note: ATPase8
C:Superfamily: H(+)-transporting ATP synthase protein 8
C:Keywords: ATP biosynthesis; hydrolase; membrane-associated complex; mitochondrion; oxid

Query Match 61.1%; Score 33; DB 2; Length 67;
Best Local Similarity 50.0%; Pred. No. 33;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 VKLGTYYFDS 10
||:|
DB 26 LKISTYYHS 35

RESULT 49
PH1485
Ig heavy chain V region (clone X74G7) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C:Accession: PH1485
R:Giusti, A.M.; Manser, T.
J. Exp. Med. 177, 797-809, 1993

A:Title: Hypermutation is observed only in antibody H chain V region transgenes that hav
d for somatic mutation.
A:Reference number: PH1482; MUID:93171820; PMID:8436910
A:Accession: PH1485
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-90 <GIU>
A:Cross-references: UNIPARC:UPI0000176A35
A:Experimental source: hybridoma cell
A:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin

Query Match 61.1%; Score 33; DB 2; Length 90;
Best Local Similarity 83.3%; Pred. No. 44;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 GYYFYD 9
|:|
DB 85 GSYFYD 90

RESULT 50
S26885
Ig heavy chain V region (DP-44) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 23-Jul-1999
C:Accession: S26885; S36596
R:Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A:Title: The repertoire of human germline V(H) sequences reveals about fifty groups of
A:Reference number: S26885; MUID:93021117; PMID:1404388
A:Accession: S26885
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-97 <TOM1>
A:Cross-references: UNIPARC:UPI0000176B67; EMBL:Z12344
R:Tomlinson, M.
submitted to the EMBL Data Library, June 1992
A:Reference number: S36596
A:Accession: S36596
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-5,'Q',7-12,'H',14-97 <TOM2>
A:Cross-references: UNIPARC:UPI000011640F; EMBL:Z12344; NID:g32908; PIDN:CAA78214.1; PI
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:15-97/Domain: immunoglobulin homology <IMM>

Query Match 61.1%; Score 33; DB 2; Length 97;
Best Local Similarity 85.7%; Pred. No. 48;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GYYFYDS 10
|||:|
DB 56 GTYYADS 62

Search completed: April 6, 2006, 08:58:30
Job time : 18 secs
```

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: April 6, 2006, 08:55:21 ; Search time 66.4407 Seconds  
(without alignments)  
106.189 Million cell updates/sec

Title: US-10-089-500-5  
Perfect score: 54  
Sequence: 1 VKLGTYYFDS 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 1000 summaries

Database :

UniProt 05.80.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	44	81.5	217	2	O6LNK3 PHOPR
2	43	79.6	424	2	O5LXP9 STRT1
3	43	79.6	424	2	Q5MZA0 STRT2
4	43	79.6	456	2	Q97H36 CLOAB
5	41	75.9	206	2	O6LUF1 PHOPR
6	41	75.9	368	2	O5FKV2 LACAC
7	41	75.9	704	2	O8DKC6 SYNEL
8	41	75.9	1040	2	O5CK18 CRYHO
9	40	74.1	368	2	Q932E5 STAM
10	40	74.1	4130	2	Q7PIA2 CHRVO
11	39	72.2	520	2	O6QC13 9CLOS
12	39	72.2	565	2	Q74IS2 LACVO
13	39	72.2	2817	2	Q97K42 CLOAB
14	38	70.4	262	2	O8CFP5 STAP
15	38	70.4	281	2	O8LTP9 9CAUD
16	38	70.4	382	2	O5HPQ7 STAP
17	38	70.4	405	2	O8AL15 THETN
18	38	70.4	423	2	Q4ZE15 9CAUD
19	38	70.4	476	2	Q4TWH9 9SPHN
20	38	70.4	587	1	COAT_PAVL3
21	38	70.4	587	2	Q84367 MUMIV
22	38	70.4	587	2	Q84364 MUMIV
23	38	70.4	708	2	O54U89 DICDI
24	38	70.4	716	1	COAT_MUMIV
25	38	70.4	718	1	COAT_MUMIM
26	38	70.4	723	2	Q84507 MUMIV
27	38	70.4	729	2	Q84366 MUMIV
28	38	70.4	847	2	O55476 SYN3
29	38	70.4	907	2	Q9FW49 ARATH
30	38	70.4	921	1	VID28 YEAST
31	38	70.4	1781	2	Q5SBLJ5_LACRE

32	38	70.4	1781	2	Q4JCS4_LACRE	O4JCS4 lactobacill
33	38	70.4	1781	2	Q4JLC7_LACRE	O4JLC7 lactobacill
34	37	68.5	221	2	Q5JCY5_PYRKO	Q5JCY5 pyrococcus
35	37	68.5	245	2	Q4KAC8_PSEFS	Q4KAC8 pseudomonas
36	37	68.5	254	2	Q67LI9_SYMTH	Q67LI9 symbiodonae
37	37	68.5	338	2	Q6CLB5_KLULA	Q6CLB5 kluyveromyc
38	37	68.5	368	2	Q5YF08_9VIRU	Q5YF08 rock bream
39	37	68.5	368	2	Q8QUM8_9VIRU	Q8QUM8 infectious
40	37	68.5	368	2	Q4KS76_9VIRU	Q4KS76 orange-spot
41	37	68.5	380	2	Q8WV03_HUMAN	Q8WV03 homo sapien
42	37	68.5	393	2	Q8NB16_HUMAN	Q8NB16 homo sapien
43	37	68.5	522	2	Q815Q4_BACCR	Q815Q4 bacillus ce
44	37	68.5	527	2	Q5UQB6_MIMIV	Q5UQB6 mimivirus
45	37	68.5	529	2	Q8RCC8_THETN	Q8RCC8 thermoanaer
46	37	68.5	798	2	Q9RKF0_STRCO	Q9RKF0 streptomyce
47	37	68.5	814	2	Q80692_ARATH	Q80692 arabidopsi
48	37	68.5	1101	2	Q8AB16_BACTN	Q8AB16 bacteroides
49	37	68.5	1297	2	Q67TF0_SYMTH	Q67TF0 symbiobacte
50	37	68.5	1772	2	Q5SBN0_LACRE	Q5SBN0 lactobacill
51	36	66.7	149	2	Q6N5D8_RHOPA	Q6N5D8 rhodopseudo
52	36	66.7	160	2	Q8DX46_STRA5	Q8DX46 streptococc
53	36	66.7	161	2	Q62210_CABER	Q62210 caenorhabdi
54	36	66.7	179	2	Q570C6_ARATH	Q570C6 arabidopsi
55	36	66.7	180	2	Q600N0_MYCHY	Q600N0 mycoplasma
56	36	66.7	195	2	Q694A2_GLOWR	Q694A2 glossina mo
57	36	66.7	198	2	Q62BG3_BURMA	Q62BG3 burkholderi
58	36	66.7	203	1	YLAE_BACSU	Q07629 bacillus su
59	36	66.7	217	2	Q63LX9_BURPS	Q63LX9 burkholderi
60	36	66.7	258	1	FLAB3_PYRKO	Q9V2W9 pyrococcus
61	36	66.7	281	2	Q60SS9_CABER	Q60SS9 caenorhabdi
62	36	66.7	313	2	Q4HPL2_CAMUP	Q4HPL2 campylobact
63	36	66.7	348	2	Q5LBF9_BACFN	Q5LBF9 bacteroides
64	36	66.7	348	2	Q64RZ1_BACFR	Q64RZ1 bacteroides
65	36	66.7	352	2	Q4QIB5_LEIMA	Q4QIB5 leishmania
66	36	66.7	361	2	Q9LZQ3_ARATH	Q9LZQ3 arabidopsi
67	36	66.7	393	2	Q8RWB1_ARATH	Q8RWB1 arabidopsi
68	36	66.7	401	2	Q9V5K2_DROME	Q9V5K2 droseophila
69	36	66.7	409	2	P91783_POLPE	P91783 polyorchis
70	36	66.7	423	2	Q5K772_CRYNE	Q5K772 crypococcu
71	36	66.7	427	2	Q5SHN2_CRYNE	Q5SHN2 cryptococcu
72	36	66.7	471	2	Q66K04_MOUSE	Q66K04 mus musculu
73	36	66.7	605	2	Q6DE64_XENLA	Q6DE64 xenopus lae
74	36	66.7	609	2	Q6P6Z9_XENLA	Q6P6Z9 xenopus lae
75	36	66.7	637	2	Q97276_SULSO	Q97276 sulfobus
76	36	66.7	675	1	C25AA_BACTY	Q87906 bacillus th
77	36	66.7	693	2	Q600J4_MYCHY	Q600J4 mycoplasma
78	36	66.7	703	2	Q6CD57_YARLI	Q6CD57 yartowia li
79	36	66.7	729	2	Q4YZ01_PLABE	Q4YZ01 plasmodium
80	36	66.7	813	2	Q7RE10_PLAYO	Q7RE10 plasmodium
81	36	66.7	889	2	Q7R9D1_PLAYO	Q7R9D1 plasmodium
82	36	66.7	1093	2	Q4PEA8_USTMA	Q4PEA8 ustilago ma
83	36	66.7	1470	2	Q5CPG5_CRYPV	Q5CPG5 cryptospori
84	36	66.7	1676	2	Q7R124_GIALA	Q7R124 giardia lam
85	36	66.7	3763	2	Q8T2A1_DICDI	Q8T2A1 dictyosteli
86	35	64.8	108	2	Q6PKZ0_RABIT	Q6PKZ0 cryctolagus
87	35	64.8	163	2	Q6MUB2_MYCMS	Q6MUB2 mycoplasma
88	35	64.8	186	2	Q4K5Q8_PSEFS	Q4K5Q8 pseudomonas
89	35	64.8	228	1	UL09_HCMVA	P16745 human cytom
90	35	64.8	263	2	Q5WJ78_BACSC	Q5WJ78 bacillus cl
91	35	64.8	271	2	Q9WZR9_THEMA	Q9WZR9 thermotoga
92	35	64.8	287	2	Q5HPU7_STAEQ	Q5HPU7 staphylococ
93	35	64.8	287	2	Q8CSU4_STABP	Q8CSU4 staphylococ
94	35	64.8	294	2	Q4LSU6_STAHJ	Q4LSU6 staphylococ
95	35	64.8	296	2	Q58LY3_9BURK	Q58LY3 deltia teu
96	35	64.8	319	2	Q5TOP4_ANOGA	Q5TOP4 anopheles g
97	35	64.8	332	2	Q7PVQ9_ANOGA	Q7PVQ9 anopheles g
98	35	64.8	333	2	Q95FA3_9AELA	Q95FA3 myodocarpus
99	35	64.8	339	2	O17844_CABEL	O17844 caenorhabdi
100	35	64.8	341	2	Q90XR1_BRARE	Q90XR1 brachydanio
101	35	64.8	341	2	Q90XR3_BRARE	Q90XR3 brachydanio
102	35	64.8	341	2	Q6DI46_BRARE	Q6DI46 brachydanio
103	35	64.8	350	2	Q5CFQ1_CRYHO	Q5CFQ1 cryptospori
104	35	64.8	358	2	Q5SE75_9STRA	Q5SE75 thalassiosi

105	35	64.8	358	2	Q95F98_9APIA	Q95F98 mydocarpus	178	34	63.0	291	2	Q7WCG1_BORPA	Q7WCG1 bordetella
106	35	64.8	358	2	Q95F99_9APIA	Q95F99 mydocarpus	179	34	63.0	291	2	Q7WQ63_BORBR	Q7WQ63 bordetella
107	35	64.8	358	2	Q95FA2_9APIA	Q95FA2 mydocarpus	180	34	63.0	294	2	Q5SVV3_MOUSE	Q5SVV3 mus musculus
108	35	64.8	358	2	Q95FA4_9APIA	Q95FA4 mydocarpus	181	34	63.0	305	2	Q83HJ2_TROW8	Q83HJ2 tropheryma
109	35	64.8	358	2	Q95FA5_9APIA	Q95FA5 mydocarpus	182	34	63.0	307	2	Q4ZUE9_PSESY	Q4ZUE9 pseudomonas
110	35	64.8	372	2	Q95CIS3_LACIA	Q95CIS3 lactococcus	183	34	63.0	309	2	Q6S213_VOICA	Q6S213 volvox cart
111	35	64.8	380	2	Q4Z028_PLABE	Q4Z028 plasmodium	184	34	63.0	314	2	Q83GP2_TROWT	Q83GP2 tropheryma
112	35	64.8	386	2	Q93JX2_PSEPU	Q93JX2 pseudomonas	185	34	63.0	333	2	Q832G4_ENTFA	Q832G4 enterococcus
113	35	64.8	394	2	Q83E19_CORBU	Q83E19 coxiella bu	186	34	63.0	334	2	Q4VIC2_BACCZ	Q4VIC2 bacillus ce
114	35	64.8	434	2	Q8RELS_ANAPH	Q8RELS anaplasmia p	187	34	63.0	335	2	Q838M0_ENTFA	Q838M0 enterococcus
115	35	64.8	439	2	Q5B6R5_EMENI	Q5B6R5 aspergillus	188	34	63.0	338	2	Q8CDY4_MOUSE	Q8CDY4 mus musculus
116	35	64.8	452	1	COQ1_YARLI	Q6CBH3 yarrowia li	189	34	63.0	355	2	Q95FA6_9APIA	Q95FA6 mydocarpus
117	35	64.8	474	2	Q51DM0_ENTHI	Q51DM0 entamoeba h	190	34	63.0	357	2	Q95ZJ9_ARATH	Q95ZJ9 arabidopsis
118	35	64.8	475	2	Q4MT9_NANEQ	Q4MT9 nancarchaeu	191	34	63.0	361	2	Q8VVF4_ARATH	Q8VVF4 arabidopsis
119	35	64.8	500	2	Q4RTP7_TETNG	Q4RTP7 tetraodon n	192	34	63.0	362	2	Q4L4L4_STAHH	Q4L4L4 staphylococ
120	35	64.8	504	2	Q5AXC4_EMENI	Q5AXC4 aspergillus	193	34	63.0	371	2	Q6M193_METMP	Q6M193 methanococ
121	35	64.8	515	2	Q5LH83_BACFN	Q5LH83 bacteroides	194	34	63.0	371	2	Q8NKL0_STAAM	Q8NKL0 staphylococ
122	35	64.8	515	2	Q64Y45_BACFR	Q64Y45 bacteroides	195	34	63.0	374	2	Q61QF7_CAEBR	Q61QF7 caenorhabdi
123	35	64.8	515	2	Q92N18_RHIME	Q92N18 rhizobium m	196	34	63.0	423	2	Q59MK9_CANAL	Q59MK9 candida alb
124	35	64.8	519	2	Q9RG14_BACFR	Q9RG14 bacteroides	197	34	63.0	433	1	SYH_CANBF	Q7VVR8 candidatus
125	35	64.8	520	2	Q8A6P9_BACTN	Q8A6P9 bacteroides	198	34	63.0	441	2	Q895H8_LACPL	Q895H8 lactobacill
126	35	64.8	563	2	Q8LN96_ORYSA	Q8LN96 oryza sativ	199	34	63.0	461	2	Q81PJ9_BACAN	Q81PJ9 bacillus an
127	35	64.8	573	2	Q4I7Y9_GIBZE	Q4I7Y9 gibberella	200	34	63.0	461	2	Q63A88_BACCZ	Q63A88 bacillus ce
128	35	64.8	579	2	Q8T4A3_DROME	Q8T4A3 drosophila	201	34	63.0	463	2	Q826D0_STRAW	Q826D0 streptomyce
129	35	64.8	579	2	Q4Y3F0_PLACH	Q4Y3F0 plasmodium	202	34	63.0	480	2	Q746Z5_GEOSL	Q746Z5 geobacter s
130	35	64.8	650	2	Q51DS3_ENTHI	Q51DS3 entamoeba h	203	34	63.0	484	2	Q4Q1K0_LEHMA	Q4Q1K0 leishmania
131	35	64.8	661	2	Q5L8E2_BACFN	Q5L8E2 bacteroides	204	34	63.0	498	2	Q8EMH2_OEBIH	Q8EMH2 oceanobacil
132	35	64.8	661	2	Q64NP2_BACFR	Q64NP2 bacteroides	205	34	63.0	504	2	Q5L1C3_GEOKA	Q5L1C3 geobacillus
133	35	64.8	663	2	Q8A4A9_BACTN	Q8A4A9 bacteroides	206	34	63.0	510	1	ABGT_ECOLI	P46133 escherichia
134	35	64.8	669	2	Q18300_CAEEL	Q18300 caenorhabdi	207	34	63.0	523	1	CDPK1_PLAF7	P62344 plasmodium
135	35	64.8	685	2	Q17378_CAEEL	Q17378 caenorhabdi	208	34	63.0	523	1	CDPK1_PLAFK	P62343 plasmodium
136	35	64.8	685	2	Q60L15_CAEER	Q60L15 caenorhabdi	209	34	63.0	523	2	Q4YRR5_PLABE	Q4YRR5 plasmodium
137	35	64.8	685	2	Q7RHP1_PLAYO	Q7RHP1 plasmodium	210	34	63.0	523	2	Q4XV45_PLACH	Q4XV45 plasmodium
138	35	64.8	685	2	Q20423_CAEEL	Q20423 caenorhabdi	211	34	63.0	532	2	Q5LAN4_BACFN	Q5LAN4 bacteroides
139	35	64.8	702	2	Q4IHZ9_GIBZE	Q4IHZ9 gibberella	212	34	63.0	532	2	Q64R32_BACFR	Q64R32 bacteroides
140	35	64.8	703	2	Q5PDW6_SALPA	Q5PDW6 salmonella	213	34	63.0	534	1	CDPK1_PLAYO	Q7Rnh3 plasmodium
141	35	64.8	705	2	Q87192_VIBPA	Q87192 vibrio para	214	34	63.0	536	2	Q7N4V3_PHOLL	Q7N4V3 photorhabdu
142	35	64.8	771	2	Q4Q7S6_LEIMA	Q4Q7S6 leishmania	215	34	63.0	537	2	Q8A1R1_BACTN	Q8A1R1 bacteroides
143	35	64.8	819	2	Q7V415_DROME	Q7V415 drosophila	216	34	63.0	565	2	Q5FJN0_LACAC	Q5FJN0 lactobacill
144	35	64.8	822	2	Q7QBNO_ANOGA	Q7QBNO anopheles g	217	34	63.0	583	2	Q8OKV4_9PHVC	Q8OKV4 ectocarpus
145	35	64.8	837	2	Q21287_CAEEL	Q21287 caenorhabdi	218	34	63.0	586	2	CYDD_HAEIN	P45082 haemophilus
146	35	64.8	850	2	Q4Q3V2_LEIMA	Q4Q3V2 leishmania	219	34	63.0	586	1	Q4QLD9_HAE18	Q4QLD9 haemophilus
147	35	64.8	936	2	Q7P2M0_FUSNV	Q7P2M0 fusobacteri	220	34	63.0	587	2	Q65U03_MANSUM	Q65U03 pasteurella
148	35	64.8	936	2	Q8R102_FUSNN	Q8R102 fusobacteri	221	34	63.0	587	2	Q9CN67_PASMU	Q9CN67 pasteurella
149	35	64.8	946	2	Q7V9M9_FROMA	Q7V9M9 prochloroco	222	34	63.0	601	2	Q6Q1P5_9VIRU	Q6Q1P5 mouse parvo
150	35	64.8	962	2	Q7LXX1_ARATH	Q7LXX1 arabidopsis	223	34	63.0	627	2	Q6CGS5_YARLI	Q6CGS5 yarrowia li
151	35	64.8	965	2	Q7PXM3_ANOGA	Q7PXM3 anopheles g	224	34	63.0	636	2	Q820J9_ANASP	Q820J9 anabaena ep
152	35	64.8	967	2	Q60LS4_CAEER	Q60LS4 caenorhabdi	225	34	63.0	636	2	Q60BX3_METCA	Q60BX3 methylococ
153	35	64.8	1009	2	Q4P4Z3_USTMA	Q4P4Z3 ustilago ma	226	34	63.0	644	2	Q75QL6_9VIRU	Q75QL6 bacterioph
154	35	64.8	1040	2	Q5CTG4_CRYPV	Q5CTG4 cryptospori	227	34	63.0	651	2	Q68WX7_RICTY	Q68WX7 rickettsia
155	35	64.8	1113	2	Q9XXK4_CAEEL	Q9XXK4 caenorhabdi	228	34	63.0	656	2	Q72YN0_BACCL	Q72YN0 bacillus ce
156	35	64.8	3895	2	Q9PZ97_9FLAV	Q9PZ97 pestivirus	229	34	63.0	692	2	Q97YM6_SULSO	Q97YM6 sulfolobus
157	34	63.0	84	1	ACHA_HERIC	P54251 herpeseste i	230	34	63.0	704	2	Q5A9E3_CANAL	Q5A9E3 candida alb
158	34	63.0	86	2	Q8ZXJ9_PYRAE	Q8ZXJ9 pyrobaculum	231	34	63.0	705	1	CDCS_YEAST	F32562 saccharomyc
159	34	63.0	110	1	UL68_HQWVA	P16748 human cytom	232	34	63.0	708	2	Q81R76_BACAN	Q81R76 bacillus an
160	34	63.0	125	2	Q6ZIF6_9VIRU	Q6ZIF6 pyrobaculum	233	34	63.0	729	2	Q83430_9VIRU	Q83430 mouse parvo
161	34	63.0	153	2	Q86F96_SCHJA	Q86F96 schistosoma	234	34	63.0	760	2	Q86ZB2_BOTCI	Q86ZB2 botrytis ci
162	34	63.0	160	2	Q8EBK2_SHEON	Q8EBK2 shewanella	235	34	63.0	762	2	Q84FS9_BACFO	Q84FS9 bacteroides
163	34	63.0	204	2	Q7AEG0_ECO57	Q7AEG0 escherichia	236	34	63.0	784	1	OSTA_SALPI	Q5PDE5 salmonella
164	34	63.0	208	2	Q4NP32_3DELT	Q4NP32 anaeromyxob	237	34	63.0	784	1	OSTA_SALTI	Q5Z916 salmonella
165	34	63.0	209	1	V1428_AQAE	Q67421 aquifex aeo	238	34	63.0	786	1	OSTA_SALTY	Q57197 salmonella
166	34	63.0	227	2	Q4YS05_PLABE	Q4YS05 plasmodium	239	34	63.0	786	1	OSTA_SALTY	Q8ZRW0 salmonella
167	34	63.0	230	2	Q8X8N7_ECO57	Q8X8N7 escherichia	240	34	63.0	791	2	Q8KH06_SPHCR	Q8KH06 sphingobium
168	34	63.0	248	2	Q5V701_HALMA	Q5V701 haloarcula	241	34	63.0	794	2	Q7UMJ5_RHOBA	Q7UMJ5 rhodopirell
169	34	63.0	257	2	Q8K6K2_STRP3	Q8K6K2 streptococ	242	34	63.0	812	2	Q4NSX6_THEHU	Q4NSX6 theileria pl
170	34	63.0	258	1	THIG_CAMJE	Q9PNP6 campylobact	243	34	63.0	881	2	Q4G377_EMITHU	Q4G377 emilia h
171	34	63.0	258	1	THIG_CAMJR	Q5HU56 campylobact	244	34	63.0	977	2	Q5A9P1_CANAL	Q5A9P1 candida alb
172	34	63.0	270	2	Q831I9_ENTFA	Q831I9 enterococcus	245	34	63.0	989	2	Q7R3Z4_GIALA	Q7R3Z4 giardia lam
173	34	63.0	277	2	Q25740_HELPJA	Q25740 helicobacte	246	34	63.0	1025	2	Q84IL2_CLOSO	Q84IL2 clostridium
174	34	63.0	277	2	Q9ZKAI_HELPJU	Q9ZKAI helicobacte	247	34	63.0	1058	2	Q8EYM9_9BACL	Q8EYM9 paenibacill
175	34	63.0	282	2	Q5B211_SCHJA	Q5B211 schistosoma	248	34	63.0	1137	2	Q8CZU0_YERPE	Q8CZU0 yersinia pe
176	34	63.0	282	2	Q8XRK0_RALSO	Q8XRK0 ralstonia s	249	34	63.0	1235	2	Q81E31_BACCE	Q81E31 bacillus ce
177	34	63.0	290	2	Q6L0C0_PICTO	Q6L0C0 microphilus	250	34	63.0	1400	2	Q4MHJ3_BACCE	Q4MHJ3 bacillus ce

251	34	63.0	1400	2	Q63B29_BACCZ	Q63b29 bacillus ce	324	61.1	277	2	Q79381_9LILI	Q79381 maranta leu
252	34	63.0	1400	2	Q6HJF3_BACHK	Q6hj3 bacillus th	325	61.1	283	2	Q4QIS6_HAB18	Q4qls6 haemophilus
253	34	63.0	1411	2	Q9S322_ARATH	Q9sfj3 arabidopsis	326	61.1	289	2	Q5DXU8_VIBF1	Q5dyu8 vibrio fisc
254	34	63.0	1440	2	Q6IY78_CAEBR	Q6iy78 caenorhabdi	327	61.1	292	2	Q4LRH8_9BORK	Q4lrh8 gibbholderi
255	34	63.0	1536	2	Q5CUC2_CRYPV	Q5cuc2 cryptospori	328	61.1	296	2	Q41292_GIBZE	Q41292 gibbholderi
256	34	63.0	1587	2	Q9SLQ0_ORISA	Q9slq0 cryza sativ	329	61.1	300	2	Q54UI0_DICDI	Q54ui0 dictyosteli
257	34	63.0	1772	2	Q5SBN3_LACRE	Q5sbn3 lactobacill	330	61.1	301	2	Q7MYE0_PHOTO	Q7mye0 photorhabdu
258	34	63.0	1773	2	Q55I70_CRYNE	Q55i70 cryptococcu	331	61.1	303	2	Q9VTM8_DROME	Q9vtm8 drosophila
259	34	63.0	1841	2	Q5K705_CRYNE	Q5k705 cryptococcu	332	61.1	310	2	Q7PZCS_ANOGA	Q7pzc5 anopheles g
260	34	63.0	1896	2	Q75076_ASHGO	Q75076 ashya goss	333	61.1	310	2	Q9N611_LEIMA	Q9n611 leishmania
261	34	63.0	1943	2	Q25331_HELFP	Q25331 helicobacte	334	61.1	318	2	Q5A462_CANAL	Q5a462 candida alb
262	34	63.0	1945	2	Q4KR25_GLOS	Q4kr25 tomato chlo	335	61.1	327	2	Q7XYP5_CHIS6	Q7xyp5 chlorarachn
263	34	63.0	2145	2	Q6BI73_DEBHA	Q6bi73 debaryomyce	336	61.1	327	2	Q6W511_MANSM	Q6w511 manheimia
264	34	63.0	2176	2	Q9UT24_SCHPO	Q9ut24 schizosacch	337	61.1	339	2	Q8SZ26_ENCCU	Q8stz6 enccephalito
265	34	63.0	2562	2	Q54827_DICDI	Q54827 dictyosteli	338	61.1	338	2	Q8PP59_XANAC	Q8pp59 xanthomonas
266	34	63.0	2857	2	Q51F00_ENTHI	Q51f00 entamoeba h	339	61.1	342	2	Q8RD75_THETN	Q8rd75 thermoanaer
267	34	63.0	3311	2	Q74QPO_YERPE	Q74qpo yersinia pe	340	61.1	343	2	Q5ZKQ0_CHICK	Q5zkg0 gallus gall
268	34	63.0	3886	2	Q666G1_YERPS	Q666g1 yersinia ps	341	61.1	346	2	Q5EMM5_YERPS	Q5emm5 yersinia ps
269	34	63.0	4767	2	Q17301_CAEBR	Q17301 caenorhabdi	342	61.1	347	2	Q4UR22_XANCP	Q4ur22 xanthomonas
270	34	63.0	7743	2	Q618P4_CAEBR	Q618p4 caenorhabdi	343	61.1	347	2	Q8PCG0_XANCP	Q8pcg0 xanthomonas
271	34	63.0	8402	2	Q4REB9_TETNG	Q4reb9 tetradoon n	344	61.1	349	2	Q9M6N2_VICFA	Q9m6n2 victa faba
272	33	61.1	60	2	Q8RBV0_THETN	Q8rbv0 thermoanaer	345	61.1	359	2	Q9HI59_THEAC	Q9hi59 thermoplasma
273	33	61.1	67	1	ATP8_ARTJA	Q99598 artibeus ja	346	61.1	360	2	Q66CG8_YERPS	Q66cg8 yersinia ps
274	33	61.1	97	2	Q4K0A5_PSEF5	Q4kd45 pseudomonas	347	61.1	360	2	Q8ZG94_YERPE	Q8z94 yersinia pe
275	33	61.1	109	2	Q68948_AZOPA	Q68948 azotobacter	348	61.1	367	2	Q74VU4_YERPE	Q74vu4 yersinia pe
276	33	61.1	109	2	Q68950_AZOSA	Q68950 azotobacter	349	61.1	367	2	Q6DFE5_XENLA	Q6dfe5 xenopus lae
277	33	61.1	109	2	Q9XB18_9BACT	Q9xb18 nitrogen-fi	350	61.1	369	1	OMPF_XENNE	Q56828 xenorhabdus
278	33	61.1	109	2	Q9XB21_9BACT	Q9xb21 nitrogen-fi	351	61.1	375	2	Q9KDV6_BACHD	Q9kdv6 bacillus ha
279	33	61.1	114	2	Q4XNC8_PLACH	Q4xnc8 plasmodium	352	61.1	376	2	Q8TJ85_METAC	Q8tj85 methanosarc
280	33	61.1	114	2	Q4Y628_PLACH	Q4y628 plasmodium	353	61.1	376	2	Q8D051_YERPE	Q8d051 yersinia pe
281	33	61.1	114	2	Q4YF22_PLABE	Q4yf22 plasmodium	354	61.1	378	2	Q8PRQ1_METMA	Q8prq1 methanosarc
282	33	61.1	114	2	Q4Y877_PLABE	Q4y877 plasmodium	355	61.1	378	2	Q8PSN2_METMA	Q8psn2 methanosarc
283	33	61.1	114	2	Q95J11_MACFA	Q95j11 macaca fasc	356	61.1	378	2	Q8Q079_METMA	Q8q079 methanosarc
284	33	61.1	118	2	Q7R973_PLAYO	Q7r973 plasmodium	357	61.1	379	2	Q8K210_MOUSE	Q8k210 mus musculu
285	33	61.1	120	1	HV03_MOUSE	P01747 mus musculu	358	61.1	383	2	Q4FRX0_9GAMM	Q4frx0 psychrobact
286	33	61.1	120	2	Q9UW04_ASCRA	Q9uw04 ascochyta r	359	61.1	387	2	Q8GRCS_PARDP	Q8grcs paracoccus
287	33	61.1	127	2	Q98RT3_GUITH	Q98rt3 guillardia	360	61.1	390	2	Q17274_CAEEL	Q17274 caenorhabdi
288	33	61.1	129	2	Q7MR60_VIBVY	Q7mr60 vibrio vuln	361	61.1	396	2	Q93A40_ENTPA	Q93a40 enterococcu
289	33	61.1	133	2	Q8DF92_VIBVU	Q8df92 vibrio vuln	362	61.1	397	2	Q9AGN0_CLOPE	Q9agn0 clostridium
290	33	61.1	161	1	FARP_ASCSU	P41854 a friramide	363	61.1	397	2	Q7A2X3_STAAM	Q7a2x3 staphylococ
291	33	61.1	164	2	Q7QFN8_ANOGA	Q7qfn8 anopheles g	364	61.1	400	2	Q8Y821_LISMO	Q8y821 listeria mo
292	33	61.1	164	2	Q6G830_STAAS	Q6g830 staphylococ	365	61.1	404	2	Q8CVG5_ECCL6	Q8cvg5 escherichia
293	33	61.1	164	2	Q6G130_STAAR	Q6g130 staphylococ	366	61.1	423	2	Q8TT73_METAC	Q8tt73 methanosarc
294	33	61.1	164	2	Q5HH14_STAAC	Q5hh14 staphylococ	367	61.1	426	2	Q6HRR5_BACAN	Q6hrr5 bacillus an
295	33	61.1	164	2	Q7ALE7_STAAM	Q7ale7 staphylococ	368	61.1	441	2	Q6LSY7_PHOPR	Q6lsy7 phocobacter
296	33	61.1	164	2	Q7AGN1_STAAN	Q7agn1 staphylococ	369	61.1	443	2	Q4QP34_HAB18	Q4qp34 haemophilus
297	33	61.1	179	2	Q9V101_STAAM	Q9v101 staphylococ	370	61.1	443	2	Q9CJS4_PASNU	Q9cjs4 pasteurella
298	33	61.1	179	2	Q870B3_9FUNG	Q870b3 piromyces s	371	61.1	444	2	Q7VP64_HABDU	Q7vp64 haemophilus
299	33	61.1	183	2	Q8GGH4_ENTCL	Q8ggh4 enterobacte	372	61.1	448	2	Q4SK23_TETNG	Q4sk23 tetradoon n
300	33	61.1	185	2	Q9F258_STRCO	Q9f258 streptomyc	373	61.1	449	2	Q6SRC6_MANSM	Q6src6 manheimia
301	33	61.1	203	2	Q4XT08_PLACH	Q4xt08 plasmodium	374	61.1	452	2	Q5ZZE8_LEGPH	Q5zze8 legionella
302	33	61.1	204	2	Q9ZVG4_ARATH	Q9zvg4 arabidopsis	375	61.1	453	2	Q7P5Y1_FUSNV	Q7p5y1 fusobacteri
303	33	61.1	205	2	Q4HMR5_CAMILA	Q4hm5 campylobact	376	61.1	453	2	Q8RE36_FUSNV	Q8re36 fusobacteri
304	33	61.1	208	2	Q5BDD3_EMENT	Q5bdd3 aspergillus	377	61.1	461	2	Q4MGA9_BACCE	Q4mga9 bacillus ce
305	33	61.1	213	2	Q5MAQ5_EACSK	Q5maq5 bacillus cl	378	61.1	468	2	Q60276_HUMAN	Q60276 homo sapien
306	33	61.1	213	2	Q5SRG9_MOUSE	Q5srg9 mus musculu	379	61.1	468	2	Q4YIJ4_PLABE	Q4yij4 plasmodium
307	33	61.1	219	2	Q5JH01_PYROCC	Q5jh01 pyrococcus	380	61.1	472	1	VNFD_AZOCH	P15332 azotobacter
308	33	61.1	226	2	Q8LDR3_ARATH	Q8ldr3 arabidopsis	381	61.1	473	1	VNFD_AZOVI	P16855 azotobacter
309	33	61.1	228	2	Q9RDU2_PSESP	Q9rd2 pseudomonas	382	61.1	474	2	Q4JLK4_AZOVI	Q4jlk4 azotobacter
310	33	61.1	236	2	Q5QWN7_IDILO	Q5qwn7 idiomarina	383	61.1	479	2	Q98D66_RHILO	Q98d66 rhizobium l
311	33	61.1	239	2	Q8CUI3_OCEIH	Q8cuy3 oceanobacil	384	61.1	496	2	Q4TRES_9SPHN	Q4tres erythrobact
312	33	61.1	247	2	Q5ESC0_VIBF1	Q5esc0 vibrio fisc	385	61.1	500	2	Q8IE44_PLAOF	Q8ie44 plasmodium
313	33	61.1	254	2	Q9SH42_ARATH	Q9sh42 arabidopsis	386	61.1	500	2	Q7UL71_RHOBA	Q7ul71 rhodospirell
314	33	61.1	255	2	Q8IY35_HUMAN	Q8iy35 homo sapien	387	61.1	512	2	Q6ASU1_PROAC	Q6asu1 propionibac
315	33	61.1	256	1	ATP6_PICCA	P48879 pichia cana	388	61.1	536	2	Q7N4I7_PHOLL	Q7n4i7 photorhabdu
316	33	61.1	256	2	Q7RMG4_PLAYO	Q7rmg4 plasmodium	389	61.1	537	1	MPBA_EGOLI	P77348 escherichia
317	33	61.1	258	1	Y984_HAEIN	P43908 haemophilus	390	61.1	537	2	Q5EHP4_SALPA	Q5ehp4 salmonella
318	33	61.1	259	1	THIG_CHLIT	Q8kej1 chlorobium	391	61.1	537	2	Q8Z7A5_SALTI	Q8z7a5 salmonella
319	33	61.1	262	2	Q9VUJ4_DROME	Q9vuj4 drosophila	392	61.1	537	2	Q8ZPE8_SALTY	Q8zpe8 salmonella
320	33	61.1	268	2	Q75806_HUMAN	Q75806 homo sapien	393	61.1	538	2	Q8ZE45_YERPE	Q8ze45 yersinia pe
321	33	61.1	271	1	HXA9_MOUSE	P09631 mus musculu	394	61.1	538	2	Q6GA74_YERPS	Q6ga74 yersinia ps
322	33	61.1	272	1	HXA9_HUMAN	P31269 homo sapien	395	61.1	538	2	Q6D5P9_ERWCT	Q6d5p9 erwina car
323	33	61.1	277	2	Q79353_9APTA	Q79353 hydrocotyle	396	61.1	540	2	Q7N3Y4_PHOLL	Q7n3y4 photorhabdu



397	33	61.1	544	2	Q5WGG1_BACSK	Q5wgg1 bacillus cl	470	33	61.1	889	2	Q889A2_PSESM	Q889a2 pseudomonas
398	33	61.1	544	2	Q8CW38_ECOL6	Q8cw38 escherichia	471	33	61.1	959	2	Q29498_ARCFU	Q29498 archaeoglob
399	33	61.1	544	2	Q83R72_SHIFL	Q83r72 shigella fl	472	33	61.1	966	1	STK10_MOUSE	Q55098 mus musculus
400	33	61.1	544	2	Q8X8M7_ECO57	Q8x8m7 escherichia	473	33	61.1	966	2	Q5SS75_MOUSE	Q5ss75 mus musculus
401	33	61.1	550	2	Q97D46_CLOAB	Q97d46 clostridium	474	33	61.1	986	2	Q5DTS2_MOUSE	Q5dts2 mus musculus
402	33	61.1	555	2	Q61UB8_CAEBR	Q61ub8 caenorhabdi	475	33	61.1	994	2	Q61KL3_CAEBR	Q61kl3 caenorhabdi
403	33	61.1	565	2	Q4RSY4_TETNG	Q4rsy4 tetraodon n	476	33	61.1	1305	2	Q5OMC6_ENTHI	Q50mc6 entamoeba h
404	33	61.1	566	2	Q60V03_CAEBR	Q60v03 caenorhabdi	477	33	61.1	1321	2	Q7S886_NEUCR	Q7s886 neurospora
405	33	61.1	572	2	Q505J3_RAT	Q505j3 rattus norv	478	33	61.1	1400	2	Q739A2_BACC1	Q739a2 bacillus ce
406	33	61.1	572	2	Q80XH4_MOUSE	Q80xh4 mus musculus	479	33	61.1	1414	2	Q5J1Q4_9NOCA	Q5j1q4 nocardia ce
407	33	61.1	575	2	Q658N2_HUMAN	Q658n2 homo sapien	480	33	61.1	1773	2	Q6AZH2_XENLA	Q6azh2 xenopus lae
408	33	61.1	575	2	Q96G45_HUMAN	Q96g45 homo sapien	481	33	61.1	1825	2	Q6FVM0_CANGA	Q6fvm0 candida gla
409	33	61.1	584	2	Q6BDY6_PAVC	Q6bdy6 canine parv	482	33	61.1	1849	2	Q8IHX8_PLAP7	Q8ihx8 plasmodium
410	33	61.1	594	2	Q4CFB8_CRYHO	Q4cfb8 cryptospori	483	33	61.1	2163	1	BRR2_YEAST	Q512s8 entamoeba h
411	33	61.1	594	2	Q4YNV1_PLABE	Q4ynv1 plasmodium	484	33	61.1	2270	2	Q512S8_ENTHI	Q512s8 entamoeba h
412	33	61.1	603	2	Q5CQ55_CRYPV	Q5cq55 cryptospori	485	33	61.1	2295	2	Q91TPI_TUHV1	Q91tp1 tupaid her
413	33	61.1	605	2	Q5DU24_MOUSE	Q5du24 mus musculus	486	33	61.1	2341	2	Q7RR45_PLAYO	Q7rr45 plasmodium
414	33	61.1	607	2	Q9FG45_ARATH	Q9fg45 arabidopsis	487	33	61.1	2971	1	YCX9_CHLRE	Q32065 chlamydomon
415	33	61.1	609	2	Q49556_ARATH	Q49556 arabidopsis	488	33	61.1	3194	2	Q9ZLM3_HELPJ	Q9zlm3 helicobacte
416	33	61.1	616	2	Q4KU04_VIRU	Q4ku04 vicia crypt	489	33	61.1	3871	2	Q20911_CAEBL	Q20911 caenorhabdi
417	33	61.1	617	2	Q8E362_STR33	Q8e362 streptococc	490	33	61.1	8243	2	Q96554_CRYPV	Q96554 cryptospori
418	33	61.1	617	2	Q8DXD8_STR45	Q8dx8 streptococc	491	33	61.1	8243	2	Q5CUM8_CRYPV	Q5cum8 cryptospori
419	33	61.1	618	2	Q99XY4_STRP	Q99xy4 streptococc	492	33	61.1	11103	2	Q54CU4_DICDI	Q54cu4 dictyosteli
420	33	61.1	618	2	Q8NZB4_STRP8	Q8nz8 streptococc	493	32.5	60.2	677	2	Q4N4R9_THEPA	Q4nm17 plasmodium
421	33	61.1	618	2	Q5X9U7_STRP6	Q5x9u7 streptococc	494	32	59.3	27	2	Q4YM17_PLABE	Q4ym17 plasmodium
422	33	61.1	618	2	Q8KS57_STRP3	Q8ks57 streptococc	495	32	59.3	45	2	Q4YIM4_PLABE	Q97km6 clostridium
423	33	61.1	620	2	Q9Y4B7_HUMAN	Q9y4b7 homo sapien	496	32	59.3	50	2	Q97KM6_CLOAB	Q97km6 clostridium
424	33	61.1	633	2	Q57NY3_SALCH	Q57ny3 salmonella	497	32	59.3	52	2	Q9JTC0_NEIMA	Q9jtc0 neisseria m
425	33	61.1	635	2	Q6CDF3_YARLI	Q6cdf3 yarrowia li	498	32	59.3	89	2	Q8TR54_METAC	Q8tr54 methanosarc
426	33	61.1	639	2	Q8ZIF2_YERPE	Q8zif2 yersinia pe	499	32	59.3	91	2	Q8PE14_XANCP	Q8pe14 xanthomonas
427	33	61.1	639	2	Q66EUG_YERPS	Q66eue yersinia ps	500	32	59.3	114	2	Q6LJG5_PHOPR	Q6ljg5 photobacter
428	33	61.1	642	2	Q73H10_WOLPM	Q73h10 wolbachia p	501	32	59.3	114	2	Q8YRZ7_ANASP	Q8yrz7 anabaena sp
429	33	61.1	647	2	Q5LKL1_SILPO	Q5lkl1 silicibacte	502	32	59.3	116	2	Q8A5V5_BACTN	Q8a5v5 bacteroides
430	33	61.1	649	2	Q8CZP1_YERPE	Q8czp1 yersinia pe	503	32	59.3	129	2	P91088_CAEBL	P91088 caenorhabdi
431	33	61.1	650	2	Q6MJ97_BDEBA	Q6mj97 bdellovibri	504	32	59.3	138	2	Q6CE93_YARLI	Q6ce93 yarrowia li
432	33	61.1	657	2	Q6HC45_BACHK	Q6hc45 bacillus th	505	32	59.3	148	2	Q7M2C9_PHOUL	Q7m2c9 photorhabdu
433	33	61.1	657	2	Q632K3_BACCZ	Q632k3 bacillus ce	506	32	59.3	156	2	Q5V8I1_PAXIN	Q5v8i1 paxillus in
434	33	61.1	659	2	Q6FJH2_CANGA	Q6fjh2 candida gla	507	32	59.3	156	2	Q5V8I4_PAXIN	Q5v8i4 paxillus in
435	33	61.1	659	2	Q4MNB9_BACCE	Q4mnb9 bacillus ce	508	32	59.3	156	2	Q5V8K0_9HOMO	Q5v8k0 gluconobact
436	33	61.1	659	2	Q816J3_BACCR	Q816j3 bacillus ce	509	32	59.3	164	2	Q5FTA8_GLUOX	Q5fta8 gluconobact
437	33	61.1	674	2	Q73JG9_TREDE	Q73jg9 treponema d	510	32	59.3	164	2	Q72UV3_LEPIC	Q72uv3 leptospira
438	33	61.1	676	2	Q5X9I0_STRP6	Q5x9i0 streptococc	511	32	59.3	164	2	Q8F037_LEPIN	Q8f037 leptospira
439	33	61.1	676	2	Q99XR5_STRP8	Q99xr5 streptococc	512	32	59.3	170	1	LSPA_BORBU	Lspa borrelia bu
440	33	61.1	676	2	Q8N252_STRP8	Q8n252 streptococc	513	32	59.3	170	2	Q6G1F0_BORGA	Q6g1f0 borrelia ga
441	33	61.1	676	2	Q8KSM1_STRP3	Q8ksm1 streptococc	514	32	59.3	176	2	Q59092_PYRHO	Q59092 pyrococcus
442	33	61.1	679	1	YB2G_SCHPO	P87317 schizosacch	515	32	59.3	181	2	Q97BJ6_THERVO	Q97bj6 thermoplasm
443	33	61.1	683	2	Q973N2_SULTO	Q973n2 sulfolobus	516	32	59.3	184	2	Q6CSM8_KLULA	Q6csm8 kluveromyc
444	33	61.1	691	2	Q93216_ARATH	Q93216 arabidopsis	517	32	59.3	185	2	Q5V8K2_PAXIN	Q5v8k2 paxillus in
445	33	61.1	691	2	SYM_PARUM	Q6mdg0 parachlamyd	518	32	59.3	189	2	Q50U77_ENTHI	Q50u77 entamoeba h
446	33	61.1	698	1	Q5N7W3_ORYSA	Q5n7w3 oryza sativ	519	32	59.3	189	2	Q51411_ENTHI	Q51411 entamoeba h
447	33	61.1	704	2	Q8L849_ARATH	Q8l849 arabidopsis	520	32	59.3	191	2	Q65Q08_MANSNM	Q65q08 manheimia
448	33	61.1	704	2	Q9FF49_ARATH	Q9ff49 arabidopsis	521	32	59.3	196	2	Q4JB89_SULAC	Q4jb89 sulfolobus
449	33	61.1	710	2	Q6FMS5_CANGA	Q6fms5 candida gla	522	32	59.3	196	2	Q749X7_GEOSL	Q749x7 geobacter a
450	33	61.1	719	2	Q9U021_GIALA	Q9u021 giardia lam	523	32	59.3	206	2	Q8EWK2_MYCPE	Q8ewk2 mycoplasma
451	33	61.1	724	2	Q6FQUB_CANGA	Q6fqub candida gla	524	32	59.3	209	2	Q9V117_PYRAB	Q9v117 pyrococcus
452	33	61.1	731	2	Q8YXU7_ANASP	Q8yxu7 anabaena sp	525	32	59.3	211	2	Q8BEC9_9PIC0	Q8bec9 foot-and-mo
453	33	61.1	788	2	Q5JEG9_PYRKO	Q5jeg9 pyrococcus	526	32	59.3	213	2	Q4JTZ0_CORJK	Q4jtz0 corynebacte
454	33	61.1	789	2	Q7RMW7_PLAYO	Q7rmw7 plasmodium	527	32	59.3	219	2	Q8UHL2_AGRRT	Q8uhl2 agrobacteri
455	33	61.1	790	2	Q4KK74_PSEF5	Q4kk74 pseudomonas	528	32	59.3	223	2	Q6ST30_SOLITU	Q6st30 solanum tub
456	33	61.1	794	2	Q8PX55_METWA	Q8px55 methanosarc	529	32	59.3	226	2	Q6X5U6_9STRA	Q6x5u6 malomonas
457	33	61.1	794	2	Q8TUU5_METAC	Q8tuu5 methanosarc	530	32	59.3	228	1	MINC_BACAN	1 minc bacillus an
458	33	61.1	807	2	Q4TAH6_TETNG	Q4tah6 tetraodon n	531	32	59.3	228	1	MINC_BACCR	1 minc bacillus ce
459	33	61.1	817	2	Q4UDN0_THEAN	Q4udn0 theileria a	532	32	59.3	228	2	O26626_METTH	2 o26626 methanobact
460	33	61.1	821	2	Q4IPB9_GIBZE	Q4ipb9 gibberella	533	32	59.3	228	2	O4MS55_BACGE	2 o4ms55 bacillus ce
461	33	61.1	826	2	Q8Z122_YERPE	Q8z122 yersinia ps	534	32	59.3	228	2	Q6HD76_BACHK	2 q6hd76 bacillus th
462	33	61.1	826	2	Q66526_YERPS	Q66526 yersinia ps	535	32	59.3	228	2	Q633Z4_BACCZ	2 q633z4 bacillus ce
463	33	61.1	847	2	Q4TOQ7_9SPHN	Q4tq7 erythrobact	536	32	59.3	230	2	Q18899_CABEL	Q18899 caenorhabdi
464	33	61.1	849	2	Q855Y9_9CAUD	Q855y9 mycobacteri	537	32	59.3	230	2	Q8STQ4_ENCCU	Q8stq4 encephalito
465	33	61.1	855	2	Q70409_MOUSE	Q70409 mus musculu	538	32	59.3	233	2	Q897T1_CLOTE	Q897t1 clostridium
466	33	61.1	855	2	Q6TAC4_MOUSE	Q6tac4 mus musculu	539	32	59.3	234	2	Q89687_CLOTE	Q89687 clostridium
467	33	61.1	864	2	Q50XS0_ENTHI	Q50xs0 entamoeba h	540	32	59.3	236	2	Q73U42_TREDE	Q73u42 treponema d
468	33	61.1	868	2	Q8A2M9_BACTN	Q8a2m9 bacteroides	541	32	59.3	236	2	Q6D4N0_ERWCT	2 q6d4n0 erwinia car
469	33	61.1	879	2	Q86Y66_HUMAN	Q86y66 homo sapien	542	32	59.3	239	2	Q6D4N0_ERWCT	2 q6d4n0 erwinia car



543	32	59.3	240	1	PADR_SHEON	Q8ed80 shewanella	616	32	59.3	391	2	Q5CE79_CRYHO	05ce79 cryptospori
544	32	59.3	246	2	Q73NX5_TREDE	Q73nx5 treponema d	617	32	59.3	393	2	Q8XNQ9_CLOPE	Q8xng9 clostroidum
545	32	59.3	248	2	Q6N7F8_RHOPA	Q6n7f8 rhodopseuad	618	32	59.3	393	2	O11412_9ADEN	O11412 duck adenov
546	32	59.3	254	2	Q6ZLM5_ORYSA	Q6zlm5 oryza sativ	619	32	59.3	394	2	O61206_CAEEL	O61206 caenorhabdi
547	32	59.3	256	2	Q5MNH9_NEOUN	Q5mnh9 neotyphodiu	620	32	59.3	394	2	Q9ZNM4_HELPF	Q9znm4 helicobacte
548	32	59.3	256	2	Q5MNH2_NEOUN	Q5mnh2 neotyphodiu	621	32	59.3	400	2	Q8NID9_TRIRU	Q8nid9 trichophyto
549	32	59.3	257	2	Q6F720_ACIAID	Q6f720 acinetobacti	622	32	59.3	403	2	P87659_9ADEN	P87659 duck adenov
550	32	59.3	260	2	Q9AS67_ORYSA	Q9as67 oryza sativ	623	32	59.3	404	2	Q8JIM0_ARTBE	Q8jlm0 arthroderma
551	32	59.3	263	2	Q4MQZ6_BACCE	Q4mqz6 bacillus ce	624	32	59.3	405	2	Q8JIL9_ARTBE	Q8jil9 arthroderma
552	32	59.3	263	2	Q6HEM7_BACHK	Q6hem7 bacillus th	625	32	59.3	405	2	Q8J077_TRISH	Q8j077 trichophyto
553	32	59.3	263	2	Q631T7_BACCZ	Q631t7 bacillus ce	626	32	59.3	406	2	Q9NKQ2_LEIMA	Q9nkq2 leishmania
554	32	59.3	263	2	Q81XG6_BACAN	Q81xg6 bacillus an	627	32	59.3	406	2	Q8TMV5_METAC	Q8tmv5 methanosaer
555	32	59.3	264	2	Q97XG4_SULSO	Q97xg4 sulfolobus	628	32	59.3	406	2	Q8RDU6_FUSNU	Q8rdu6 fusobacteri
556	32	59.3	264	2	Q6DC12_BRARE	Q6dc12 brachydanio	629	32	59.3	407	2	Q8HW65_9MAGN	Q8hw65 cocculus or
557	32	59.3	264	2	Q90Z20_BRARE	Q90z20 brachydanio	630	32	59.3	411	2	Q4YUHS_PLABE	Q4yuh5 plasmodium
558	32	59.3	273	2	Q6N5V8_RHOPA	Q6n5v8 rhodopseuad	631	32	59.3	413	1	SYC_MYCMO	K61c2 mycoplasma
559	32	59.3	281	2	Q45568_CAEEL	Q45568 caenorhabdi	632	32	59.3	419	2	Q4HPF8_CAMUP	Q4hpf8 campylobact
560	32	59.3	282	2	Q5Y815_9GAMM	Q5y815 shewanella	633	32	59.3	428	2	Q4IMQ9_GIBZE	Q4imq9 gibberella
561	32	59.3	287	1	Y1304_SYNY3	P73599 synechocyst	634	32	59.3	439	2	Q7SI20_NEURC	Q7sl20 neurospora
562	32	59.3	288	2	Q66454_AQUAE	Q66454 aquifex ae	635	32	59.3	439	2	Q4FP98_9RICK	Q4fp98 candidatus
563	32	59.3	289	2	Q4YT28_PLABE	Q4yt28 plasmodium	636	32	59.3	441	2	Q76DQ8_9ALTE	Q76dq8 microbulbif
564	32	59.3	292	2	Q8JIM2_ARTBE	Q8jlm2 arthroderma	637	32	59.3	441	2	CSN2_DROME	Q94899 drosophila
565	32	59.3	292	2	Q8JIM1_ARTBE	Q8jlm1 arthroderma	638	32	59.3	445	2	Q69HS3_CIOIN	Q69hs3 ciona intes
566	32	59.3	293	2	Q97W77_SULSO	Q97w77 sulfolobus	639	32	59.3	445	2	Q7PPL9_ANOGA	Q7ppl9 anopheles g
567	32	59.3	294	2	Q48432_9CAUD	Q48432 lactobacill	640	32	59.3	445	2	Q5P9C4_ANAMM	Q5p9c4 anaplasma m
568	32	59.3	296	2	Q9RHV7_COMTE	Q9rhv7 comamonas t	641	32	59.3	446	1	TBB2_DROER	P63130 drosophila
569	32	59.3	303	2	Q9WYP7_9REOV	Q9wyp7 kadipiro vi	642	32	59.3	446	1	TBB2_DROHY	P61858 drosophila
570	32	59.3	305	2	O01427_CAEEL	O01427 caenorhabdi	643	32	59.3	446	1	TBB2_DROME	P61857 drosophila
571	32	59.3	306	2	Q4KIR8_PSEEF	Q4kir8 pseudomonas	644	32	59.3	446	1	Q540X8_DROME	Q540x8 drosophila
572	32	59.3	310	2	P74948_VIBCH	P74948 vibrio chol	645	32	59.3	454	2	Q5WAD9_BACSK	Q5wad9 bacillus cl
573	32	59.3	310	2	Q87138_VIBCH	Q87138 vibrio chol	646	32	59.3	455	2	Q9K9J6_BACHD	Q9k9j6 bacillus ha
574	32	59.3	310	2	Q6PPR3_MOUSE	Q6ppr3 mus musculu	647	32	59.3	458	2	Q9CEF8_LACLA	Q9cef8 lactococcus
575	32	59.3	311	2	Q92U52_RHIME	Q92u52 rhizobium m	648	32	59.3	459	2	Q8DSX2_STRMU	Q8dsx2 streptococc
576	32	59.3	312	2	Q5HX13_CAMJR	Q5hx13 campylobact	649	32	59.3	459	2	Q8DYE6_STRAS	Q8dye6 streptococc
577	32	59.3	312	2	Q9PIX5_CAMJE	Q9pix5 campylobact	650	32	59.3	459	2	Q8E409_STRAS	Q8e409 streptococc
578	32	59.3	315	2	Q977D2_SULCO	Q977d2 sulfolobus	651	32	59.3	459	2	Q87R46_STRPN	Q87r46 streptococc
579	32	59.3	315	2	Q4HFU9_CAMCO	Q4hfu9 campylobact	652	32	59.3	460	2	Q7LIU4_9STRE	Q7liu4 streptococc
580	32	59.3	317	1	RNZ_METJA	Q58897 methanococc	653	32	59.3	460	2	Q8GQP7_9STRE	Q8gqp7 streptococc
581	32	59.3	328	2	Q9WZB6_THEME	Q9wzb6 thermotoga	654	32	59.3	460	2	Q82UI1_NITBU	Q82ui1 nitrosomona
582	32	59.3	333	2	Q55NH2_CRYNE	Q55nh2 cryptococcu	655	32	59.3	460	2	Q5M0U2_STRT1	Q5m0u2 streptococc
583	32	59.3	333	2	Q5KBV7_CRYNE	Q5kbv7 cryptococcu	656	32	59.3	460	2	Q5M5C8_STRT2	Q5m5c8 streptococc
584	32	59.3	334	2	Q61DE3_CAEER	Q61de3 caenorhabdi	657	32	59.3	460	2	Q9A163_STRPY	Q9a163 streptococc
585	32	59.3	337	1	YBZ1_YEAST	P38278 saccharomyc	658	32	59.3	460	2	Q8P286_STRP8	Q8p286 streptococc
586	32	59.3	338	2	Q8DR52_STRR6	Q8dr52 streptococc	659	32	59.3	460	2	Q6D4Z7_ERWCT	Q6d4z7 erwinia car
587	32	59.3	339	2	Q513Q2_ENTHI	Q513q2 entamoeba h	660	32	59.3	460	2	Q8K8F5_STRP3	Q8k8f5 streptococc
588	32	59.3	340	2	Q97SI4_STRPN	Q97si4 streptococc	661	32	59.3	462	2	Q5UY76_HALMA	Q5uy76 haloarcula
589	32	59.3	341	1	OMPL_PHOPR	Q52591 photobacter	662	32	59.3	466	2	Q8EYD9_LEPIN	Q8eyd9 leptospira
590	32	59.3	341	2	Q719E8_9MAGN	Q719e8 cocculus la	663	32	59.3	467	2	Q8DAT8_VIBVU	Q8dat8 vibrio vuln
591	32	59.3	342	2	Q6TRI9_CULQU	Q6tri9 culex quinq	664	32	59.3	470	2	Q5GZAI_REOVL	Q5gzai reovirus ty
592	32	59.3	343	2	Q9XWP5_CAEEL	Q9xwp5 caenorhabdi	665	32	59.3	474	2	Q6CDP7_YARUI	Q6cdp7 yarrowia li
593	32	59.3	348	1	RTCA_ANASP	Q8yvg3 anabaena sp	666	32	59.3	474	2	Q8SYD5_DROME	Q8syd5 drosophila
594	32	59.3	348	2	Q8VPR9_ACIRA	Q8vpr9 acinetobact	667	32	59.3	474	2	Q9U6P7_DROME	Q9u6p7 drosophila
595	32	59.3	348	2	Q9Z6M9_CHLPA	Q9z6m9 chlamydia p	668	32	59.3	475	2	Q757K8_ASHGO	Q757k8 ashbya gos
596	32	59.3	350	2	Q4YKD7_PLABE	Q4ykd7 plasmodium	669	32	59.3	479	2	Q8DQ18_STRR6	Q8dq18 streptococc
597	32	59.3	354	2	Q4XQW7_PLACH	Q4xqw7 plasmodium	670	32	59.3	479	2	Q89161_ERAJA	Q89161 bradyrhizob
598	32	59.3	355	2	Q8IIP1_PLAF7	Q8iip1 plasmodium	671	32	59.3	481	2	Q5AXY6_EMENI	Q5axy6 aspergillus
599	32	59.3	355	2	Q7RCL6_PLAYO	Q7rc16 plasmodium	672	32	59.3	484	1	DNB2_ADE12	P04498 human adeno
600	32	59.3	356	2	Q4UIK2_THEAN	Q4uik2 theileria a	673	32	59.3	484	2	Q5L8K0_BACFN	Q5l8k0 bacteroides
601	32	59.3	358	2	Q6RW54_ENTAE	Q6rw54 enterobacte	674	32	59.3	484	2	Q64NU6_BACFR	Q64nu6 bacteroides
602	32	59.3	358	2	Q6RW56_ENTAE	Q6rw56 enterobacte	675	32	59.3	485	2	Q5XDJ2_STRP6	Q5xdj2 streptococc
603	32	59.3	358	2	Q6RW57_ENTAE	Q6rw57 enterobacte	676	32	59.3	491	2	Q9FNC1_ARATH	Q9fnc1 arabidopsis
604	32	59.3	358	2	Q6MR95_PARUM	Q6mr95 parachlamyd	677	32	59.3	496	1	GLPK_BACCR	Q81u58 bacillus an
605	32	59.3	364	2	Q83YL3_BACTM	Q83yl3 bacillus th	678	32	59.3	496	1	GLPK_BACCR	Q81922 bacillus ce
606	32	59.3	368	2	Q9LAJ4_ACISP	Q9laj4 acinetobact	679	32	59.3	496	1	GLPK_BACSU	P18157 bacillus eu
607	32	59.3	370	2	Q51326_ENTHI	Q51326 entamoeba h	680	32	59.3	496	1	GLPK_THEAO	Q9wx53 thermus aqu
608	32	59.3	374	2	Q8Y6K4_LISMO	Q8y6k4 listeria mo	681	32	59.3	496	2	Q8GN30_BACNA	Q8gn30 bacillus eu
609	32	59.3	375	2	Q7VT70_BORPE	Q7vt70 bordetella	682	32	59.3	496	2	Q5L091_GEOKA	Q5l091 geobacillus
610	32	59.3	375	2	Q7W292_BORPE	Q7w292 bordetella	683	32	59.3	496	2	Q63EX2_BACCZ	Q63ex2 bacillus ce
611	32	59.3	375	2	Q7WR59_BORER	Q7wr59 bordetella	684	32	59.3	496	2	Q6HMD5_BACHK	Q6hmd5 bacillus th
612	32	59.3	378	2	Q4L7F0_STAHL	Q4l7f0 staphylococ	685	32	59.3	496	2	Q65M11_BACLD	Q65ml1 bacillus li
613	32	59.3	379	2	Q5NGS5_FRATT	Q5ngs5 francisella	686	32	59.3	497	1	GLPK_BACHD	Q9kdw8 bacillus ha
614	32	59.3	380	2	Q832U1_ENTFA	Q832u1 enterococcu	687	32	59.3	497	2	Q4K3N7_PSEF5	Q4k3n7 pseudomonas
615	32	59.3	382	2	Q4ZUC3_PSESY	Q4zuc3 pseudomonas	688	32	59.3	497	2	Q8PP40_XANAC	Q8pp40 xanthomonas

689	32	59.3	498	1	GLPK_STAAC	Q5hgd2 staphylococ	762	32	59.3	709	2	Q5QY9_IDILO	Q5qye9 idiomarina
690	32	59.3	498	1	GLPK_STAAM	P63741 staphylococ	763	32	59.3	711	2	Q5ONR2_ENTHI	Q5onr2 entamoeba h
691	32	59.3	498	1	GLPK_STAAN	P99113 staphylococ	764	32	59.3	726	2	Q5XDK4_STRP6	Q5xdk4 streptococ
692	32	59.3	498	1	GLPK_STAAR	Q6ghd5 staphylococ	765	32	59.3	726	2	Q8K8G3_STRP3	Q8k8g3 streptococ
693	32	59.3	498	1	GLPK_STAAS	Q6g9f3 staphylococ	766	32	59.3	726	2	Q8P295_STRP8	Q8p295 streptococ
694	32	59.3	498	1	GLPK_STAAM	Q8nwx7 staphylococ	767	32	59.3	726	2	Q9A175_STRP1	Q9a175 streptococ
695	32	59.3	498	2	Q9I748_PSEAE	Q8nwx7 pseudomonas	768	32	59.3	733	1	KS6AA_XENLA	P10665 xenopus lae
696	32	59.3	498	2	Q5WCJ3_BACSK	Q5wcj3 bacillus cl	769	32	59.3	733	2	Q6DE78_XENLA	Q6de78 xenopus lae
697	32	59.3	499	1	GLPK_STAEP	Q8cse0 staphylococ	770	32	59.3	733	2	Q6GR32_XENLA	Q6gr32 xenopus lae
698	32	59.3	499	1	GLPK_STAEP	Q8cse0 staphylococ	771	32	59.3	733	2	Q9ASK6_RANDY	Q9ask6 rana dybows
699	32	59.3	499	2	Q4L607_STAHO	Q5hnp1 staphylococ	772	32	59.3	735	1	MCN5_XENLA	P55862 xenopus lae
700	32	59.3	499	2	Q97KV1_CLOAB	Q4l607 staphylococ	773	32	59.3	735	2	Q5DOA3_XENLA	Q5doa3 xenopus lae
701	32	59.3	500	1	GLPK_OCEIH	Q97kv1 clostridium	774	32	59.3	740	2	Q4WQ14_ASEFU	Q4wq14 aspergillus
702	32	59.3	500	1	Y039_BORBU	Q8enx7 oceanobacil	775	32	59.3	740	2	Q6FEQ0_ACIAD	Q6feq0 acinetobact
703	32	59.3	500	2	Q66Z33_BORCA	Q51068 borrelia bu	776	32	59.3	740	2	Q6GTY4_MOUSE	Q6gty4 mus musculu
704	32	59.3	500	2	Q5WILL_BACSK	Q66z33 borrelia ga	777	32	59.3	743	2	Q6N780_RHOPA	Q6n780 rhodopseudo
705	32	59.3	510	2	Q73CE0_BACCI	Q5w111 bacillus cl	778	32	59.3	754	2	Q4I4B6_GIBZE	Q4i4b6 gibberella
706	32	59.3	510	2	Q64FJ8_9DEIN	Q73ce0 bacillus ce	779	32	59.3	757	2	Q5CT46_CRYPV	Q5ct46 cryptospori
707	32	59.3	514	2	Q8J0U7_ASPNG	Q64fj8 thermus sp.	780	32	59.3	757	2	Q8W5V7_9CAUD	Q8w5v7 bacterioph
708	32	59.3	516	2	Q94D96_ORYSA	Q8j0u7 aspergillus	781	32	59.3	757	2	Q928E8_LISIN	Q928e8 listeria in
709	32	59.3	520	2	Q9CM64_PASMU	Q94d96 oryza aativ	782	32	59.3	758	2	Q4TNY9_9SPHN	Q4tny9 erythroba
710	32	59.3	521	1	CYOA_HAEIN	Q9cm64 pasteurella	783	32	59.3	758	2	Q8D6I2_VIBVU	Q8d6i2 vibrio vuln
711	32	59.3	521	2	Q4TN94_9SPHN	F45021 haemophilus	784	32	59.3	758	2	Q7MDD9_VIBVY	Q7md9 vibrio vuln
712	32	59.3	521	2	Q4QLL3_HAEI8	Q4tn94 erythroba	785	32	59.3	759	2	Q4VBE3_XENTR	Q4vbe3 xenopus tro
713	32	59.3	523	2	Q65UN8_MANSM	Q4ql13 haemophilus	786	32	59.3	772	2	Q5YOM4_9ARCH	Q5yom4 uncultured
714	32	59.3	525	2	Q9C736_ARATH	Q65un8 manhelmia	787	32	59.3	773	2	Q8Z2G0_PYRAE	Q8z2g0 pyrobaculum
715	32	59.3	528	2	Q4WDS9_ASPFU	Q9c736 arabidopsis	788	32	59.3	773	2	Q553Z6_DICDI	Q553z6 dictyosteli
716	32	59.3	528	2	Q945G7_PRUSE	Q4wds9 aspergillus	789	32	59.3	774	2	Q6I4B34_9ARCH	Q6i4b34 uncultured
717	32	59.3	530	2	Q985N6_RHILO	Q945g7 prunus sero	790	32	59.3	776	2	Q5RIK6_BRARE	Q5rik6 brachydanio
718	32	59.3	536	2	Q54VA7_DICDI	Q985n6 rhizobium l	791	32	59.3	790	1	SEL1L_MOUSE	Q92z96 mus musculu
719	32	59.3	537	2	Q4IAE8_GIBZE	Q54va7 dictyosteli	792	32	59.3	794	1	SEL1L_HUMAN	Q9ubv7 mesocricetu
720	32	59.3	540	2	Q5BBM2_EMENI	Q4iae8 gibberella	793	32	59.3	794	1	SEL1L_MESAU	Q9esm7 mesocricetu
721	32	59.3	543	2	Q6LQK9_PHOPR	Q5bbm2 aspergillus	794	32	59.3	794	2	SEL1L_RAT	Q80z70 rattus norv
722	32	59.3	548	2	Q8DXJ4_STRAS	Q6lqk9 photobacter	795	32	59.3	794	2	Q7Y5H6_9CAUD	Q7y5h6 xanthomonas
723	32	59.3	548	2	Q8E451_STRAS	Q8dxj4 streptococ	796	32	59.3	799	1	TMPS6_MOUSE	Q9dbi0 mus musculu
724	32	59.3	552	2	Q6LPY6_PHOPR	Q8e451 streptococ	797	32	59.3	799	2	TMPS6_HUMAN	Q8iuh0 homo sapien
725	32	59.3	553	2	Q4Q984_PRUSE	Q6lpv6 photobacter	798	32	59.3	802	1	Q4K456_PSEF5	Q4k456 pseudomonas
726	32	59.3	559	2	Q80VC0_MOUSE	Q4q984 prunus sero	799	32	59.3	806	2	Q501Q8_XENLA	Q501q8 xenopus lae
727	32	59.3	573	2	Q9C735_ARATH	Q80vc0 mus musculu	800	32	59.3	822	2	Q61CC2_HUMAN	Q61cc2 homo sapien
728	32	59.3	575	2	Q8IM39_PLAF7	Q9c735 arabidopsis	801	32	59.3	824	2	Q5DTL8_MOUSE	Q5dtl8 mus musculu
729	32	59.3	576	2	Q4FSJ6_9GAMM	Q8im39 plasmodium	802	32	59.3	832	2	Q4YTM9_PLABE	Q4ytm9 plasmodium
730	32	59.3	578	2	Q6BRE6_DEBHA	Q4fsj6 psychrobact	803	32	59.3	833	2	Q582L3_9TRYP	Q582l3 trypanosoma
731	32	59.3	579	2	Q4JRC2_9VIRU	Q6bre6 debaryomyce	804	32	59.3	845	2	Q7WTU0_9GAMM	Q7wtu0 shewanella
732	32	59.3	581	2	Q9FHN7_ARATH	Q4jrc2 hepatopancr	805	32	59.3	854	2	Q5LIG5_CRYNE	Q5lig5 cryptococcu
733	32	59.3	585	1	GH39_ARATH	Q9fhn7 arabidopsis	806	32	59.3	902	2	Q5KA31_CRYNE	Q5ka31 cryptococcu
734	32	59.3	589	2	Q4QCF1_LEIMA	Q82243 arabidopsis	807	32	59.3	902	2	Q9ITX3_CASBL	Q9itx3 caenorhabdi
735	32	59.3	589	2	Q4SHG4_TETNG	Q4qcf1 leishmania	808	32	59.3	909	2	Q4SUH6_TETNG	Q4sjh6 tetraodon n
736	32	59.3	604	2	Q8MPF3_TOXGO	Q4shg4 tetraodon n	809	32	59.3	913	2	Q6MJ54_BDEBA	Q6mj54 bdellovibri
737	32	59.3	608	2	Q5MY92_PLABE	Q8mpf3 toxoplasma	810	32	59.3	926	1	CLAA_LYCES	P31541 theileria a
738	32	59.3	613	2	Q8CVU4_MOUSE	Q8vcx7 mus musculu	811	32	59.3	929	2	Q4UIW7_THERAN	Q4uiw7 theileria a
739	32	59.3	625	1	TBP2_HAEIN	Q8cvu4 mus musculu	812	32	59.3	929	2	Q8DHU4_SYNEL	Q8dhua synchococc
740	32	59.3	625	1	Q55FK0_DICDI	P44971 haemophilus	813	32	59.3	930	2	Q8YMS8_ANASP	Q8ym8 anabaena sp
741	32	59.3	625	2	Q836L8_ENTFA	Q55fk0 dictyosteli	814	32	59.3	930	2	SECA_SYNY3	Q55709 synchocyst
742	32	59.3	625	2	Q5JDT8_PYRKO	Q836l8 enterococcu	815	32	59.3	932	1	Q4N6P9_THERPA	Q4n6p9 theileria p
743	32	59.3	626	2	KS6AB_XENLA	Q5jdt8 pyrococcus	816	32	59.3	937	2	Q7UA15_SYNPX	Q7ua15 synchococc
744	32	59.3	629	1	Q56AB_XENLA	P10666 xenopus lae	817	32	59.3	937	2	Q7U2M1_PROMP	Q7u2m1 prochloroco
745	32	59.3	630	2	Q48042_HAEIN	Q91158 oryza sativ	818	32	59.3	943	1	SECA_SYNP7	Q55357 synchococc
746	32	59.3	631	2	Q6PGQ0_XENLA	Q48042 haemophilus	819	32	59.3	948	2	Q7V975_PROMM	Q7v975 prochloroco
747	32	59.3	630	2	Q919A8_XENLA	Q6pgq0 xenopus lae	820	32	59.3	948	2	Q5N2Q7_SYNP6	Q5n2q7 synchococc
748	32	59.3	650	2	Q918K0_XENLA	Q919a8 xenopus lae	821	32	59.3	948	2	Q6L1C5_PHOPR	Q6l1c5 photobacter
749	32	59.3	651	2	Q918K0_XENLA	Q918k0 xenopus lae	822	32	59.3	960	2	DAL81_YEAST	P21657 saccharomyc
750	32	59.3	651	2	Q91869_XENLA	Q91869 xenopus lae	823	32	59.3	970	1	Q5HCH8_HUMAN	Q5hch8 homo sapien
751	32	59.3	656	2	Q81DES_BACCR	Q8ides bacillus ce	824	32	59.3	972	2	Q4PER8_USTWA	Q4per8 ustilago ma
752	32	59.3	657	2	Q86ID0_DICDI	Q86id0 dictyosteli	825	32	59.3	979	2	Q58KE7_9BACT	Q58ke7 leptospiril
753	32	59.3	663	2	Q7ZYL5_XENLA	Q7zy15 xenopus lae	826	32	59.3	1012	2	Q7RLC7_PLAYO	Q7rlc7 plasmodium
754	32	59.3	670	2	Q7MT53_PORGI	Q7mt53 porphyromon	827	32	59.3	1014	2	LARP1_HUMAN	Q7ric7 bacterioph
755	32	59.3	677	2	Q9VRK9_PROME	Q9vrk9 drosophila	828	32	59.3	1096	1	O60460_HUMAN	Q6p460 homo sapien
756	32	59.3	682	2	Q4WYB6_ASPFU	Q4wyb6 aspergillus	829	32	59.3	1104	2	Q815P9_PLAF7	Q815p9 plasmodium
757	32	59.3	687	2	Q8RB53_THETN	Q8rb53 thermocnaer	830	32	59.3	1140	2	Q8L3Z0_SQDDE	Q8l3z0 solanum dem
758	32	59.3	695	2	Q8AB98_BACTN	Q8ab98 bacteroides	831	32	59.3	1141	2	O88341_RAT	Q88341 rattus norv
759	32	59.3	698	2	Q5FPC6_GLUOX	Q5fpc6 gluconobact	832	32	59.3	1175	2	Q7MX74_PORGI	Q7mx74 porphyromon
760	32	59.3	706	2	Q51C31_ENTHI	Q51c31 entamoeba h	833	32	59.3	1200	2	Q5WTG0_LEGFL	Q5wtg0 legionella
761	32	59.3	707	2	Q75BV3_ASHGO	Q75bv3 ashbya goss	834						

835	32	59.3	1200	2	Q5ZS80	LEGPH	Q5ZS80	legionella	908	31	57.4	86	2	Q91GE7	NPVEP	Q91GE7	epiphyas po
836	32	59.3	1200	2	Q5X1Q1	LEGPH	Q5X1Q1	legionella	909	31	57.4	87	2	Q4XVJ0	PLACH	Q4XVJ0	plasmodium
837	32	59.3	1201	2	Q9XDH8	LEGPH	Q9XDH8	legionella	910	31	57.4	91	2	Q9GM24	MACFA	Q9GM24	macaca faec
838	32	59.3	1214	2	Q50P00	ENTHI	Q50P00	entamoeba h	911	31	57.4	91	2	Q4TC74	TETNG	Q4TC74	tetraodon n
839	32	59.3	1217	2	Q84IM4	CLOSG	Q84IM4	clostridium	912	31	57.4	92	2	Q45640	BACSU	Q45640	bacillus su
840	32	59.3	1268	2	Q5YFG1	9VIRU	Q5YFG1	singapore g	913	31	57.4	93	2	Q9FH49	ARATH	Q9FH49	arabidopsis
841	32	59.3	1268	2	Q5GAF7	9VIRU	Q5GAF7	grouper iri	914	31	57.4	103	2	Q6MHP1	BDBBA	Q6MHP1	bdellovibri
842	32	59.3	1271	2	Q941Q7	LYCES	Q941Q7	lycopersico	915	31	57.4	99	2	Q956P6	9EMBR	Q956P6	anthoceros
843	32	59.3	1284	2	Q7QON5	GIALA	Q7QON5	giardia lam	916	31	57.4	105	2	Q4Y275	PLACH	Q4Y275	plasmodium
844	32	59.3	1338	2	Q9WXJ4	9STRE	Q9WXJ4	streptococc	917	31	57.4	109	2	Q9XBZ8	9BACT	Q9XBZ8	nitrogen-fl
845	32	59.3	1373	2	Q75372	HUMAN	Q75372	homo sapien	918	31	57.4	109	2	Q9XC01	9BACT	Q9XC01	nitrogen-fl
846	32	59.3	1407	2	Q582F4	9TRYP	Q582F4	trypanosoma	919	31	57.4	109	2	Q9XC04	9BACT	Q9XC04	nitrogen-fl
847	32	59.3	1412	2	Q8UW84	PAROL	Q8UW84	paralichthy	920	31	57.4	117	2	Q5D8Y2	SCHJA	Q5D8Y2	schistosoma
848	32	59.3	1440	2	Q27395	CABEL	Q27395	caenorhabdi	921	31	57.4	119	2	Q9X7X6	SULSO	Q9X7X6	schulobus
849	32	59.3	1463	2	Q5SBM6	LACHE	Q5SBM6	lactobacilli	922	31	57.4	119	2	Q9UL73	HUMAN	Q9UL73	homo sapien
850	32	59.3	1518	2	Q00600	STRSL	Q00600	streptococc	923	31	57.4	119	2	Q5LI06	GEOKA	Q5LI06	geobacillus
851	32	59.3	1521	2	Q7RQNZ	PLAYO	Q7RQNZ	plasmodium	924	31	57.4	121	1	YS49	CABEL	YS49	caenorhabdi
852	32	59.3	1550	2	Q6LB69	OLICA	Q6LB69	oligotropha	925	31	57.4	123	2	Q93Y85	NICAM	Q93Y85	nicotiana a
853	32	59.3	1554	2	Q8KZL5	9STRE	Q8KZL5	streptococc	926	31	57.4	128	2	Q5HWQ0	CAMJR	Q5HWQ0	campylobact
854	32	59.3	1561	2	Q5SBM8	9LACO	Q5SBM8	lactobacilli	927	31	57.4	129	2	Q87RV1	VIBPA	Q87RV1	vibrio para
855	32	59.3	1628	2	Q98QZ7	MYCPU	Q98QZ7	mycoplasma	928	31	57.4	131	2	Q5OS73	ENTHI	Q5OS73	entamoeba h
856	32	59.3	1764	2	Q4IKX9	GIBZE	Q4IKX9	gibberella	929	31	57.4	132	2	Q4QIC3	LEIMA	Q4QIC3	leishmania
857	32	59.3	1784	2	Q5OTZ6	ENTHI	Q5OTZ6	entamoeba h	930	31	57.4	133	2	Q6T2B6	STRDI	Q6T2B6	streptomyces
858	32	59.3	1994	2	Q4QIK5	LEIMA	Q4QIK5	leishmania	931	31	57.4	136	2	Q6LWF4	LACPL	Q6LWF4	lactobacilli
859	32	59.3	2195	2	Q54G57	DICDI	Q54G57	dictyosteli	932	31	57.4	138	2	Q7QGS9	ANOGA	Q7QGS9	anopheles g
860	32	59.3	2234	2	Q4IN78	GIBZE	Q4IN78	gibberella	933	31	57.4	140	2	Q5ZLS1	CHICK	Q5ZLS1	gallus gall
861	32	59.3	2237	2	Q5CIC8	DICDI	Q5CIC8	dictyosteli	934	31	57.4	145	2	Q4WGF2	ASFPD	Q4WGF2	aspergillus
862	32	59.3	2448	2	Q8WMO5	HUMAN	Q8WMO5	homo sapien	935	31	57.4	148	2	Q8W2K6	9SOLN	Q8W2K6	solanum ame
863	32	59.3	2687	2	Q4QJD3	LEIMA	Q4QJD3	leishmania	936	31	57.4	149	2	Q7CMC4	BACAN	Q7CMC4	bacillus an
864	32	59.3	3103	2	Q666M9	YERPS	Q666M9	yersinia ps	937	31	57.4	149	2	Q9X392	BACAN	Q9X392	bacillus an
865	32	59.3	3110	2	Q74QH9	YERPE	Q74QH9	yersinia pe	938	31	57.4	152	2	Q5UYL9	HALMA	Q5UYL9	halocaula
866	32	59.3	3110	2	Q8ZHP2	YERPE	Q8ZHP2	yersinia pe	939	31	57.4	154	2	Q5PC42	SALPA	Q5PC42	salmonella
867	32	59.3	3126	2	Q65TD6	MANSM	Q65TD6	mannheimia	940	31	57.4	154	2	Q8Z2J0	SALTI	Q8Z2J0	salmonella
868	32	59.3	3184	2	Q5CSC7	CRYPV	Q5CSC7	cryptospori	941	31	57.4	154	2	Q9Z624	SALTY	Q9Z624	salmonella
869	32	59.3	3481	2	Q7QWH2	GIALA	Q7QWH2	giardia lam	942	31	57.4	160	2	Q57177	SALCH	Q57177	salmonella
870	32	59.3	3451	2	Q7R2V8	GIALA	Q7R2V8	giardia lam	943	31	57.4	160	2	Q5LAL8	BACFN	Q5LAL8	bacteroides
871	32	59.3	5222	2	Q54L33	DICDI	Q54L33	dictyosteli	944	31	57.4	160	2	Q64R16	BACFR	Q64R16	bacteroides
872	32	59.3	7312	2	Q58LL8	9CAUD	Q58LL8	cyanophage	945	31	57.4	164	2	Q4YX88	PLABE	Q4YX88	plasmodium
873	31.5	58.3	185	2	Q5VNI1	ORYSA	Q5VNI1	oryza sativ	946	31	57.4	164	2	Q6LR37	PROPR	Q6LR37	photobacter
874	31.5	58.3	208	1	SCML1	HUMAN	Q9UN30	homo sapien	947	31	57.4	165	2	Q8U317	9YRPU	Q8U317	pyrococcus
875	31.5	58.3	208	2	Q5H969	HUMAN	Q5H969	homo sapien	948	31	57.4	165	2	Q9KFT9	BACHD	Q9KFT9	bacillus ha
876	31.5	58.3	302	2	Q5H968	HUMAN	Q5H968	homo sapien	949	31	57.4	167	2	Q7RLM9	PLAYO	Q7RLM9	plasmodium
877	31.5	58.3	396	2	Q8GZ55	PSEPK	Q8GZ55	pseudomonas	950	31	57.4	167	2	Q4Y1T4	PLACH	Q4Y1T4	plasmodium
878	31.5	58.3	676	2	Q97LI4	CLOAB	Q97LI4	clostridium	951	31	57.4	170	2	Q5FID7	LACAC	Q5FID7	lactobacilli
879	31.5	58.3	1466	2	Q7Z241	BRARE	Q7Z241	brachydanio	952	31	57.4	170	2	Q8CV18	OCETH	Q8CV18	oceanobacil
880	31.5	58.3	2854	2	Q6GSH5	BARHE	Q6GSH5	bartonella	953	31	57.4	171	2	Q5M927	TOBAC	Q5M927	nicotiana t
881	31.5	58.3	2855	2	Q6G0X6	BARQU	Q6G0X6	bartonella	954	31	57.4	171	2	Q6HHE8	BACCH	Q6HHE8	bacillus th
882	31	57.4	58	2	Q4XHX1	PLACH	Q4XHX1	plasmodium	955	31	57.4	171	2	Q81P52	BACAN	Q81P52	bacillus an
883	31	57.4	63	2	Q22742	CABEL	Q22742	caenorhabdi	956	31	57.4	171	2	Q639Z7	BACCH	Q639Z7	bacillus ce
884	31	57.4	67	2	Q5FR65	LACAC	Q5FR65	lactobacilli	957	31	57.4	172	2	Q4ML63	BACCE	Q4ML63	bacillus ce
885	31	57.4	80	2	Q6R830	9CAUD	Q6R830	bacteriopho	958	31	57.4	172	2	Q735Z7	BACC1	Q735Z7	bacillus ce
886	31	57.4	80	2	Q9B0F4	9CAUD	Q9B0F4	staphylococ	959	31	57.4	172	2	Q7WMB8	BORBR	Q7WMB8	borderella
887	31	57.4	80	2	Q4ZBT7	9VIRU	Q4ZBT7	bacteriopho	960	31	57.4	174	2	Q88088	ENTFA	Q88088	enterococcu
888	31	57.4	80	2	Q4ZCH1	9VIRU	Q4ZCH1	bacteriopho	961	31	57.4	174	2	Q87MP7	CLOAB	Q87MP7	clostridium
889	31	57.4	80	2	Q4ZDX4	9CAUD	Q4ZDX4	bacteriopho	962	31	57.4	175	2	Q870W7	NEUCR	Q870W7	neurospora
890	31	57.4	80	2	Q4ZDP7	9CAUD	Q4ZDP7	bacteriopho	963	31	57.4	176	1	TNR23	MOUSE	Q9E63	mus musculu
891	31	57.4	80	2	Q4ZBD5	9CAUD	Q4ZBD5	bacteriopho	964	31	57.4	180	2	Q4Y3Y9	PLACH	Q4Y3Y9	plasmodium
892	31	57.4	80	2	Q6GF76	STAAR	Q6GF76	staphylococ	965	31	57.4	180	2	Q7YA36	9ERIC	Q7YA36	clenatoclet
893	31	57.4	80	2	Q6GGN4	STAAR	Q6GGN4	staphylococ	966	31	57.4	182	2	Q83F58	COXBU	Q83F58	coxella bu
894	31	57.4	80	2	Q5HJ14	STAAC	Q5HJ14	staphylococ	967	31	57.4	186	2	Q9LYB9	ARATH	Q9LYB9	arabidopsis
895	31	57.4	80	2	Q8NWH8	STAAM	Q8NWH8	staphylococ	968	31	57.4	186	2	Q98HJ3	RHILLO	Q98HJ3	rhizobium l
896	31	57.4	80	2	Q931K8	STAAM	Q931K8	staphylococ	969	31	57.4	186	2	Q727B2	DESVM	Q727B2	desulfovibr
897	31	57.4	82	2	Q8SDL7	BPPHD	Q8SDL7	bacteriopho	970	31	57.4	187	2	Q7YA38	9ERIC	Q7YA38	actinidia a
898	31	57.4	82	2	Q8SDR2	9CAUD	Q8SDR2	staphylococ	971	31	57.4	187	2	Q7YA39	ACTDE	Q7YA39	actinidia d
899	31	57.4	82	2	Q8SDV6	BPPHA	Q8SDV6	bacteriopho	972	31	57.4	187	2	Q7YA40	9ERIC	Q7YA40	actinidia l
900	31	57.4	82	2	Q9M8R3	9CAUD	Q9M8R3	staphylococ	973	31	57.4	188	2	Q7YA41	9ERIC	Q7YA41	actinidia p
901	31	57.4	82	2	Q4ZAY1	9VIRU	Q4ZAY1	bacteriopho	974	31	57.4	188	2	Q7YA37	ACTCH	Q7YA37	actinidia c
902	31	57.4	82	2	Q4ZCV9	9VIRU	Q4ZCV9	bacteriopho	975	31	57.4	189	2	Q8A2M8	BACTN	Q8A2M8	bacteroides
903	31	57.4	82	2	Q4ZAR4	9CAUD	Q4ZAR4	bacteriopho	976	31	57.4	191	2	Q4UPE8	XANCP	Q4UPE8	xanthomonas
904	31	57.4	82	2	Q931Z8	STAAM	Q931Z8	staphylococ	977	31	57.4	191	2	Q8P3X1	XANCP	Q8P3X1	xanthomonas
905	31	57.4	85	2	Q9SR55	STAAM	Q9SR55	staphylococ	978	31	57.4	192	1	VIF	HVOY	P20890	human immun
906	31	57.4	86	2	Q4ZCP1	9VIRU	Q4ZCP1	bacteriopho	979	31	57.4	192	2	O16505	CAEEL	O16505	caenorhabdi
	31	57.4			Q5YA82	9CAUD	Q5YA82	bacillus cl	980	31	57.4	192	2	Q6D8Z2	ERWCT	Q6D8Z2	erwinia car

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981 31 57.4 192 2 057303_9HIV1 057303 human immun
982 31 57.4 192 2 055976_9HIV1 055976 human immun
983 31 57.4 192 2 055977_9HIV1 055977 human immun
984 31 57.4 192 2 055978_9HIV1 055978 human immun
985 31 57.4 192 2 055979_9HIV1 055979 human immun
986 31 57.4 192 2 055980_9HIV1 055980 human immun
987 31 57.4 192 2 055981_9HIV1 055981 human immun
988 31 57.4 192 2 055982_9HIV1 055982 human immun
989 31 57.4 192 2 055983_9HIV1 055983 human immun
990 31 57.4 192 2 055984_9HIV1 055984 human immun
991 31 57.4 192 2 055985_9HIV1 055985 human immun
992 31 57.4 192 2 055987_9HIV1 055987 human immun
993 31 57.4 192 2 055988_9HIV1 055988 human immun
994 31 57.4 192 2 055989_9HIV1 055989 human immun
995 31 57.4 192 2 055990_9HIV1 055990 human immun
996 31 57.4 192 2 055991_9HIV1 055991 human immun
997 31 57.4 192 2 055993_9HIV1 055993 human immun
998 31 57.4 192 2 055994_9HIV1 055994 human immun
999 31 57.4 192 2 055995_9HIV1 055995 human immun
1000 31 57.4 192 2 Q90210_9HIV1 Q90210 human immun
```

## ALIGNMENTS

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RESULT 1
Q6LNK3_PROPR
ID Q6LNK3_PROPR PRELIMINARY; PRT; 217 AA.
AC Q6LNK3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=PBPR2751;
OS Photobacterium profundum (Photobacterium sp. (strain SS9)).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Photobacterium.
OX NCBI_TaxID=74109;
[1]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RP PubMed=15746425; DOI=10.1126/science.1103341;
RX Vezzi A., Campanaro S., D'Angelo M., Simonato F., Vitulo N.,
RA Lauro F.M., Cestaro A., Malacrida G., Simonati B., Cannata N.,
RA Romualdi C., Bartlett D.H., Valle G.;
RT "Life at depth: Photobacterium profundum genome sequence and
RT expression analysis."
RL Science 307:1459-1461(2005).
DR EMBL; CR378672; CAG21123.1; -; Genomic_DNA.
KW Complete proteome.
SQ SEQUENCE 217 AA; 24557 MW; F477AC11AF24BA6 CRC64;
```

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Query Match 81.5%; Score 44; DB 2; Length 217;
Best Local Similarity 70.0%; Pred. No. 6.1;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VKLGTYFDS 10
||:||||:
Db 155 VKIGTYHFDN 164
```

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RESULT 2
Q5LXP9_STRT1
ID Q5LXP9_STRT1 PRELIMINARY; PRT; 424 AA.
AC Q5LXP9;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=stl1951;
OS Streptococcus thermophilus (strain CNRZ 1066).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=299768;
```

```

[1]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RP PubMed=15543133; DOI=10.1038/nbt1034;
RX Bolotin A., Quinquis B., Renault P., Sorokin A., Ehrlich S.D.,
RA Kulakauskas S., Lapidus A., Goldsman E., Mazur M., Pusch G.D.,
RA Fonstein M., Overbeek R., Kyprides N., Purnelle B., Prozzi D.,
RA Ngui K., Masuy D., Hancy F., Burtreau S., Boutry M., Delcours J.,
RA Goffeau A., Hols P.;
RT "Complete sequence and comparative genome analysis of the dairy
bacterium Streptococcus thermophilus.";
RL Nat. Biotechnol. 22:1554-1558(2004).
DR EMBL; CP000024; AAV63463.1; -; Genomic DNA.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0005506; F:iron ion binding; IEA.
DR InterPro; IPR000385; MoaA_NiFB_PQQE.
DR InterPro; IPR007197; Radical_SAM.
DR Pfam; PF04055; Radical_SAM; 1.
DR PROSITE; PS01305; MOAA_NiFB_PQQE; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 424 AA; 49050 MW; 2AA11D9CDE1AC84A CRC64;
```

```

Query Match 79.6%; Score 43; DB 2; Length 424;
Best Local Similarity 87.5%; Pred. No. 18;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```

QY 3 LGTYTFDS 10
:|||||
Db 34 IGTYTFDS 41
```

```

RESULT 3
Q5M2A0_STRT2
ID Q5M2A0_STRT2 PRELIMINARY; PRT; 424 AA.
AC Q5M2A0;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=stl1951;
OS Streptococcus thermophilus (strain ATCC BAA-250 / LMG 18311).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=264199;
[1]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RP PubMed=15543133; DOI=10.1038/nbt1034;
RX Bolotin A., Quinquis B., Renault P., Sorokin A., Ehrlich S.D.,
RA Kulakauskas S., Lapidus A., Goldsman E., Mazur M., Pusch G.D.,
RA Fonstein M., Overbeek R., Kyprides N., Purnelle B., Prozzi D.,
RA Ngui K., Masuy D., Hancy F., Burtreau S., Boutry M., Delcours J.,
RA Goffeau A., Hols P.;
RT "Complete sequence and comparative genome analysis of the dairy
bacterium Streptococcus thermophilus.";
RL Nat. Biotechnol. 22:1554-1558(2004).
DR EMBL; CP000023; AAV61546.1; -; Genomic DNA.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0005506; F:iron ion binding; IEA.
DR InterPro; IPR000385; MoaA_NiFB_PQQE.
DR InterPro; IPR007197; Radical_SAM.
DR Pfam; PF04055; Radical_SAM; 1.
DR PROSITE; PS01305; MOAA_NiFB_PQQE; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 424 AA; 49050 MW; 2AA11D9CDE1AC84A CRC64;
```

```

Query Match 79.6%; Score 43; DB 2; Length 424;
Best Local Similarity 87.5%; Pred. No. 18;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```

QY 3 LGTYTFDS 10
:|||||
Db 34 IGTYTFDS 41
```

```
RESULT 4
Q97H36_CLOAB
ID Q97H36_CLOAB PRELIMINARY; PRT; 456 AA.
AC Q97H36;
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Ucharacterized protein, CGEB homolog.
GN OrderedLocusNames=CAC2177;
OS Clostridium acetobutylicum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1488;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC 824 / DSM 792 / VM B-1787;
RX MEDLINE=21359325; PubMed=11466286;
RX DOI=10.1128/JB.183.16.4823-4838.2001;
RA Noelting J., Breton G., Onelchenko M.V., Makarova K.S., Zeng Q.,
RA Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,
RA Tatusov R.L., Sabathe F., Doucette-Stamm L.A., Soucaille P.,
RA Daly M.J., Bennett G.N., Koonin E.V., Smith D.R.;
RT "Genome sequence and comparative analysis of the solvent-producing
bacterium Clostridium acetobutylicum.";
RL J. Bacteriol. 183:4823-4838(2001).
DR ENBL; AE007718; AAK80135.1; -; Genomic_DNA.
DR PIR; D97168; D97168.
KW Complete proteome.
SQ SEQUENCE 456 AA; 53855 MW; 11BDB94E1F86E7F4 CRC64;

Query Match 79.6%; Score 43; DB 2; Length 456;
Best Local Similarity 70.0%; Pred. No. 19;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 VKLGYTFDS 10
:|:|||||
Db 380 IKNTYTFDS 389

RESULT 5
Q6LUF1_PROPR
ID Q6LUF1_PROPR PRELIMINARY; PRT; 206 AA.
AC Q6LUF1;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=PPRA0653;
OS Photobacterium profundum (Photobacterium sp. (strain SS9)).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Photobacterium.
OX NCBI_TaxID=74109;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=15746425; DOI=10.1126/science.1103341;
RA Vezzi A., Campanaro S., D'Angelo M., Simonato F., Vitulo N.,
RA Lauro F.M., Cestaro A., Malacrida G., Simonati B., Cannata N.,
RA Romaldi C., Bartlett D.H., Valle G.;
RT "Life at depth: Photobacterium profundum genome sequence and
expression analysis.";
RL Science 307:1459-1461(2005).
DR ENBL; CR378665; CAG19074.1; -; Genomic DNA.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 206 AA; 23833 MW; 0F43398D786D3E77 CRC64;

Query Match 75.9%; Score 41; DB 2; Length 206;
Best Local Similarity 66.7%; Pred. No. 21;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KLGYTFDS 10
:|:|||||
Db 153 KIGTYTFET 161
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```
RESULT 6
Q5FKV2_LACAC
ID Q5FKV2_LACAC PRELIMINARY; PRT; 368 AA.
AC Q5FKV2;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE P-N-acetylmuramoyl-pentapeptide-transferase (EC 2.7.8.13).
GN Namesmurg; OrderedLocusNames=LBA0809;
OS Lactobacillus acidophilus.
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC Lactobacillus.
OX NCBI_TaxID=1579;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NCFM;
RX PubMed=15671160; DOI=10.1073/pnas.0409188102;
RA Altermann E., Russell W.M., Azcarate-Peril M.A., Barrangou R.,
RA Buck B.L., McAuliffe O., Souther N., Dobson A., Duong T., Callanan M.,
RA Lick S., Hamrick A., Cano R., Klaenhammer T.R.;
RT "Complete genome sequence of the probiotic lactic acid bacterium
Lactobacillus acidophilus NCFM.";
RL Proc. Natl. Acad. Sci. U.S.A. 102:3906-3912(2005).
DR ENBL; CP000033; AAV42672.1; -; Genomic_DNA.
DR GO; GO:0019866; C:inner membrane; IEA.
DR GO; GO:0030246; F:carbohydrate binding; IEA.
DR GO; GO:0008963; F:phospho-N-acetylmuramoyl-pentapeptide-trans. ; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0016758; F:transferase activity, transferring hexosyl ; IEA.
DR GO; GO:0050511; F:undecaprenyldiphospho-muramoylpentapeptide ; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR GO; GO:0030259; P:lipid glycosylation; IEA.
DR GO; GO:0019277; P:UDP-N-acetylgalactosamine biosynthesis; IEA.
DR InterPro; IPR004276; Glyco_tran_28.
DR InterPro; IPR007235; Glyco_tran_28_C.
DR InterPro; IPR006009; MurG.
DR Pfam; PF03033; Glyco_transf_28; 1.
DR Pfam; PF04101; Glyco_tran_28_C; 1.
DR TIGRPFAMs; TIGR01133; murG; 1.
KW Complete proteome; Transferase.
SQ SEQUENCE 368 AA; 40630 MW; 938599A97B91F040 CRC64;

Query Match 75.9%; Score 41; DB 2; Length 368;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GTYTFDS 10
|||||
Db 229 GTYTFDS 235

RESULT 7
Q8DKC6_SYNEL
ID Q8DKC6_SYNEL PRELIMINARY; PRT; 704 AA.
AC Q8DKC6;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Tl10933 protein.
GN OrderedLocusNames=tl10933;
OS Synecococcus elongatus (Thermosynechococcus elongatus).
OC Bacteria; Cyanobacteria; Chroococcales; Synecococcus.
OX NCBI_TaxID=32046;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BP-1;
RX MEDLINE=22225144; PubMed=12240834;
RA Nakamura Y., Kaneko T., Sato S., Ikeuchi M., Katoh H., Sasamoto S.,
RA Watanabe A., Iriguchi M., Kawashima K., Kimura T., Kiehida Y.,
RA Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Nakazaki N.,
RA Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of the thermophilic cyanobacterium
```

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RT Thermosynechococcus elongatus BP-1." ;
RL DNA Res. 9:123-130(2002)
DR EMBL; BA000039; BAC08485.1; -; Genomic_DNA.
DR GO; GO:0005488; F:binding; IEA.
DR GO; GO:0015979; P:photosynthesis; IEA.
DR InterPro; IPR008258; LT catalytic.
DR InterPro; IPR001440; TPR.
DR InterPro; IPR011990; TPR-like_helical.
DR Pfam; PF01464; SLT; 1.
DR PROSITE; PS0293; TPR_REGION; 1.
KW Complete proteome.
SQ SEQUENCE 704 AA; 81126 MW; 0DE8D9216268B52C CRC64;

Query Match 75.9%; Score 41; DB 2; Length 704;
Best Local Similarity 66.7%; Pred. No. 70;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VKLGTYYFD 9
Db :|||||
627 IRLGTWYFD 635

RESULT 8
Q5CK18 CRYHO
ID Q5CK18_CRYHO PRELIMINARY; PRT; 1040 AA.
AC Q5CK18
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE Hypothetical protein.
DE Hypothetical protein.
GN ORFNames=Chro.20326;
OS Cryptosporidium hominis.
OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
OC Cryptosporidiidae; Cryptosporidium.
OX NCBI_TaxID=237895;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=TU502;
RA Xu P., Widmer G., Wang Y., Ozaki L.S., Alves J.M., Serrano M.G.,
RA Puiu D., Manque P., Akiyoshi D., Mackey A.J., Pearson W.R., Dear P.H.,
RA Bankier A.T., Peterson D.L., Abrahamson M.S., Kapur V., Tzipori S.,
RA Buck G.A.;
RT "The genome of Cryptosporidium hominis."
RL Nature 431:1107-1112(2004).
DR EMBL; AAEL01000101; EAL36950.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 1040 AA; 115095 MW; 16181F65A9F31E0B CRC64;

Query Match 75.9%; Score 41; DB 2; Length 1040;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GTYYFDS 10
Db :|||||
522 GTYYFDS 528

RESULT 9
Q932E5 STAAH
ID Q932E5_STAAH PRELIMINARY; PRT; 368 AA.
AC Q932E5
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Integrase.
GN OrderedLocusNames=SAV0783;
OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158878;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,

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RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
aureus." ;
RL Lancet 357:1225-1240(2001).
DR EMBL; BA000017; BAB56945.1; -; Genomic_DNA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0015074; P:DNA integration; IEA.
DR GO; GO:0006310; P:DNA recombination; IEA.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR002104; Phage integrase.
DR Pfam; PF00589; Phage_integrase; 1.
DR PRINTS; PR01415; ANKYRIN.
KW Complete proteome.
SQ SEQUENCE 368 AA; 43818 MW; 14B83C72100292DE CRC64;

Query Match 74.1%; Score 40; DB 2; Length 368;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KLGTYYF 8
Db :|||||
16 KLGTYYF 22

RESULT 10
Q7PIA2 CHRVO
ID Q7PIA2_CHRVO PRELIMINARY; PRT; 4130 AA.
AC Q7PIA2
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Probable RTX (Repeat in structural toxin).
GN OrderedLocusNames=CV0311;
OS Chromobacterium violaceum.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Chromobacterium.
OX NCBI_TaxID=536;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC 12472 / DSM 30191;
RX MEDLINE=22862880; PubMed=14500782; DOI=10.1073/pnas.1832124100;
RA Vasconcelos A.T.R.; de Almeida D.F., Hungria M., Guimaraes C.T.,
RA Antonio R.V., Almeida F.C., de Almeida L.G.P., de Almeida R.,
RA Alves-Gomes J.A., Andrade E.M., Araripa J., de Araujo M.F.P.,
RA Astolfi-Pilho S., Azevedo V., Baptista A.J., Bataus L.A.M.,
RA Batista J.S., Belo A., van den Berg C., Bogo M., Bonatto S.,
RA Bordignon J., Brígido M.M., Brito C.A., Brocchi M., Burity H.A.,
RA Camargo A.A., Cardoso D.D.P., Carneiro N.P., Carraro D.M.,
RA Carvalho C.M.B., Cascardo J.C.M., Cavada B.S., Chueire L.M.O.,
RA Creczynski-Pasa T.B., Cunha-Junior N.C., Fagnundes N., Falcao C.L.,
RA Fantinatti F., Farias I.P., Felipe M.S.S., Ferrari L.P., Ferro J.A.,
RA Ferro M.I.T., Franco G.R., Freitas N.S.A., Furlan L.R.,
RA Gazzinelli R.T., Gomes E.A., Goncalves P.R., Grangeiro T.B.,
RA Grattapaglia D., Grissard E.C., Hanna E.S., Jardim S.N., Laurino J.,
RA Leoi L.C.T., Lima L.F.A., Loureiro M.F., Lyra M.C.C.P.,
RA Madeira H.M.F., Manfio G.P., Maranhao A.Q., Martins W.S.,
RA di Mauro S.M.Z., de Medeiros S.R.B., Meisner R.V., Moreira M.A.M.,
RA Nascimento F.F., Nicolas M.F., Oliveira J.G., Oliveira S.C.,
RA Paixao R.F.C., Parente J.A., Pedrosa F.O., Pena S.D.J., Pereira J.O.,
RA Pereira M., Pinto L.S.R.C., Pinto L.S., Porto J.I.R., Potrich D.P.,
RA Ramalho-Neto C.E., Reis A.M.M., Rigo L.U., Rondinelli E.,
RA Santos E.B.P., Santos F.R., Schneider M.P.C., Senanez H.N.,
RA Silva A.M.R., da Silva A.L.C., Silva D.W., Silva R., Simoes I.C.,
RA Simon D., Soares C.M.A., Soares R.B.A., Souza E.M., Souza K.R.L.,
RA Souza R.C., Steffens M.B.R., Steindel M., Teixeira S.R., Umenyi T.,
RA Vettore A., Wassem R., Zaha A., Simpson A.J.G.;
RT "The complete genome sequence of Chromobacterium violaceum reveals
remarkable and exploitable bacterial adaptability." ;

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RL Proc. Natl. Acad. Sci. U.S.A. 100:11660-11665(2003).  
 DR EMBL: AE016911; AA057990.1; -, Genomic DNA.  
 DR GO: GO:0005509; F:calcium ion binding; IEA.  
 DR InterPro: IPR001343; Hemlysn\_Ca\_bind.  
 DR InterPro: IPR010221; VCBs.  
 DR Pfam: PF00353; HemolysinCabin; 4.  
 DR PRINTS: PR00313; CABNDNGRPT.  
 DR TIGRFAMs: TIGR01965; VCBs\_repeat; 25.  
 KW Complete proteome.  
 SQ SEQUENCE 4130 AA; 431836 MW; E78381A3C0C6F00E CRC64;

Query Match 74.1%; Score 40; DB 2; Length 4130;  
 Best Local Similarity 70.0%; Pred. No. 6.1e+02;  
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VKLGYTFYFDS 10  
 ||| ||| |||  
 Db 2460 VKYGFTHFDS 2469

RESULT 11  
 Q6QC13\_9CLOS PRELIMINARY; PRT; 520 AA.  
 AC Q6QC13;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DE Polymerase (Fragment).  
 OS Mint vein banding virus.  
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Closteroviridae;  
 OC unclassified Closteroviridae.  
 OX NCBI\_TaxID=265877;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Tranetakakis I.E.; DOI=10.1016/j.jviromet.2004.11.006;  
 RA Tranetakakis I.E.; Keller K.E.; Martin R.R.;  
 RT "The use of reverse transcriptase for efficient first- and second-  
 RT strand cDNA synthesis from single- and double-stranded RNA  
 RT templates.";  
 RL J. Virol. Methods 124:73-77(2005).  
 RN [2]

RP NUCLEOTIDE SEQUENCE.  
 RA Tranetakakis I.E.; Postman J.D.; Martin R.R.;  
 RT "A member of the Closteroviridae from mint with similarities to all  
 RT three genera of the family.";  
 RL Plant Dis. 99:654-658(2005).  
 DR EMBL: AY548173; AAS57939.1; -, Genomic\_RNA.  
 DR GO: GO:0003723; F:RNA binding; IEA.  
 DR GO: GO:0003968; F:RNA-directed RNA polymerase activity; IEA.  
 DR GO: GO:0006350; P:transcription; IEA.  
 DR GO: GO:0019079; P:viral genome replication; IEA.  
 DR InterPro: IPR001788; RNA\_dep\_RNApol2.  
 DR InterPro: IPR007095; RNA\_pol\_DS\_PS.  
 DR InterPro: IPR007094; RNA\_pol\_PSVir.  
 DR InterPro: IPR001680; WD40.  
 DR Pfam: PF00978; RdRP\_2; 1.  
 DR PROSITE: PS00678; WD\_REPEATS\_1; UNKNOWN\_1.  
 FT NON TER 1  
 SQ SEQUENCE 520 AA; 59370 MW; C0244E817FD88627 CRC64;

Query Match 72.2%; Score 39; DB 2; Length 520;  
 Best Local Similarity 80.0%; Pred. No. 1.2e+02;  
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 VKLGYTFYFDS 10  
 ||| ||| |||  
 Db 426 VKLGKSYFDS 435

RESULT 12  
 Q74IS2\_LACJO PRELIMINARY; PRT; 565 AA.  
 ID Q74IS2\_LACJO  
 AC Q74IS2;

DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Prolyl-tRNA synthetase.  
 GN OrderedLocusNames=LJ1493;  
 OS Lactobacillus johnsonii.  
 OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;  
 OC Lactobacillus.  
 OX NCBI\_TaxID=33959;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RC STRAIN=NCC 533;  
 RX PubMed=14983040; DOI=10.1073/pnas.0307327101;  
 RA Pidmore R.D.; Berger B.; Desiere F.; Vilanova D.; Barretto C.;  
 RA Pittet A.-C.; Zwanen M.-C.; Rouvet M.; Altermann E.; Barrangou R.;  
 RA Mollet B.; Mercenier A.; Klaenhammer T.; Arigoni F.; Schell M.A.;  
 RT "The genome sequence of the probiotic intestinal bacterium  
 RT Lactobacillus johnsonii NCC 533.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 101:2512-2517(2004).  
 DR EMBL: AE017204; AAS09261.1; -, Genomic\_DNA.  
 DR GO: GO:0005737; C:cytoplasm; IEA.  
 DR GO: GO:0005524; F:ATP binding; IEA.  
 DR GO: GO:0016874; F:ligase activity; IEA.  
 DR GO: GO:0004827; F:proline-tRNA ligase activity; IEA.  
 DR GO: GO:0006433; P:prolyl-tRNA aminoacylation; IEA.  
 DR GO: GO:0006412; P:protein biosynthesis; IEA.  
 DR InterPro: IPR004154; anticodon\_bd.  
 DR InterPro: IPR004500; ProS\_fam\_II.  
 DR InterPro: IPR002314; tRNA-synt\_2b.  
 DR InterPro: IPR002316; tRNA-synt\_pro.  
 DR InterPro: IPR006195; tRNA\_ligase\_II.  
 DR InterPro: IPR007214; YbaK.  
 DR Pfam: PF03129; HGTP-anticodon; 1.  
 DR Pfam: PF00587; tRNA-synt\_2b; 1.  
 DR Pfam: PF04073; YbaK; 1.  
 DR PRINTS: PR01046; TRNASYNTHPRO.  
 DR TIGRFAMs: TIGR00409; ProS\_fam\_II; 1.  
 DR PROSITE: PS00862; AA\_TRNA\_LIGASE\_II; 1.  
 KW Aminoacyl-tRNA synthetase; Complete proteome.  
 SQ SEQUENCE 565 AA; 63242 MW; F655C682A39D68D4 CRC64;

Query Match 72.2%; Score 39; DB 2; Length 565;  
 Best Local Similarity 77.8%; Pred. No. 1.3e+02;  
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 KLGTYTFYFDS 10  
 ||| ||| |||  
 Db 413 KLGTYTYTDT 421

RESULT 13  
 Q97K42\_CLOAB PRELIMINARY; PRT; 2817 AA.  
 ID Q97K42\_CLOAB  
 AC Q97K42;  
 DT 01-OCT-2001 (TrEMBLrel. 18, Created)  
 DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Uncharacterized protein, related to enterotoxins of other  
 DE Clostridiales.  
 GN OrderedLocusNames=CAC1079;  
 OS Clostridium acetobutylicum.  
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;  
 OC Clostridium.  
 OX NCBI\_TaxID=1488;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=ATCC 824 / DSM 792 / VKM B-1787;  
 RX MEDLINE=21359325; PubMed=11466286;  
 RA DOI=10.1128/JB.183.16.4823-4838.2001;  
 RA Noelling J.; Berton G.; Omelchenko M.V.; Makarova K.S.; Zeng Q.;  
 RA Gibson R.; Lee H.M.; Dubois J.; Qiu D.; Hitti J.; Wolf Y.I.;  
 RA Tatusov R.L.; Sabathe F.; Doucette-Stamm L.A.; Soucaille P.;  
 RA Daly M.J.; Bennett G.N.; Koonin E.V.; Smith D.R.;



RT "Genome sequence and comparative analysis of the solvent-producing  
bacterium *Clostridium acetobutylicum*."  
J. Bacteriol. 183:4823-4838(2001).  
RL EMBL; AB007623; AAK79053.1; -; Genomic\_DNA.  
DR PIR; B97033; B97033.  
DR HSP; P06653; LHXC.  
DR InterPro; IPR002479; CW binding.  
DR InterPro; IPR006626; PbH1.  
DR Pfam; PF01473; CW binding\_1; 54.  
DR SMART; SM00710; PbH1; 10.  
KW Complete proteome.  
SQ SEQUENCE 2817 AA; 318226 MW; 1851D0D4FFBEE921 CRC64;

Query Match 72.2%; Score 39; DB 2; Length 2817;  
Best Local Similarity 70.0%; Pred. No. 6.4e+02;  
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 VKLGYTFDS 10  
:|||||  
Db 612 IKGNTYFDS 621

RESULT 14  
Q8CPFS STAEF  
ID Q8CPFS STAEF PRELIMINARY; PRT; 262 AA.  
AC Q8CPFS  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Competence-damage inducible protein cina.  
GN OrderedLocusNames=SE0962;  
OS *Staphylococcus epidermidis*.  
OC Bacteria; Firmicutes; Bacillales; *Staphylococcus*.  
OX NCBI\_TaxID=1282;  
RN [1]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
RC STRAIN=ATCC 12228.  
RX PubMed=12950922; DOI=10.1046/j.1365-2958.2003.03671.x;  
RA Zhang Y.-Q., Ren S.-X., Li H.-L., Wang Y.-X., Fu G., Yang J.,  
Qin Z.-Q., Miao Y.-G., Wang W.-Y., Chen R.-S., Shen Y., Chen Z.,  
Yuan Z.-H., Zhao G.-P., Qu D., Danchin A., Wen Y.-M.;  
RT "Genome-based analysis of virulence genes in a non-biofilm-forming  
*Staphylococcus epidermidis* strain (ATCC 12228).";  
RL Mol. Microbiol. 49:1577-1593(2003).  
DR EMBL; AE016747; AA004559.1; -; Genomic DNA.  
DR GO; GO:0006777; P:Mo-molybdopterin cofactor biosynthesis; IEA.  
DR InterPro; IPR001453; MoCF\_bios.  
DR Pfam; PF00994; MoCF\_biosynth; 1.  
KW Complete proteome.  
SQ SEQUENCE 262 AA; 29694 MW; C4EB5FF6572CE347 CRC64;

Query Match 70.4%; Score 38; DB 2; Length 262;  
Best Local Similarity 66.7%; Pred. No. 98;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 KLGTYYFDS 10  
:|||||  
Db 124 RIGTYFDS 132

RESULT 15  
Q8LTG9\_9CAUD  
ID Q8LTG9\_9CAUD PRELIMINARY; PRT; 281 AA.  
AC Q8LTG9  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
DE Hypothetical protein (fragment).  
OS *Staphylococcus* phase 187.  
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.  
OX NCBI\_TaxID=55511;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.

RA Pantucek R., Doskar J., Ruzickova V., Kasparek P., Oracova E.,  
RA Kvardova V., Rosypal S.;  
RT "Identification of bacteriophage types and their carriage in  
RT *Staphylococcus aureus*."  
RL Arch. Virol. 149:1689-1703(2004).  
DR EMBL; AF515457; AAMS4032.1; -; Genomic\_DNA.  
KW Hypothetical protein.  
FT NON\_TER 281  
SQ SEQUENCE 281 AA; 31326 MW; E6D0D2C8C0FA2790 CRC64;  
Query Match 70.4%; Score 38; DB 2; Length 281;  
Best Local Similarity 77.8%; Pred. No. 1e+02;  
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 KLGTYYFDS 10  
:|||||  
Db 244 KSGIYFDS 252

RESULT 16  
Q5HPQ7 STAEQ  
ID Q5HPQ7 STAEQ PRELIMINARY; PRT; 382 AA.  
AC Q5HPQ7  
DT 10-MAY-2005 (TrEMBLrel. 30, Created)  
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)  
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)  
DE Competence/damage-inducible protein Cina, putative.  
GN OrderedLocusNames=SERP0851;  
OS *Staphylococcus epidermidis* (strain ATCC 35984 / RP62A).  
OC Bacteria; Firmicutes; Bacillales; *Staphylococcus*.  
OX NCBI\_TaxID=176279;  
RN [1]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
RX PubMed=15774886; DOI=10.1128/JB.187.7.2426-2438.2005;  
RA Gill S.R., Fouts D.E., Archer G.L., Mongodin E.F., DeBoy R.T.,  
Ravel J., Paulsen I.T., Kolonay J.F., Brinkac L.M., Beanan M.J.,  
Dodson R.J., Daugherty S.C., Madupu R., Angiuoli S.V., Durkin A.S.,  
Haft D.H., Vamathevan J.J., Khouri H., Utterback T.R., Lee C.,  
Dimitrov G., Jiang L., Qin H., Weidman J., Tran K., Kang K.H.,  
Hance I.R., Nelson K.E., Fraser C.M.;  
RT "Insights on evolution of virulence and resistance from the complete  
genome analysis of an early methicillin-resistant *Staphylococcus*  
RT *aureus* strain and a biofilm-producing methicillin-resistant  
RT *Staphylococcus epidermidis* strain.";  
RL J. Bacteriol. 187:2426-2438(2005).  
DR EMBL; CF000029; AAW54235.1; -; Genomic\_DNA.  
DR TIGR; SERP0851;  
DR GO; GO:0006777; P:Mo-molybdopterin cofactor biosynthesis; IEA.  
DR InterPro; IPR008135; Cina.  
DR Pfam; PF00994; MoCF\_bios.  
DR FIRSF; FIRSF006728; Cina; 1.  
DR ProDom; PD002460; MoCF\_biosynth; 1.  
DR TIGRFAMs; TIGR00200; cina\_nterm; 1.  
KW Complete proteome.  
SQ SEQUENCE 382 AA; 42815 MW; 51119DC04862F3EF CRC64;

Query Match 70.4%; Score 38; DB 2; Length 382;  
Best Local Similarity 66.7%; Pred. No. 1.4e+02;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 KLGTYYFDS 10  
:|||||  
Db 244 RIGTYFDS 252

RESULT 17  
Q8RAL5\_THETN  
ID Q8RAL5\_THETN PRELIMINARY; PRT; 405 AA.  
AC Q8RAL5;  
DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)



DE ABC-type transport systems, involved in lipoprotein release, permease  
DE components.  
GN OrderedLocusNames=TTE1198;  
OC Thermoanaerobacter tengcongensis.  
OC Bacteria; Firmicutes; Clostridia; Thermoanaerobacteriales;  
OC Thermoanaerobacteriaceae; Thermoanaerobacter.  
OX NCBI\_TaxID=119072;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.

RA STRAIN=MB4;  
RC MEDLINE=2192816; PubMed=11997336; DOI=10.1101/gr.219302;  
RA Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,  
Chen Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,  
Tan H., Chen R., Wang J., Yu J., Yang H.;  
RT "A complete sequence of the T. tengcongensis genome.";  
RL Genome Res. 12:689-700(2002).  
DR EMBL; AE013082; AAW24428.1; -; Genomic\_DNA.  
DR GO; GO:0016020; C:membrane; IEA.  
DR InterPro; IPR003838; DUF214.  
DR Pfam; PF02687; FtsX; 1.  
KW Complete proteome.  
SQ SEQUENCE 405 AA; 44689 MW; 0AC9708B2F873306 CRC64;

Query Match 70.4%; Score 38; DB 2; Length 405;  
Best Local Similarity 62.5%; Pred. No. 1.5e+02;  
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VKLGTYTF 8  
Db 173 IKIGTYTY 180  
:|:||||:

## RESULT 18

ID Q4ZE15\_9CAUD PRELIMINARY; PRT; 423 AA.  
AC Q4ZE15;  
DT 13-SEP-2005 (T-EMBLrel. 31, Created)  
DT 13-SEP-2005 (T-EMBLrel. 31, Last sequence update)  
DT 13-SEP-2005 (T-EMBLrel. 31, Last annotation update)  
DE ORF006.  
OS Bacteriophage 187.  
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.  
OX NCBI\_TaxID=320833;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX PubMed=15788529; DOI=10.1073/pnas.0501140102;  
RA Kwan T., Liu J., Dubow M., Gros P., Pelletier J.;  
RT "The complete genomes and proteomes of 27 Staphylococcus aureus  
bacteriophages";  
RL Proc. Natl. Acad. Sci. U.S.A. 102:5174-5179(2005).  
DR EMBL; AY54950; AAX90884.1; -; Genomic DNA.  
SQ SEQUENCE 423 AA; 46939 MW; 6D9BFED313CF142D CRC64;

Query Match 70.4%; Score 38; DB 2; Length 423;  
Best Local Similarity 77.8%; Pred. No. 1.6e+02;  
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 KLGTYYFDS 10  
Db 250 KSGIYYFDS 258  
|:|||||

## RESULT 19

ID Q4TMH9\_9SPHN PRELIMINARY; PRT; 476 AA.  
AC Q4TMH9;  
DT 13-SEP-2005 (T-EMBLrel. 31, Created)  
DT 13-SEP-2005 (T-EMBLrel. 31, Last sequence update)  
DT 13-SEP-2005 (T-EMBLrel. 31, Last annotation update)  
DE Uracil-DNA glycosylase.  
GN ORFNames=ELI1948;  
OS Erythrobacter litoralis HTCC2594.

OC Bacteria; Proteobacteria; Alphaproteobacteria; Sphingomonadales;  
Query Match 70.4%; Score 38; DB 1; Length 587;  
Best Local Similarity 85.7%; Pred. No. 2.1e+02;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OC Sphingomonadaceae; Erythrobacter.  
OX NCBI\_TaxID=314225;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=HTCC2594;  
RA Giovannoni S.J., Cho J.-C., Ferriera S., Johnson J., Kravitz S.,  
Halpern A., Remington K., Beeson K., Tran B., Rogers Y.-H.,  
Friedman R., Venter J.C.;  
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.  
CC -!- CAUTION: The sequence shown here is derived from an  
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
preliminary data.  
DR EMBL; AAGG01000005; EAL75437.1; -; Genomic DNA.  
SQ SEQUENCE 476 AA; 53590 MW; 4B46734034FDBAD6 CRC64;

Query Match 70.4%; Score 38; DB 2; Length 476;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VKLGTYTY 7  
Db 7 VKLGTYTY 13  
|||||||

## RESULT 20

ID COAT\_PAVL3 STANDARD; PRT; 587 AA.  
AC F36310;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 13-SEP-2005 (Rel. 48, Last annotation update)  
DE Coat protein VP2.  
OS Parvovirus LuIII.  
OC Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.  
OX NCBI\_TaxID=35339;  
RN [1]  
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].  
RX MEDLINE=93297126; PubMed=8517025;  
RA Difford N., Chen K.C., Bates R.C., Lederma M.;  
RT "The complete nucleotide sequence of parvovirus LuIII and localization  
of a unique sequence possibly responsible for its encapsidation  
pattern.";  
RL Virology 192:339-345(1993).  
CC -!- SIMILARITY: Belongs to the parvoviruses coat protein family.  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
between the Swiss Institute of Bioinformatics and the EMBL outstation -  
the European Bioinformatics Institute. There are no restrictions on its  
use as long as its content is in no way modified and this statement is not  
removed.  
CC EMBL; M61888; -; NOT\_ANNOTATED\_CDS; Genomic\_DNA.  
DR PIR; B44276; B44276.  
DR HSP; P07302; 1MVM.  
DR InterPro; IPR001403; Parvo\_coat.  
DR Pfam; PF00740; Parvo\_coat; 1.  
KW Capsid protein; Glycoprotein; Structural protein.  
FT COMPBIAS 26 41 Gly-rich.  
FT CARBOHYD 49 49 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 90 90 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 220 220 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 304 304 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 371 371 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 503 503 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 511 511 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 514 514 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 539 539 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 571 571 N-linked (GlcNAc...) (Potential).  
SQ SEQUENCE 587 AA; 65429 MW; 523E6B9CBF2EBB74 CRC64;

Query Match 70.4%; Score 38; DB 1; Length 587;  
Best Local Similarity 85.7%; Pred. No. 2.1e+02;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY      4 GTTYFDS 10
Db      267 GTTYFDT 273
|||||:

RESULT 21
Q84367 MUMIV
ID      Q84367 MUMIV PRELIMINARY; PRT; 587 AA.
AC      Q84367
DT      01-NOV-1996 (TrEMBLrel. 01, Created)
DT      01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT      01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE      VP1 protein.
GN      Name=VP1;
OS      Murine minute virus (Murine parvovirus).
OC      Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
OX      NCBI_TaxID=10794;
RN      [1]
RP      NUCLEOTIDE SEQUENCE.
RC      STRAIN=MVM;
RX      MEDLINE=83143341; PubMed=6298737;
RA      Astell C.R., Thomson M., Merchlinsky M., Ward D.C.;
RT      "The complete DNA sequence of minute virus of mice, an autonomous
RT      parvovirus.";
RL      Nucleic Acids Res. 11:999-1018(1983).
RN      [2]
RP      NUCLEOTIDE SEQUENCE.
RC      STRAIN=MVM;
RX      MEDLINE=86115415; PubMed=3502703;
RA      Astell C.R., Gardiner E.M., Tattersall P.;
RT      "DNA sequence of the lymphotropic variant of minute virus of mice,
RT      MVM(1), and comparison with the DNA sequence of the fibrotropic
RT      prototype strain.";
RL      J. Virol. 57:656-669(1986).
RN      [3]
RP      NUCLEOTIDE SEQUENCE.
RC      STRAIN=MVM;
RX      MEDLINE=87061199; PubMed=3783817;
RA      Morgan W.R., Ward D.C.;
RT      "Three splicing patterns are used to excise the small intron common to
RT      all minute virus of mice RNAs.";
RL      J. Virol. 60:1170-1174(1986).
DR      EMBL; J02275; AAA67114.1; -: Genomic_DNA.
DR      HSP; P30129; 4DPV.
DR      GO; GO:0019028; C:viral capsid; IEA.
DR      GO; GO:0005198; F:structural molecule activity; IEA.
DR      InterPro; IPR001403; Parvo_coat.
DR      Pfam; PF00740; Parvo_coat; 1.
SQ      SEQUENCE 587 AA; 64534 MW; 9B8A75280D755056 CRC64;

Query Match      70.4%; Score 38; DB 2; Length 587;
Best Local Similarity 85.7%; Pred. No. 2.1e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      4 GTTYFDS 10
Db      268 GTTYFDT 274
|||||:

RESULT 22
Q84364 MUMIV
ID      Q84364 MUMIV PRELIMINARY; PRT; 587 AA.
AC      Q84364;
DT      01-NOV-1996 (TrEMBLrel. 01, Created)
DT      01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT      01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE      VP2 protein.
GN      Name=VP2;
OS      Murine minute virus (Murine parvovirus).
OC      Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
OX      NCBI_TaxID=10794;
RN      [1]
RP      NUCLEOTIDE SEQUENCE.
RC      STRAIN=MVM;
RX      MEDLINE=86115415; PubMed=3502703;
RA      Astell C.R., Gardiner E.M., Tattersall P.;
RT      "DNA sequence of the lymphotropic variant of minute virus of mice,
RT      MVM(1), and comparison with the DNA sequence of the fibrotropic
RT      prototype strain.";
RL      J. Virol. 57:656-669(1986).
RN      [2]
RP      NUCLEOTIDE SEQUENCE.
RC      STRAIN=MVM;
RX      MEDLINE=87061199; PubMed=3783817;
RA      Morgan W.R., Ward D.C.;
RT      "Three splicing patterns are used to excise the small intron common to
RT      all minute virus of mice RNAs.";
RL      J. Virol. 60:1170-1174(1986).
DR      EMBL; J02275; AAA67114.1; -: Genomic_DNA.
DR      HSP; P30129; 4DPV.
DR      GO; GO:0019028; C:viral capsid; IEA.
DR      GO; GO:0005198; F:structural molecule activity; IEA.
DR      InterPro; IPR001403; Parvo_coat.
DR      Pfam; PF00740; Parvo_coat; 1.
SQ      SEQUENCE 587 AA; 64534 MW; 9B8A75280D755056 CRC64;

Query Match      70.4%; Score 38; DB 2; Length 587;
Best Local Similarity 85.7%; Pred. No. 2.1e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      4 GTTYFDS 10
Db      268 GTTYFDT 274
|||||:

RESULT 23
Q54U89 DICDI
ID      Q54U89 DICDI PRELIMINARY; PRT; 708 AA.
AC      Q54U89;
DT      13-SEP-2005 (TrEMBLrel. 31, Created)
DT      13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT      13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE      Hypothetical protein.
GN      ORFNames=DOB0204083;
OS      Dictyostelium discoideum (Slime mold).
OC      Eukaryota; Mycetozoa; Dictyostellida; Dictyostelium.
OX      NCBI_TaxID=44689;
RN      [1]
RP      NUCLEOTIDE SEQUENCE.
RC      STRAIN=AX4;
RA      Eichinger L., Pachebat J.A., Gloeckner G., Rajandream M.-A.,
RA      Sugang R., Berriman M., Song J., Olsen E., Szafranski K., Xu Q.,
RA      Tunggal B., Kummerfeld S., Madera M., Konfortov B.A., Rivero F.,
RA      Bankier A.T., Lehmann R., Hamlin N., Davies R., Gaudet P., Fey P.,
RA      Pilcher K., Chen G., Saunders D., Sodergren E., Davis P.,
RA      Kerhornou A., Nie X., Hall N., Anjard C., Hemphill L., Bason N.,
RA      Farbrother P., Desany B., Just E., Morio T., Roat R., Churcher C.,
RA      Cooper J., Haydock S., van Driessche N., Cronin A., Goodhead I.,
RA      Muzny D., Mourier T., Pain A., Lu M., Harper D., Lindsey R.,
RA      Hauser H., James K., Quiles M., Mohan M.B., Saito T., Buchrieser C.,
RA      Wardrop A., Felder M., Thangavelu M., Johnson D., Knights A.,
RA      Loulsegod H., Mungall K., Oliver K., Price C., Quail M.A.,
RA      Urushihara H., Hernandez J., Rabinowitsch E., Steffen D., Sanders M.,
RA      Ma J., Kohara Y., Sharp S., Simmonds M., Spiegler S., Tivey A.,
RA      Sugano S., White B., Walker D., Woodward J., Winckler T., Tanaka Y.,
RA      Shaulsky G., Schleicher M., Weinstock G., Rosenthal A., Cox E.C.,
RA      Chisholm R.L., Gibbs R., Loomis W.F., Platzer M., Kay R.R.,
RA      Williams J., Dear P.H., Noegel A.A., Barrell B., Kuapa A.;
RT      "The genome of the social amoeba Dictyostelium discoideum.";
RL      Nature 0:0-0(2005).
CC      -!- CAUTION: The sequence shown here is derived from an
CC      EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC      preliminary data.
KW      Hypothetical protein.
SQ      SEQUENCE 708 AA; 78002 MW; C20804F008331288 CRC64;

Query Match      70.4%; Score 38; DB 2; Length 708;
Best Local Similarity 75.0%; Pred. No. 2.6e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      2 KGTYYFD 9
Db      129 KGTYYFN 136
|||||:

```

## RESULT 24

COAT\_MUMIM  
ID AC P03137;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 13-SEP-2005 (Rel. 48, Last annotation update)  
DE Coat protein VP1 [Contains: Coat protein VP2].  
OS Murine minute virus (Murine parvovirus).  
OC Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.  
OX NCBI\_TaxID=10794;  
RN [1]  
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].  
RX MEDLINE=83143341; PubMed=6298737;  
RA Astell C.R., Thomson M., Merchlinsky M., Ward D.C.;  
RT "The complete DNA sequence of minute virus of mice, an autonomous parvovirus."  
RL Nucleic Acids Res. 11:999-1018(1983).  
CC -1- SIMILARITY: Belongs to the parvoviruses coat protein family.  
CC  
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CC  
CC EMBL; V01115; CAA24310.1; ALT\_SEQ; Genomic\_DNA.  
DR PIR; A03700; VCPV2M.  
DR HSP; P07302; LMVM.  
DR InterPro; IPR001403; Parvo\_coat.  
DR Pfam; PF00740; Parvo\_coat; 1.  
DR Capsid protein; Glycoprotein; Structural protein.  
FT CHAIN 1 716 Coat protein VP1.  
FT CHAIN 131 716 Gly-rich.  
FT COMPTAS 156 171 N-linked (GlcNAc. . .) (Potential).  
FT CARBOHYD 179 179 N-linked (GlcNAc. . .) (Potential).  
FT CARBOHYD 218 218 N-linked (GlcNAc. . .) (Potential).  
FT CARBOHYD 500 500 N-linked (GlcNAc. . .) (Potential).  
FT CARBOHYD 633 633 N-linked (GlcNAc. . .) (Potential).  
FT CARBOHYD 669 669 N-linked (GlcNAc. . .) (Potential).  
SQ SEQUENCE 716 AA; 78708 MW; 6A7229A91161F4C6 CRC64;

Query Match 70.4%; Score 38; DB 1; Length 716;  
Best Local Similarity 85.7%; Pred. No. 2.6e+02;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 4 GTYYFDS 10  
Db 397 GTYYFDT 403

## RESULT 25

COAT\_MUMIM  
ID AC P07302; Q9WMH2; Q9WMH3;  
DT 01-APR-1988 (Rel. 07, Created)  
DT 01-APR-1988 (Rel. 07, Last sequence update)  
DT 13-SEP-2005 (Rel. 48, Last annotation update)  
DE Coat protein VP1 [Contains: Coat protein VP2].  
OS Murine minute virus (strain MMV1) (Murine parvovirus).  
OC Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.  
OX NCBI\_TaxID=10795;  
RN [1]  
RP NUCLEOTIDE SEQUENCE  
RX MEDLINE=86115415; PubMed=3502703;  
RA Astell C.R., Gardiner E.M., Tattersall P.;  
RT "DNA sequence of the lymphotropic variant of minute virus of mice, MMV(1), and comparison with the DNA sequence of the fibrotropic prototype strain."  
RL J. Virol. 57:656-669(1986).  
RN [2]

RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=85242059; PubMed=3855242;  
RA Sahli R., McMaster G.K., Hirt B.;  
RT "DNA sequence comparison between two tissue-specific variants of the autonomous parvovirus, minute virus of mice."  
RL Nucleic Acids Res. 13:3617-3633(1985).  
RN [3]  
RP X-RAY CRYSTALLOGRAPHY (3.5 ANGSTROMS) OF 132-718.  
RX PubMed=15299974; DOI=10.1107/S0907444996010566;  
RA Llamas-Saiz A.L., Agbandje-Mckenna M., Wikoff W.R., Bratton J., Tattersall P., Rossmann M.G.;  
RT "Structure determination of Minute Virus of mice."  
RL Acta Crystallogr. D 53:93-100(1997).  
CC -1- SIMILARITY: Belongs to the parvoviruses coat protein family.  
CC  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.  
CC  
CC EMBL; X02481; CAB46507.1; -; Genomic\_DNA.  
DR EMBL; X02481; CAB46508.1; -; Genomic\_DNA.  
DR EMBL; M12032; AAA69569.1; ALT\_INIT; Genomic\_DNA.  
DR PIR; B23008; VCPVIM.  
DR PDB; 1MWM; X-ray; A=132-718.  
DR InterPro; IPR001403; Parvo\_coat.  
DR Pfam; PF00740; Parvo\_coat; 1.  
DR 3D-structure; Capsid protein; Glycoprotein; Structural protein.  
FT CHAIN 1 718 Coat protein VP1.  
FT CHAIN 132 718 Gly-rich.  
FT COMPTAS 157 172 N-linked (GlcNAc. . .) (Potential).  
FT CARBOHYD 180 180 N-linked (GlcNAc. . .) (Potential).  
FT CARBOHYD 219 219 N-linked (GlcNAc. . .) (Potential).  
FT CARBOHYD 502 502 N-linked (GlcNAc. . .) (Potential).  
FT CARBOHYD 635 635 N-linked (GlcNAc. . .) (Potential).  
FT CARBOHYD 671 671 N-linked (GlcNAc. . .) (Potential).  
FT CONFLICT 144 144 A -> G (in Ref. 2).  
FT STRAND 182 186  
FT STRAND 191 204  
FT STRAND 213 217  
FT TURN 220 221  
FT TURN 228 231  
FT STRAND 235 245  
FT TURN 251 253  
FT HELIX 256 265  
FT STRAND 266 266  
FT STRAND 268 269  
FT STRAND 274 289  
FT STRAND 296 301  
FT TURN 303 304  
FT STRAND 307 307  
FT STRAND 309 312  
FT HELIX 322 325  
FT TURN 326 326  
FT TURN 333 334  
FT STRAND 337 338  
FT STRAND 340 345  
FT STRAND 351 351  
FT TURN 357 358  
FT STRAND 367 367  
FT TURN 373 375  
FT HELIX 381 384  
FT STRAND 390 390  
FT STRAND 396 397  
FT STRAND 408 409  
FT STRAND 428 428  
FT STRAND 438 438  
FT TURN 442 444  
FT TURN 458 460  
FT STRAND 466 467  
FT TURN 473 474  
FT STRAND 477 477

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FT STRAND 484 484
FT TURN 494 496
FT TURN 499 503
FT TURN 509 509
FT TURN 512 513
FT STRAND 525 525
FT STRAND 534 536
FT HELIX 546 546
FT TURN 557 558
FT STRAND 559 559
FT TURN 575 577
FT TURN 583 584
FT STRAND 585 586
FT STRAND 600 600
FT STRAND 618 618
FT STRAND 627 630
FT STRAND 636 636
FT STRAND 649 649
FT STRAND 652 668
FT STRAND 683 683
FT STRAND 691 691
FT STRAND 692 694
FT HELIX 718 AA; B43C1762ED5F74B9 CRC64;
SQ SEQUENCE 718 AA; 79017 MW; B43C1762ED5F74B9 CRC64;

Query Match 70.4%; Score 38; DB 1; Length 718;
Best Local Similarity 85.7%; Pred. No. 2.6e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GTTYFDS 10
Db 399 GTTYFDT 405

RESULT 26
Q84207 MUMIV
ID Q84207 MUMIV PRELIMINARY; PRT; 723 AA.
AC Q84207;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Coding sequence (Fragment).
OS Murine minute virus (Murine parvovirus).
OC Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
OX NCBI_TaxID=10794;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=83143341; PubMed=6298737;
RA Astell C.R., Thomson M., Merchlinsky M., Ward D.C.;
RT "The complete DNA sequence of minute virus of mice, an autonomous
parvovirus."
RL Nucleic Acids Res. 11:999-1018(1983).
DR HSSP; P30129; 4DPV.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR001403; Parvo_coat.
DR Pfam; PF00740; Parvo_coat; 1.
DR NON TER 1
SQ SEQUENCE 723 AA; 79492 MW; F805707524126980 CRC64;

Query Match 70.4%; Score 38; DB 2; Length 723;
Best Local Similarity 85.7%; Pred. No. 2.6e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GTTYFDS 10
Db 404 GTTYFDT 410

RESULT 27
Q84366 MUMIV
ID Q84366 MUMIV PRELIMINARY; PRT; 729 AA.
AC Q84366;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Soluble lytic transglycosylase.
GN Namesalt; OrderedLocustNames=slr0534;
OS Synechocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
OX NCBI_TaxID=1148;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=97061201; PubMed=8905231;
RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
Miyajima N., Hirose M., Sugita M., Sasamoto S., Kimura T.,
Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.,
Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
Tabata S.;
RL "Sequence analysis of the genome of the unicellular cyanobacterium
Synechocystis sp. strain PCC6803. II. Sequence determination of the
entire genome and assignment of potential protein-coding regions."
RT
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RL DNA Res. 3:109-136(1996).
DR EMBL; BA000022; BAA10822.1; -; Genomic_DNA.
DR PIR; S75975; S75975.
DR GO; GO:0005488; P:binding; IEA.
DR GO; GO:0015979; P:photosynthesis; IEA.
DR InterPro; IPR008258; LT catalytic.
DR InterPro; IPR011990; TPR-like_helical.
DR Pfam; PF01464; SLT; 1.
KW Complete proteome.
SQ SEQUENCE 847 AA; 95980 MW; A84B878873EE00AF CRC64;

Query Match 70.4%; Score 38; DB 2; Length 847;
Best Local Similarity 66.7%; Pred. No. 3.1e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VKLGTYYFD 9
Db 759 VNMGTWYFD 767

RESULT 29
Q9FW49 ARATH
ID Q9FW49 ARATH PRELIMINARY; PRT; 907 AA.
AC Q9FW49;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein TIE4.10.
GN Name=TIE4.10;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
OC NCBI_TaxID=3702;
OX NCBI_TaxID=3702;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.J., Wu D.,
RA Maiti R., Ronning C.M., Koo H., Fujii C.Y., Uterback T.R., Wu D.,
RA Barnstead M.E., Bowman C.L., White O., Nierman W.C., Fraser C.M.;
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC069299; AACG26079.1; -; Genomic_DNA.
DR PIR; A86460; A86460.
DR InterPro; IPR000413; Integrin_alpha.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR007090; LRR_plant.
DR Pfam; PF00560; LRR_1; 16.
DR PRINTS; PR00019; LEURICHRPT.
DR PROSITE; PS00242; INTEGRIN ALPHA; UNKNOWN 1.
KW Hypothetical protein; Leucine-rich repeat_Repeat.
SQ SEQUENCE 907 AA; 99879 MW; 60BA983FB32F0009 CRC64;

Query Match 70.4%; Score 38; DB 2; Length 907;
Best Local Similarity 85.7%; Pred. No. 3.3e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GTTYFDS 10
Db 795 GTTYDS 801

RESULT 30
VID28_YEAST
ID VID28_YEAST STANDARD; PRT; 921 AA.
AC P40547;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Vacuolar import and degradation protein VID28 (Glucose-induced
DE degradation protein 5).
GN Name=VID28; Synonyms=GID5; OrderedLocusNames=YIL017C;
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.

OX NCBI_TaxID=4932;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=S288C / AB972;
RX MEDLINE=97313266; PubMed=9169870;
RA Churchill C.M., Bowman S., Badcock K., Bankier A.T., Brown D.,
RA Chillingworth T., Connor R., Devlin K., Gentles S., Hamlin N.,
RA Harris D.E., Horsnell T., Hunt S., Jagels K., Jones M., Lyne G.,
RA Moulé S., Odell C., Pearson D., Rajandream M.A., Rice P., Rowley N.,
RA Skelton J., Smith V., Walsh S.V., Whitehead S., Barrell B.G.;
RL "The nucleotide sequence of Saccharomyces cerevisiae chromosome IX.";
RN Nature 387:84-87(1997).
RN [2]
RP FUNCTION
RP PubMed=12686616; DOI=10.1091/mbc.E02-08-0456;
RA Regelmann J., Schuele T., Joespeit F.S., Horak J., Rose M.,
RA Entian K.-D., Thumm M., Wolf D.H.;
RT "Catabolite degradation of fructose-1,6-bisphosphatase in the yeast
RT Saccharomyces cerevisiae: a genome-wide screen identifies eight novel
RT GID genes and indicates the existence of two degradation pathways.";
RL Mol. Biol. Cell 14:1652-1663(2003).
RN [3]
RP SUBCELLULAR LOCATION.
RX MEDLINE=22923954; PubMed=14562095; DOI=10.1038/nature02026;
RA Hub W.-K., Falvo J.V., Gerke L.C., Carroll A.S., Howson R.W.,
RA Weisman J.S., O'Shea E.K.;
RT "Global analysis of protein localization in budding yeast.";
RL Nature 425:686-691(2003).
CC -!- FUNCTION: Has a role in the negative regulation of
CC gluconeogenesis. Required for both proteosome-dependent and
CC vacuolar catabolite degradation of fructose-1,6-bisphosphatase
CC (FBPase).
CC -!- SUBCELLULAR LOCATION: Nuclear, and cytoplasmic.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; Z46881; CAA86975.1; -; Genomic_DNA.
CC PIR; S49965; S49965.
CC IntAct; P40547; -.
CC Germline; 139554; -.
CC Ensembl; YIL017C; Saccharomyces cerevisiae.
CC SGD; S00001279; VID28.
CC GO; GO:0005737; C:cytoplasm; IDA.
CC GO; GO:0005634; C:nucleus; IDA.
CC GO; GO:0045721; P:negative regulation of gluconeogenesis; IMP.
CC InterPro; IPR011989; ARM-like.
CC Complete proteome; Nuclear protein; Ubl conjugation pathway.
KW SEQUENCE 921 AA; 105491 MW; DDPAS50E2E846A0 CRC64;

Query Match 70.4%; Score 38; DB 1; Length 921;
Best Local Similarity 85.7%; Pred. No. 3.3e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LGTYFD 9
Db 72 VGTYFD 78

RESULT 31
Q5SBL9 LACRE
ID Q5SBL9 LACRE PRELIMINARY; PRT; 1781 AA.
AC Q5SBL9;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Glucanucrase (EC 2.4.1.5).
OS Lactobacillus reuteri.
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC Lactobacillus.

```

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OX NCBI_TaxID=1598;
RN [1] NUCLEOTIDE SEQUENCE.
RP STRAIN=121;
RC PubMed=1528655; DOI=10.1099/mic.0.27321-0;
RX Kralj S., van Geel-Schutten G.H., Dondorf M.M.G., Kirsanovs S.,
RA van der Maarel M.J.E.C., Dijkhuizen L.;
RT "Glucan synthesis in the genus Lactobacillus: isolation and
RT characterization of glucanucrase genes, enzymes and glucan products
RT from six different strains.";
RL Microbiology 150:3681-3690 (2004).
[2]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=121;
RC MEDLINE=22188232; PubMed=12200277;
RX DOI=10.1128/AEM.68.9.4283-4291.2002;
RA Kralj S., van Geel-Schutten G.H., Rahaoui H., Leer R.J., Faber E.J.,
RA van der Maarel M.J., Dijkhuizen L.;
RT "Molecular characterization of a novel glucosyltransferase from
RT Lactobacillus reuteri strain 121 synthesizing a unique, highly
RT branched glucan with alpha-(1-->4) and alpha-(1-->6) glucosidic
RT bonds.";
RL Appl. Environ. Microbiol. 68:4283-4291 (2002).
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=ATCC 55730;
RC EMBL: AY697435; AAU08015.1; -; Genomic DNA.
DR GO: GO:0047849; F:dextranucrase activity; IEA.
DR GO: GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
DR GO: GO:0016757; F:transferase activity, transferring glycosyl. .; IEA.
DR GO: GO:0005975; P:carbohydrate metabolism; IEA.
DR GO: GO:0030245; P:cellulose catabolism; IEA.
DR GO: GO:0009250; P:glucan biosynthesis; IEA.
DR GO: GO:000272; P:polysaccharide catabolism; IEA.
DR InterPro: IPR002479; CW binding.
DR InterPro: IPR003318; Glyco_hydro_70.
DR Pfam: PF01473; CW binding_1; 1.
DR Pfam: PF02324; Glyco_hydro_70; 1.
KW Glycosyltransferase; Transferase.
SQ SEQUENCE 1781 AA; 198608 MW; 4E352FEAAAF915F6E CRC64;

Query Match 70.4%; Score 38; DB 2; Length 1781;
Best Local Similarity 85.7%; Pred. No. 6.3e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 GTTYFDS 10
Db 1724 GTTYFDN 1730
|||||:

RESULT 32
Q4JCS4_LACRE PRELIMINARY; PRT; 1781 AA.
AC Q4JCS4;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DE Glucanucrase (SC 2.4.1.5).
OC Lactobacillus reuteri.
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC Lactobacillus.
OX NCBI_TaxID=1598;
RN [1] NUCLEOTIDE SEQUENCE.
RP STRAIN=ATCC 55730;
RX PubMed=1600808;
RA Kralj S., Strippling E., Sanders P., van Geel-Schutten G.H.,
RA Dijkhuizen L.;
RT "Highly Hydrolytic Reuteranucrase from Probiotic Lactobacillus reuteri Strain ATCC 55730.";
RL Appl. Environ. Microbiol. 71:3942-3950 (2005).
DR EMBL: AY911856; AA957502.1; -; Genomic_DNA.
KW Glycosyltransferase; Transferase.
SQ SEQUENCE 1781 AA; 196912 MW; BB0D5D5B80EB46FD CRC64;

Query Match 70.4%; Score 38; DB 2; Length 1781;
Best Local Similarity 85.7%; Pred. No. 6.3e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 GTTYFDS 10
Db 1724 GTTYFDN 1730
|||||:

RESULT 33
Q4JLC7_LACRE PRELIMINARY; PRT; 1781 AA.
AC Q4JLC7;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DE Lr1943.
GN ORFNames=lrl943;
OS Lactobacillus reuteri.
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC Lactobacillus.
OX NCBI_TaxID=1598;
RN [1] NUCLEOTIDE SEQUENCE.
RP STRAIN=ATCC 55730;
RC Wall T., Bath K., Roos S., Jonsson H.;
RT "Bioinformatic identification of the secretome of Lactobacillus reuteri ATCC 55730.";
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL: DQ074948; AA986923.1; -; Genomic_DNA.
SQ SEQUENCE 1781 AA; 197203 MW; 8B7C05D18CA8B7FE CRC64;

Query Match 70.4%; Score 38; DB 2; Length 1781;
Best Local Similarity 85.7%; Pred. No. 6.3e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 GTTYFDS 10
Db 1724 GTTYFDN 1730
|||||:

RESULT 34
Q5JCV5_PYRKO PRELIMINARY; PRT; 221 AA.
AC Q5JCV5;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE Polichol-phosphate mannosyltransferase.
GN OrderedLocusNames=TK0364;
OS Pyrococcus kodakaraensis (Thermococcus kodakaraensis).
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Thermococcus.
OX NCBI_TaxID=69014;
RN [1] NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RP STRAIN=KOD1;
RX PubMed=15710748; DOI=10.1101/gr.3003105;
RA Fukui T., Atomi H., Kanai T., Matsumi R., Fujiwara S., Imanaka T.;
RT "Complete genome sequence of the hyperthermophilic archaeon Thermococcus kodakaraensis KOD1 and comparison with Pyrococcus genomes.";
RL Genome Res. 15:352-363 (2005).
DR EMBL: AP006878; BAD84553.1; -; Genomic_DNA.
DR GO: GO:0016757; F:transferase activity, transferring glycosyl. .; IEA.
DR InterPro: IPR001173; Glyco_transf_2.
DR Pfam: PF00535; Glycosyltransf_2; 1.
KW Complete proteome; Glycosyltransferase; Transferase.
SQ SEQUENCE 221 AA; 24928 MW; 0BA21EB88A0AB2A1 CRC64;

Query Match 68.5%; Score 37; DB 2; Length 221;
Best Local Similarity 60.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
```

QY 1 VKLGTYYFDS 10  
:|||||:|:  
Db 144 LKLGTYVYDT 153

RESULT 35  
Q4KAC8\_PSEF5  
ID Q4KAC8\_PSEF5 PRELIMINARY; PRT; 245 AA.  
AC Q4KAC8\_PSEF5  
DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
DE Hypothetical protein.  
GN ORFNAMES-PFL 3703;  
OS Pseudomonas fluorescens (strain Pf-5).  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
OC Pseudomonadaceae; Pseudomonas.  
OX NCBI\_TaxID=220664;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=PF-5;  
RX PubMed=15980861; DOI=10.1038/nbr1110;  
RA Paulsen I.T., Press C., Ravel J., Kobayashi D., Myers G.S.,  
RA Pavlenti D., DeBoy R.T., Seshadri R., Ren O., Madupu R., Dodson R.J.,  
RA Durkin S., Brinkac L.M., Daugherty S.C., Sullivan S.A., Rosovitz M.,  
RA Gwinn M.L., Zhou L., Nelson W.C., Weidman J., Watkins K., Tran K.,  
RA Khouri H.M., Pierson E., Pierson L. III, Thomashow L., Loper J.;  
RT "Complete genome sequence of the plant commensal Pseudomonas  
fluorescens Pf-5.";  
RL Nat. Biotechnol. 23:873-878(2005).  
DR EMBL: CP000076; AAY92969.1; -; Genomic\_DNA.  
KW Hypothetical protein.  
SQ SEQUENCE 245 AA; 27173 MW; 248E924B5449F3F6 CRC64;

Query Match 68.5%; Score 37; DB 2; Length 245;  
Best Local Similarity 77.8%; Pred. No. 1.4e+02;  
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 VKLGTYYFD 9  
:|||||:  
Db 132 VKLGAYYSD 140

RESULT 36  
Q67LI9\_SYTH  
ID Q67LI9\_SYTH PRELIMINARY; PRT; 254 AA.  
AC Q67LI9;  
DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
DE Hypothetical protein.  
GN OrderedLocusNames=STH2472;  
OS Symbiobacterium thermophilum.  
OC Bacteria; Actinobacteria; Symbiobacterium.  
OX NCBI\_TaxID=2734;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=JAM14863;  
RX PubMed=15383646; DOI=10.1093/nar/gkh830;  
RA Usda K., Yanashita A., Ishikawa J., Shimada M., Watsuji T.,  
RA Morimura K., Ikeda H., Hattori M., Beppu T.;  
RT "Genome sequence of Symbiobacterium thermophilum, an uncultivable  
bacterium that depends on microbial commensalism.";  
RL Nucleic Acids Res. 32:4937-4944(2004).  
DR EMBL: AP006840; BAD41457.1; -; Genomic DNA.  
KW Complete proteome; Hypothetical protein.  
SQ SEQUENCE 254 AA; 30085 MW; 4B891DE2B8FC8A85 CRC64;

Query Match 68.5%; Score 37; DB 2; Length 254;  
Best Local Similarity 60.0%; Pred. No. 1.5e+02;  
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 VKLGTYYFDS 10

Db 66 VREGWYFDA 75  
:|:|:|:|:

RESULT 37  
Q6CLB5\_KLULA  
ID Q6CLB5\_KLULA PRELIMINARY; PRT; 338 AA.  
AC Q6CLB5\_KLULA  
DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
DE Similar to sp|P38235 Saccharomyces cerevisiae YBR053c singleton.  
GN OrderedLocusNames=KLJA0F04301g;  
OS Kluyveromyces lactis (Yeast).  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.  
OX NCBI\_TaxID=28985;  
RN [1]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
RX PubMed=1529592; DOI=10.1038/nature02579;  
RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,  
RA Lafontaine I., de Montigny J., March C., Neuvéglise C., Talla E.,  
RA Goffard N., Frangoul L., Aigle M., Anthouard V., Babour A., Barbe V.,  
RA Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,  
RA Boissière A., Boyer J., Cattolico L., Confantolero F., de Barovar A.,  
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi R.,  
RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,  
RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Müller H.,  
RA Nicaud J.-M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,  
RA Pellenz S., Potier S., Richard G.-P., Straub M.-L., Suleau A.,  
RA Svennen D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,  
RA Zenit-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,  
RA Bouchier C., Caudron B., Scarpelli C., Gallardin C., Weissenbach J.,  
RA Wincker P., Souciet J.-L.;  
RT "Genome evolution in yeasts.";  
RL Nature 430:35-44(2004).  
DR EMBL: CR382126; CAG97982.1; -; Genomic\_DNA.  
DR InterPro: IPR005511; SMP-30.  
DR Pfam: PF03758; SMP-30; 1.  
KW Complete proteome.  
SQ SEQUENCE 338 AA; 38362 MW; DBD1603F135D96D5 CRC64;

Query Match 68.5%; Score 37; DB 2; Length 338;  
Best Local Similarity 77.8%; Pred. No. 1.9e+02;  
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 KLGTYFDS 10  
:|:|:|:|:  
Db 10 KNGPYFDS 18

RESULT 38  
Q5YF08\_9VIRU  
ID Q5YF08\_9VIRU PRELIMINARY; PRT; 368 AA.  
AC Q5YF08;  
DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
DE ORF079L.  
OS Rock bream iridovirus.  
OC Viruses; dsDNA viruses, no RNA stage; Iridoviridae; Megalocytivirus.  
OX NCBI\_TaxID=263891;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=BBIV-KOR-TV1.  
RX PubMed=15246274; DOI=10.1016/j.virol.2004.05.008;  
RA Do J.W., Moon C.H., Kim H.J., Ko M.S., Kim S.B., Son J.H., Kim J.S.,  
RA An E.J., Kim M.K., Lee S.K., Han M.S., Cha S.J., Park M.S., Park M.A.,  
RA Lee J.S., Kim Y.C., Choi D.L., Kim J.W., Park J.W.;  
RT "Complete genomic DNA sequence of rock bream iridovirus.";  
RL Virology 325:351-363(2004).  
DR EMBL: AY532606; AAT71894.1; -; Genomic\_DNA.  
SQ SEQUENCE 368 AA; 40820 MW; 801B9BD1D123C903 CRC64;

Query Match 68.5%; Score 37; DB 2; Length 368;  
Best Local Similarity 66.7%; Pred. No. 2.1e+02;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 KLGTYFYFDS 10  
Db 231 KMGTYFYDS 239

RESULT 39  
Q8QUM8\_9VIRU PRELIMINARY; PRT; 368 AA.  
AC Q8QUM8\_9VIRU PRELIMINARY; PRT; 368 AA.  
DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
DE 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE ORF082L.  
OS Infectious spleen and kidney necrosis virus.  
OC Viruses; dsDNA viruses, no RNA stage; Iridoviridae; Megalocytivirus.  
OX NCBI\_TaxID=180170;  
RN [1]  
RN NUCLEOTIDE SEQUENCE.  
RP MEDLINE=21874810; PubMed=11878882; DOI=10.1006/viro.2001.1208;  
RX He J.G., Deng M., Weng S.P., Li Z., Zhou S.Y., Long Q.X., Wang X.Z.,  
RA Chan S.M.;  
RA "Complete genome analysis of the mandarin fish infectious spleen and  
RT kidney necrosis iridovirus";  
RT Virology 291:126-139(2001).  
RL EMBL; AF371960; AAL9806.1; -; Genomic DNA.  
SQ SEQUENCE 368 AA; 40658 MW; D8E08B028DDA0CB6 CRC64;

Query Match 68.5%; Score 37; DB 2; Length 368;  
Best Local Similarity 66.7%; Pred. No. 2.1e+02;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 KLGTYFYFDS 10  
Db 231 KMGTYFYDS 239

RESULT 40  
Q4KS76\_9VIRU PRELIMINARY; PRT; 368 AA.  
AC Q4KS76\_9VIRU PRELIMINARY; PRT; 368 AA.  
DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
DE ORF81L.  
OS Orange-spotted grouper iridovirus.  
OC Viruses; dsDNA viruses, no RNA stage; Iridoviridae; Iridovirus.  
OX NCBI\_TaxID=322017;  
RN [1]  
RN NUCLEOTIDE SEQUENCE.  
RP Zhou S.Y., Lv L., Chen C., Weng S.P., Chan S.M., He J.G.;  
RA Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY894343; AAL82390.1; -; Genomic DNA.  
SQ SEQUENCE 368 AA; 40781 MW; 98039BC9C923C903 CRC64;

Query Match 68.5%; Score 37; DB 2; Length 368;  
Best Local Similarity 66.7%; Pred. No. 2.1e+02;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 KLGTYFYFDS 10  
Db 231 KMGTYFYDS 239

RESULT 41  
Q8WV03\_HUMAN PRELIMINARY; PRT; 380 AA.  
ID Q8WV03\_HUMAN PRELIMINARY; PRT; 380 AA.  
AC Q8WV03\_HUMAN PRELIMINARY; PRT; 380 AA.  
DT 01-MAR-2002 (TrEMBLrel. 20, Created)

DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)  
DE Chromosome 3 open reading frame 21.  
GN Name=C3orf21; (Human).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RN NUCLEOTIDE SEQUENCE.  
RP TISSUE=Colon, and Kidney;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Dege J.G.,  
RA Klausner R.D., Collins E.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullen P.H.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Smallos D.E.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smallos D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RN NUCLEOTIDE SEQUENCE.  
RC TISSUE=Kidney;  
RA Director MGC Project;  
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RN NUCLEOTIDE SEQUENCE.  
RP TISSUE=Colon;  
RA Director MGC Project;  
RA Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.  
RL EMBL; BC019036; AAH19036.1; -; mRNA.  
DR EMBL; BC039067; AAH39067.1; -; mRNA.  
SQ SEQUENCE 380 AA; 42510 MW; 108A64F4EAF8FB3F CRC64;

Query Match 68.5%; Score 37; DB 2; Length 380;  
Best Local Similarity 87.5%; Pred. No. 2.2e+02;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 LGTYFYFDS 10  
Db 183 LGTYFYDS 190

RESULT 42  
Q8NB16\_HUMAN PRELIMINARY; PRT; 393 AA.  
ID Q8NB16\_HUMAN PRELIMINARY; PRT; 393 AA.  
AC Q8NB16\_HUMAN PRELIMINARY; PRT; 393 AA.  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE CDNA FSEC0251 fis, clone NT2RP3003097.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RN NUCLEOTIDE SEQUENCE.  
RA Otsuki T., Ota T., Nishikawa T., Hayaashi K., Suzuki Y., Yamamoto J.,  
RA Wakamatsu A., Kimura K., Sakamoto K., Hatano N., Kawai Y., Ishii S.,



RA	Saito K., Kojima S., Sugiyama T., Ono T., Okano K., Yoshikawa Y., Aotogai S., Sasaki N., Hattori A., Okumura K., Nagai K., Sugano S., Isegai T.;
RA	"Signal Sequence and Keyword Trap in silico for Selection of Full-length Human cDNAs Encoding Secretion or Membrane Proteins from Oligo-Capped cDNA Libraries.";
RL	DNA Res. 12:117-126(2005).
DR	EMBL; AK075551; BAC11694.1; -; mRNA.
DR	Ensembl; ENSG0000173950; Homo sapiens.
DR	HGNC; HGNC:26639; C3orf21.
SQL	SEQUENCE 393 AA; 43807 MW; 3C789AFDF933A23D CRC64;
 Query Match 68.5%; Score 37; DB 2; Length 393; Best Local Similarity 87.5%; Pred.No. 2.2e+02; Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
Qy	3 LGTYFYDS 10 
Db	196 LGTYISDS 203 
 RESULT 43	
Q81504_BACCR	
ID	Q81504_BACCR PRELIMINARY; PRT; 522 AA.
AC	Q81504;
DT	01-JUN-2003 (TrEMBLrel. 24, Created)
DT	01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE	NADH oxidase (NOXASE) [EC 1.6.99.3].
GN	OrdersLocusNames=BC5081;
OS	Bacillus cereus (strain ATCC 14579 / DSM 31).
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC	Bacillus cereus group.
NCBI_TaxID	=226900;
RN	[1]
RP	NUCLEOTIDE SEQUENCE.
RX	MEDLINE=22608415; PubMed=12721630; DOI=10.1038/nature01582;
RA	Ivanova N., Sorokin A., Anderson I., Galleron N., Candelson B., Kapatral V., Bhattacharyya A., Reznik G., Mikhailova N., Lapidus A., Chu L., Mazur M., Golteman E., Larsen N., D'Souza M., Walunas T., Grachkin Y., Pusch G., Haselkorn R., Fongstein M., Ehrlich S.D., Overbeek R., Kyprides N.C.;
RT	"Genome sequence of Bacillus cereus and comparative analysis with Bacillus anthracis.";
RL	Nature 423:87-91(2003).
DR	EMBL; AE017014; AAP11950.1; -; Genomic DNA.
DR	GO; GO:0003954; F:NADH dehydrogenase activity; IEA.
DR	GO; GO:0016491; F:oxidoreductase activity; IEA.
KW	Complete proteome; Oxidoreductase.
SQL	SEQUENCE 522 AA; 61087 MW; 551097794FD59855 CRC64;
 Query Match 68.5%; Score 37; DB 2; Length 522; Best Local Similarity 66.7%; Pred.No. 3e+02; Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;	
Qy	1 VKLGYYFD 9 :
Db	127 IKSLYYFD 135 :
 RESULT 44	
Q5UQB6_MIMIV	
ID	Q5UQB6_MIMIV PRELIMINARY; PRT; 527 AA.
AC	Q5UQB6;
DT	01-FEB-2005 (TrEMBLrel. 29, Created)
DT	01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT	01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE	Hypothetical protein.
GN	ORFNames=MIMI_R225;
OS	Mimivirus.
OC	Viruses; dsDNA viruses, no RNA stage; Mimivirus.
OC	NCBI_TaxID=212035;
RN	[1]

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Db      126 KIGAYIDS 134

RESULT 46
Q9RKFO_STRCO PRELIMINARY; PRT; 798 AA.
AC Q9RKFO_0
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Putative hydrolase.
GN OrderedLocusNames=SC03487; ORFNames=SCB65.23;
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
[1]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=A3(2) / M145;
RX MEDLINE=21996410; PubMed=12000953; DOI=10.1038/417141a;
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kieser T., Larke L., Larke L., Murphy J.D., Oliver K., O'Neil S.,
RA Rabinowitsch E., Rajandream M.A., Rutherford K.M., Rutter S.,
RA Seger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J.R., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
PT Complete genome sequence of the model actinomycete Streptomyces
RT Coelicolor A3(2).";
RL Nature 417:141-147(2002).
DR EMBL; AL939116; CAB61811.1; -; Genomic DNA.
GO; GO:0016787; F:hydrolase activity; IEA.
KW Complete proteome; Hydrolase.
SQ SEQUENCE 798 AA; 88594 MW; 47244CE6F0FC555C CRC64;

Query Match 68.5%; Score 37; DB 2; Length 798;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GTTYFD 9
Db 157 GTTYFD 162

RESULT 47
O80692_ARATH PRELIMINARY; PRT; 814 AA.
AC O80692_0
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE F8K4.5 protein.
GN Name=F8K4.5;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosidia II; Brassicales; Brassicaceae; Arabidopsia.
OX NCBI_TaxID=3702;
[1]
RN NUCLEOTIDE SEQUENCE.
RC Vysotskaia V.S., Schwartz J.R., Toriumi M., Kwan A., Yu G., Oji O.,
RA Liu S., Li J., Araujo R., Au M., Brendel V., Buehler E., Conway A.B.,
RA Conway A.P., Dewar K., Feng J., Kim C., Kurtz D., Li Y., Palm C.J.,
RA Shin P., Sun H., Davis R.W., Ecker J.R., Federspiel N.A.,
RA Theologis A.;
RL Submitted (JUL-1998) to the EMBL/GenBank/DBSJ databases.
[2]
RN NUCLEOTIDE SEQUENCE.
RA Theologis;
RL Submitted (AUG-1998) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AC004392; AAC28517.1; -; Genomic_DNA.

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DR PIR; T02130; T02130.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR011424; Cl_3.
DR InterPro; IPR002219; DAG_PE-bind.
DR InterPro; IPR004146; DC1.
DR InterPro; IPR000834; Peptidase_M14.
DR InterPro; IPR001965; Znf_PHD.
DR Pfam; PF03107; Cl_2; 3.
DR Pfam; PF07649; Cl_3; 4.
DR SMART; SM00109; Cl; 2.
DR SMART; SM00249; PHD; 4.
DR PROSITE; PS00133; CARBOXYPEPT_ZN_2; UNKNOWN_1.
SQ SEQUENCE 814 AA; 93000 MW; EE8E79A280002C74 CRC64;

Query Match 68.5%; Score 37; DB 2; Length 814;
Best Local Similarity 70.0%; Pred. No. 4.6e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 VKLGYTFDS 10
Db 758 LKLGKVFDS 767

RESULT 48
Q8AB16_BACTN PRELIMINARY; PRT; 1101 AA.
AC Q8AB16_0
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative xanthan lyase XalB.
GN OrderedLocusNames=ST0296;
OS Bacteroides thetaiotaomicron.
OC Bacteria; Bacteroidetes; Bacteroidia (class); Bacteroidales;
OC Bacteroidaceae; Bacteroides.
OX NCBI_TaxID=818;
[1]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=VP1-3482 / ATCC 29148;
RX MEDLINE=22550858; PubMed=12663928; DOI=10.1126/science.1080029;
RA Xu J., Bjursell M.K., Himrod J., Deng S., Carmichael L.K.,
RA Chiang H.C., Hooper L.V., Gordon J.I.;
PT "A genomic view of the human-Bacteroides thetaiotaomicron symbiosis.";
RL Science 299:2074-2076(2003).
DR EMBL; AE016927; AA075403.1; -; Genomic_DNA.
DR GO; GO:0016829; F:lyase activity; IEA.
KW Complete proteome; Lyase.
SQ SEQUENCE 1101 AA; 127580 MW; 6B3BE78F465E6E09 CRC64;

Query Match 68.5%; Score 37; DB 2; Length 1101;
Best Local Similarity 66.7%; Pred. No. 6.1e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 KLGTYTFDS 10
Db 1067 QLGTYTFSA 1075

RESULT 49
Q67TF0_SYMTX PRELIMINARY; PRT; 1297 AA.
AC Q67TF0_0
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Putative middle wall protein.
GN OrderedLocusNames=STH58;
OS Symbiobacterium thermophilum.
OC Bacteria; Actinobacteria; Symbiobacterium.
OX NCBI_TaxID=2734;
[1]

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RP NUCLEOTIDE SEQUENCE.
RC STRAIN=IAM14863; DOI=10.1093/nar/gkh830;
RX PubMed=15383846;
RA Ueda K., Yamashita A., Ishikawa J., Shimada M., Watsuji T.,
RA Morimura K., Ikeda H., Hattori M., Beppu T.;
RT "Genome sequence of Symbiobacterium thermophilum, an uncultivable
RT bacterium that depends on microbial commensalism.";
RL Nucleic Acids Res. 32:4937-4944(2004).
DR EMBL; AP006840; BAD39043.1; -; Genomic_DNA.
DR GO; GO:0005618; C:cell wall; IEA.
DR InterPro; IPR001119; SLH.
DR Pfam; PF00395; SLH; 2.
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DE Glucansucrase (EC 2.4.1.5).
OS Lactobacillus reuteri.
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RA Kralj S., van Geel-Schutten G.H., Dondorff M.M.G., Kirsanova S.,
RA van der Maarel M.J.E.C., Dijkhuizen L.;
RT "Glucan synthesis in the genus Lactobacillus: isolation and
RT characterization of glucansucrase genes, enzymes and glucan products
RT from six different strains.";
RL Microbiology 150:3681-3690(2004).
DR EMBL; AY697431; AAU08004.1; -; Genomic DNA.
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DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
DR GO; GO:0016757; F:transferase activity, transferring glycosyl. .; IEA.
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DR GO; GO:0000272; P:polysaccharide catabolism; IEA.
DR InterPro; IPR002479; CW binding.
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GenCore version 5.1.7  
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OM protein - protein search, using sw model

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Scoring table: BLOSUM62  
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Searched: 572060 seqs, 82675679 residues

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Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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166	31	57.4	321	2	US-09-107-433-2895	Sequence 2895, Ap	239	31	57.4	660	1	US-08-337-483-8	Sequence 8, Appl
167	31	57.4	367	2	US-09-198-452A-562	Sequence 562, App	240	31	57.4	660	1	US-08-337-483-10	Sequence 10, Appl
168	31	57.4	367	2	US-09-438-185A-526	Sequence 526, App	241	31	57.4	660	1	US-08-478-373-8	Sequence 8, Appl
169	31	57.4	371	2	US-09-902-540-13676	Sequence 13676, A	242	31	57.4	660	1	US-08-478-373-10	Sequence 10, Appl
170	31	57.4	391	2	US-09-134-000C-6210	Sequence 6210, Ap	243	31	57.4	660	2	US-08-474-671-8	Sequence 8, Appl
171	31	57.4	393	2	US-09-107-532A-6010	Sequence 6010, Ap	244	31	57.4	660	2	US-08-474-671-10	Sequence 10, Appl
172	31	57.4	409	2	US-09-134-000C-5085	Sequence 5085, Ap	245	31	57.4	660	2	US-08-483-577A-8	Sequence 8, Appl
173	31	57.4	420	2	US-09-107-532A-4045	Sequence 4045, Ap	246	31	57.4	660	2	US-08-483-577A-10	Sequence 10, Appl

247	31	57.4	660	2	US-08-897-438-8	Sequence 8, Appl	Sequence 8, Appl	320	30	55.6	167	2	US-09-270-767-56620	Sequence 56620, A
248	31	57.4	660	2	US-08-897-438-10	Sequence 10, Appl	Sequence 10, Appl	321	30	55.6	170	2	US-09-134-001C-5447	Sequence 5447, Ap
249	31	57.4	660	2	US-08-637-654-8	Sequence 8, Appl	Sequence 8, Appl	322	30	55.6	175	2	US-09-830-230A-493	Sequence 493, App
250	31	57.4	660	2	US-08-637-654-10	Sequence 10, Appl	Sequence 10, Appl	323	30	55.6	179	2	US-10-104-047-2630	Sequence 2630, Ap
251	31	57.4	660	2	US-08-649-518-8	Sequence 8, Appl	Sequence 8, Appl	324	30	55.6	185	2	US-09-475-136A-15	Sequence 15, Appl
252	31	57.4	660	2	US-08-649-518-10	Sequence 10, Appl	Sequence 10, Appl	325	30	55.6	185	2	US-09-704-640-15	Sequence 15, Appl
253	31	57.4	683	2	US-09-620-412C-357	Sequence 357, App	Sequence 357, App	326	30	55.6	186	1	US-08-026-758-24	Sequence 24, Appl
254	31	57.4	683	2	US-09-598-419-357	Sequence 357, App	Sequence 357, App	327	30	55.6	187	2	US-09-902-540-14690	Sequence 14690, A
255	31	57.4	758	2	US-09-949-016-9816	Sequence 9816, Ap	Sequence 9816, Ap	328	30	55.6	209	2	US-09-134-000C-4198	Sequence 4198, Ap
256	31	57.4	782	2	US-09-585-858-29	Sequence 29, Appl	Sequence 29, Appl	329	30	55.6	211	2	US-09-270-767-46118	Sequence 46118, A
257	31	57.4	782	2	US-10-270-878-29	Sequence 29, Appl	Sequence 29, Appl	330	30	55.6	227	2	US-09-248-796A-17223	Sequence 17223, A
258	31	57.4	796	2	US-09-107-532A-7065	Sequence 7065, Ap	Sequence 7065, Ap	331	30	55.6	287	2	US-09-134-000C-4978	Sequence 4978, Ap
259	31	57.4	910	2	US-09-134-000C-4288	Sequence 4288, Ap	Sequence 4288, Ap	332	30	55.6	293	2	US-09-270-767-45409	Sequence 45409, A
260	31	57.4	948	2	US-09-556-877-194	Sequence 194, App	Sequence 194, App	333	30	55.6	299	2	US-08-944-483-66	Sequence 66, Appl
261	31	57.4	948	2	US-09-620-412C-194	Sequence 194, App	Sequence 194, App	334	30	55.6	308	2	US-09-248-796A-16365	Sequence 16365, A
262	31	57.4	948	2	US-09-598-419-194	Sequence 194, App	Sequence 194, App	335	30	55.6	310	2	US-09-563-269-16	Sequence 16, Appl
263	31	57.4	1014	2	US-10-101-464A-807	Sequence 807, App	Sequence 807, App	336	30	55.6	317	2	US-09-902-540-11936	Sequence 11936, A
264	31	57.4	1024	2	US-09-562-737-86	Sequence 86, Appl	Sequence 86, Appl	337	30	55.6	319	2	US-09-386-642-12	Sequence 12, Appl
265	31	57.4	1045	1	US-07-596-467-6	Sequence 6, Appl	Sequence 6, Appl	338	30	55.6	319	2	US-09-248-796A-17153	Sequence 17153, A
266	31	57.4	1045	1	US-07-934-374-6	Sequence 6, Appl	Sequence 6, Appl	339	30	55.6	328	2	US-09-386-642-11	Sequence 11, Appl
267	31	57.4	1045	1	US-07-783-861C-6	Sequence 6, Appl	Sequence 6, Appl	340	30	55.6	330	2	US-09-248-796A-18497	Sequence 18497, A
268	31	57.4	1074	2	US-09-071-033C-358	Sequence 358, App	Sequence 358, App	341	30	55.6	332	2	US-09-583-110-3964	Sequence 3964, Ap
269	31	57.4	1074	2	US-09-071-035-394	Sequence 394, App	Sequence 394, App	342	30	55.6	332	2	US-09-769-787-190	Sequence 190, App
270	31	57.4	1074	2	US-10-206-576-358	Sequence 358, App	Sequence 358, App	343	30	55.6	333	2	US-09-107-433-4789	Sequence 4789, Ap
271	31	57.4	1074	2	US-10-206-576-394	Sequence 394, App	Sequence 394, App	344	30	55.6	337	2	US-09-252-991A-23552	Sequence 23552, A
272	31	57.4	1095	2	US-09-107-532A-3855	Sequence 3855, Ap	Sequence 3855, Ap	345	30	55.6	342	2	US-10-037-417-133	Sequence 133, App
273	31	57.4	1096	2	US-09-134-000C-5764	Sequence 5764, Ap	Sequence 5764, Ap	346	30	55.6	342	2	US-10-037-417-134	Sequence 134, App
274	31	57.4	1150	2	US-09-002-285-74	Sequence 74, Appl	Sequence 74, Appl	347	30	55.6	343	2	US-09-109-204-32	Sequence 32, Appl
275	31	57.4	1150	2	US-09-589-477-74	Sequence 74, Appl	Sequence 74, Appl	348	30	55.6	343	2	US-09-490-032-32	Sequence 32, Appl
276	31	57.4	1150	2	US-10-099-285A-74	Sequence 74, Appl	Sequence 74, Appl	349	30	55.6	343	2	US-09-464-377-7	Sequence 7, Appl
277	31	57.4	1202	2	US-09-328-353-6889	Sequence 6889, Ap	Sequence 6889, Ap	350	30	55.6	343	2	US-09-948-094-2	Sequence 2, Appl
278	31	57.4	1222	1	US-08-682-517-15	Sequence 15, Appl	Sequence 15, Appl	351	30	55.6	343	2	US-10-037-417-130	Sequence 130, App
279	31	57.4	1252	1	US-08-682-517-9	Sequence 9, Appl	Sequence 9, Appl	352	30	55.6	344	2	US-09-252-991A-25863	Sequence 25863, A
280	31	57.4	1332	1	US-08-971-244-2	Sequence 2, Appl	Sequence 2, Appl	353	30	55.6	347	2	US-09-543-681A-6950	Sequence 6950, Ap
281	31	57.4	1332	1	US-09-286-891-2	Sequence 2, Appl	Sequence 2, Appl	354	30	55.6	349	2	US-09-543-681A-6158	Sequence 6158, Ap
282	31	57.4	1419	2	US-10-197-220-173	Sequence 173, App	Sequence 173, App	355	30	55.6	355	1	US-08-444-646-6	Sequence 6, Appl
283	31	57.4	1776	2	US-09-556-877-179	Sequence 179, App	Sequence 179, App	356	30	55.6	355	2	US-08-875-811-41	Sequence 41, Appl
284	31	57.4	1776	2	US-09-620-412C-179	Sequence 179, App	Sequence 179, App	357	30	55.6	355	2	US-08-875-811-49	Sequence 49, Appl
285	31	57.4	1776	2	US-09-598-419-179	Sequence 179, App	Sequence 179, App	358	30	55.6	355	2	US-08-875-811-64	Sequence 64, Appl
286	31	57.4	2057	2	US-09-499-203-2	Sequence 2, Appl	Sequence 2, Appl	359	30	55.6	355	2	US-09-992-807A-6	Sequence 6, Appl
287	31	57.4	2504	2	US-08-851-567B-12	Sequence 12, Appl	Sequence 12, Appl	360	30	55.6	358	2	US-08-875-811-45	Sequence 45, Appl
288	31	57.4	2504	2	US-09-817-514A-8	Sequence 8, Appl	Sequence 8, Appl	361	30	55.6	358	2	US-08-875-811-51	Sequence 51, Appl
289	31	57.4	3025	6	5223423-3	Patent No. 5223423	Patent No. 5223423	362	30	55.6	360	2	US-08-875-811-47	Sequence 47, Appl
290	30.5	56.5	219	2	US-09-107-433-4147	Sequence 4147, Ap	Sequence 4147, Ap	363	30	55.6	369	2	US-09-948-016-7375	Sequence 7375, Ap
291	30.5	56.5	239	2	US-09-485-885-12	Sequence 12, Appl	Sequence 12, Appl	364	30	55.6	379	2	US-08-875-811-43	Sequence 43, Appl
292	30.5	56.5	292	2	US-09-485-885-10	Sequence 10, Appl	Sequence 10, Appl	365	30	55.6	381	2	US-09-270-767-41595	Sequence 41595, A
293	30.5	56.5	318	2	US-09-583-110-3652	Sequence 3652, Ap	Sequence 3652, Ap	366	30	55.6	385	2	US-09-134-000C-4393	Sequence 4393, Ap
294	30.5	56.5	318	2	US-09-769-787-192	Sequence 192, App	Sequence 192, App	367	30	55.6	406	2	US-09-491-577-38	Sequence 38, Appl
295	30.5	56.5	390	2	US-09-485-885-14	Sequence 14, Appl	Sequence 14, Appl	368	30	55.6	419	2	US-09-540-236-3629	Sequence 3629, Ap
296	30.5	56.5	432	2	US-09-252-991A-31253	Sequence 31253, A	Sequence 31253, A	369	30	55.6	420	2	US-09-270-767-42980	Sequence 42980, A
297	30	55.6	13	1	US-08-787-547-10	Sequence 10, Appl	Sequence 10, Appl	370	30	55.6	457	1	US-08-278-635B-3	Sequence 3, Appl
298	30	55.6	14	2	US-09-424-712-30	Sequence 30, Appl	Sequence 30, Appl	371	30	55.6	457	2	US-08-471-961-3	Sequence 3, Appl
299	30	55.6	75	2	US-09-248-796A-25260	Sequence 25260, A	Sequence 25260, A	372	30	55.6	457	2	US-09-345-109C-3	Sequence 3, Appl
300	30	55.6	97	2	US-09-513-999C-6077	Sequence 6077, Ap	Sequence 6077, Ap	373	30	55.6	457	2	US-09-595-990A-2	Sequence 2, Appl
301	30	55.6	101	2	US-09-605-703B-2176	Sequence 2176, Ap	Sequence 2176, Ap	374	30	55.6	457	2	US-08-991-143A-2	Sequence 2, Appl
302	30	55.6	109	1	US-08-428-197-3	Sequence 3, Appl	Sequence 3, Appl	375	30	55.6	458	2	US-08-464-238B-3	Sequence 3, Appl
303	30	55.6	109	4	PC7-US933-10555-3	Sequence 3, Appl	Sequence 3, Appl	376	30	55.6	468	2	US-09-134-000C-4768	Sequence 4768, Ap
304	30	55.6	110	2	US-09-270-767-60913	Sequence 60913, A	Sequence 60913, A	377	30	55.6	481	2	US-09-215-694-17	Sequence 17, Appl
305	30	55.6	117	2	US-09-157-370-2	Sequence 2, Appl	Sequence 2, Appl	378	30	55.6	481	2	US-10-109-310-17	Sequence 17, Appl
306	30	55.6	117	2	US-09-583-110-3184	Sequence 3184, Ap	Sequence 3184, Ap	379	30	55.6	486	2	US-10-012-819-146	Sequence 146, App
307	30	55.6	118	2	US-09-107-433-2670	Sequence 2670, Ap	Sequence 2670, Ap	380	30	55.6	488	2	US-09-248-796A-18644	Sequence 18644, A
308	30	55.6	119	2	US-09-025-769B-26	Sequence 26, Appl	Sequence 26, Appl	381	30	55.6	493	2	US-09-252-991A-23214	Sequence 23214, A
309	30	55.6	119	2	US-09-490-070A-26	Sequence 26, Appl	Sequence 26, Appl	382	30	55.6	494	2	US-09-800-729-216	Sequence 216, App
310	30	55.6	119	2	US-09-490-153-26	Sequence 26, Appl	Sequence 26, Appl	383	30	55.6	500	2	US-09-489-039A-10995	Sequence 10995, A
311	30	55.6	119	2	US-09-490-324-26	Sequence 26, Appl	Sequence 26, Appl	384	30	55.6	503	2	US-09-583-110-4277	Sequence 4277, Ap
312	30	55.6	126	2	US-09-840-459-74	Sequence 74, Appl	Sequence 74, Appl	385	30	55.6	503	2	US-09-769-787-74	Sequence 74, Appl
313	30	55.6	126	2	US-09-497-625A-74	Sequence 74, Appl	Sequence 74, Appl	386	30	55.6	504	2	US-09-134-000C-5485	Sequence 5485, Ap
314	30	55.6	153	2	US-09-710-279-2826	Sequence 2826, Ap	Sequence 2826, Ap	387	30	55.6	530	2	US-09-800-729-112	Sequence 112, App
315	30	55.6	155	2	US-09-134-001C-3125	Sequence 3125, Ap	Sequence 3125, Ap	388	30	55.6	531	2	US-09-902-540-13847	Sequence 13847, A
316	30	55.6	156	2	US-09-487-792-20	Sequence 20, Appl	Sequence 20, Appl	389	30	55.6	536	2	US-09-107-433-2945	Sequence 2945, Ap
317	30	55.6	156	2	US-09-908-594-20	Sequence 20, Appl	Sequence 20, Appl	390	30	55.6	538	2	US-09-328-352-6530	Sequence 6530, Ap
318	30	55.6	161	2	US-09-830-230A-494	Sequence 494, Appl	Sequence 494, Appl	391	30	55.6	542	2	US-09-543-681A-6864	Sequence 6864, Ap
319	30	55.6	167	2	US-09-270-767-41404	Sequence 41404, A	Sequence 41404, A	392	30	55.6	586	2	US-09-489-039A-10912	Sequence 10912, A

393	30	55.6	614	2	US-09-328-352-4256	Sequence 4256, Ap	466	29	53.7	201	2	US-10-115-701A-5	Sequence 5, Appli
394	30	55.6	614	2	US-09-328-352-6185	Sequence 6185, Ap	467	29	53.7	201	2	US-09-940-308A-5	Sequence 5, Appli
395	30	55.6	626	2	US-09-489-039A-9106	Sequence 9106, Ap	468	29	53.7	201	2	US-09-940-308A-5	Sequence 5, Appli
396	30	55.6	662	2	US-09-902-540-11249	Sequence 11249, A	469	29	53.7	201	4	PCT-US96-00596-8	Sequence 8, Appli
397	30	55.6	692	2	US-09-252-991A-27997	Sequence 27997, A	470	29	53.7	203	2	US-09-248-796A-18629	Sequence 18629, A
398	30	55.6	708	2	US-09-252-991A-25303	Sequence 25303, A	471	29	53.7	203	2	US-09-902-540-15197	Sequence 15197, A
399	30	55.6	741	1	US-08-849-480A-9	Sequence 9, Appli	472	29	53.7	205	2	US-09-248-796A-15989	Sequence 15989, A
400	30	55.6	778	2	US-09-134-000C-6443	Sequence 6443, Ap	473	29	53.7	207	2	US-08-657-749D-29	Sequence 29, Appli
401	30	55.6	817	2	US-09-543-681A-4637	Sequence 4637, Ap	474	29	53.7	213	2	US-09-208-718-5	Sequence 5, Appli
402	30	55.6	936	4	PCT-US94-05905-22	Sequence 22, Appli	475	29	53.7	214	2	US-09-208-718-1	Sequence 1, Appli
403	30	55.6	939	4	PCT-US94-05905-20	Sequence 20, Appli	476	29	53.7	214	2	US-08-545-573A-41	Sequence 41, Appli
404	30	55.6	942	2	US-09-543-681A-6154	Sequence 6154, Ap	477	29	53.7	214	2	US-09-252-991A-21440	Sequence 21440, A
405	30	55.6	974	2	US-09-710-092-2	Sequence 2, Appli	478	29	53.7	214	2	US-09-270-767-32127	Sequence 32127, A
406	30	55.6	972	2	US-10-231-354-2	Sequence 2, Appli	479	29	53.7	214	2	US-09-270-767-47344	Sequence 47344, A
407	30	55.6	1056	2	US-09-710-092-6	Sequence 6, Appli	480	29	53.7	214	2	US-09-949-016-7004	Sequence 7004, Ap
408	30	55.6	1056	2	US-10-231-354-6	Sequence 6, Appli	481	29	53.7	215	2	US-09-134-000C-3957	Sequence 3957, Ap
409	30	55.6	1270	2	US-09-710-092-10	Sequence 10, Appli	482	29	53.7	224	2	US-09-248-796A-14204	Sequence 14204, A
410	30	55.6	1270	2	US-10-231-354-10	Sequence 10, Appli	483	29	53.7	228	2	US-09-270-767-59471	Sequence 59471, A
411	30	55.6	1381	2	US-09-540-245A-16	Sequence 16, Appli	484	29	53.7	231	2	US-09-248-796A-15355	Sequence 15355, A
412	30	55.6	1381	2	US-10-289-776-16	Sequence 16, Appli	485	29	53.7	235	2	US-09-248-796A-17542	Sequence 17542, A
413	30	55.6	1426	2	US-09-710-092-14	Sequence 14, Appli	486	29	53.7	237	1	US-08-224-591-16	Sequence 16, Appli
414	30	55.6	1426	2	US-10-231-354-14	Sequence 14, Appli	487	29	53.7	237	1	US-08-926-789-16	Sequence 16, Appli
415	30	55.6	1740	2	US-09-377-285B-40	Sequence 40, Appli	488	29	53.7	237	2	US-09-710-279-162	Sequence 162, App
416	30	55.6	1740	2	US-10-192-381-40	Sequence 40, Appli	489	29	53.7	241	1	US-08-224-591-18	Sequence 18, Appli
417	30	55.6	1751	2	US-09-136-574A-44	Sequence 44, Appli	490	29	53.7	241	1	US-08-926-789-18	Sequence 18, Appli
418	30	55.6	1783	2	US-09-362-336A-2	Sequence 2, Appli	491	29	53.7	243	2	US-09-328-352-7321	Sequence 7321, Ap
419	30	55.6	1804	2	US-09-362-336A-4	Sequence 4, Appli	492	29	53.7	245	2	US-09-069-821-5	Sequence 5, Appli
420	30	55.6	3165	1	US-08-459-146-3	Sequence 3, Appli	493	29	53.7	245	2	US-09-956-086-5	Sequence 5, Appli
421	30	55.6	3165	1	US-08-459-065-3	Sequence 3, Appli	494	29	53.7	245	2	US-09-956-086-5	Sequence 5, Appli
422	30	55.6	4968	2	US-09-424-783-5	Sequence 5, Appli	495	29	53.7	245	2	US-09-956-086-5	Sequence 5, Appli
423	29	53.7	17	2	US-09-157-210-13	Sequence 13, Appli	496	29	53.7	245	2	US-09-956-086-5	Sequence 5, Appli
424	29	53.7	50	2	US-10-101-464A-590	Sequence 590, App	497	29	53.7	249	2	US-09-543-681A-8153	Sequence 8153, Ap
425	29	53.7	56	2	US-09-270-767-60348	Sequence 60348, A	498	29	53.7	255	2	US-09-949-016-10004	Sequence 10004, A
426	29	53.7	86	2	US-09-910-430-8	Sequence 8, Appli	499	29	53.7	257	2	US-09-198-452A-644	Sequence 644, App
427	29	53.7	109	2	US-09-248-796A-21837	Sequence 21837, A	500	29	53.7	259	2	US-09-134-000C-6773	Sequence 6773, Ap
428	29	53.7	111	2	US-08-858-207A-375	Sequence 375, App	501	29	53.7	262	2	US-09-438-185A-606	Sequence 606, App
429	29	53.7	117	2	US-08-752-693A-3	Sequence 3, Appli	502	29	53.7	265	2	US-09-420-592A-5	Sequence 5, Appli
430	29	53.7	117	2	US-08-752-693A-4	Sequence 4, Appli	503	29	53.7	265	2	US-09-985-440-5	Sequence 5, Appli
431	29	53.7	118	2	US-08-545-573A-17	Sequence 17, Appli	504	29	53.7	265	2	US-09-983-580-5	Sequence 5, Appli
432	29	53.7	118	2	US-08-545-573A-19	Sequence 19, Appli	505	29	53.7	279	2	US-09-248-796A-18859	Sequence 18859, A
433	29	53.7	123	1	US-08-199-911-4	Sequence 4, Appli	506	29	53.7	282	2	US-09-583-110-3134	Sequence 3134, Ap
434	29	53.7	124	2	US-09-270-767-62168	Sequence 62168, A	507	29	53.7	282	2	US-09-107-433-3050	Sequence 3050, Ap
435	29	53.7	129	1	US-10-000-489-74	Sequence 74, Appli	508	29	53.7	293	2	US-09-252-991A-22441	Sequence 22441, A
436	29	53.7	136	1	US-08-253-877C-57	Sequence 57, Appli	509	29	53.7	297	2	US-09-270-767-46574	Sequence 46574, A
437	29	53.7	136	1	US-08-452-164A-57	Sequence 57, Appli	510	29	53.7	324	1	US-08-793-410-30	Sequence 30, Appli
438	29	53.7	136	2	US-08-976-183A-31	Sequence 31, Appli	511	29	53.7	324	2	US-08-505-012-12	Sequence 12, Appli
439	29	53.7	136	2	US-08-976-183A-32	Sequence 32, Appli	512	29	53.7	324	4	PCT-US96-00996-11	Sequence 11, Appli
440	29	53.7	136	2	US-08-976-183A-33	Sequence 33, Appli	513	29	53.7	325	1	US-08-377-309-8	Sequence 8, Appli
441	29	53.7	136	2	US-08-976-183A-34	Sequence 34, Appli	514	29	53.7	325	2	US-09-186-723-8	Sequence 8, Appli
442	29	53.7	150	2	US-08-976-183A-55	Sequence 55, Appli	515	29	53.7	325	2	US-08-505-012-11	Sequence 11, Appli
443	29	53.7	152	2	US-09-605-703B-1678	Sequence 1678, Ap	516	29	53.7	325	2	US-09-186-949A-9	Sequence 9, Appli
444	29	53.7	155	2	US-09-857-896A-24	Sequence 24, Appli	517	29	53.7	325	2	US-08-758-757-8	Sequence 8, Appli
445	29	53.7	162	2	US-09-583-110-3482	Sequence 3482, Ap	518	29	53.7	325	2	US-08-187-978-8	Sequence 8, Appli
446	29	53.7	163	2	US-09-949-016-7503	Sequence 7503, Ap	519	29	53.7	325	2	US-10-115-701A-8	Sequence 8, Appli
447	29	53.7	169	2	US-09-583-110-4656	Sequence 4656, Ap	520	29	53.7	325	2	US-09-940-308A-8	Sequence 8, Appli
448	29	53.7	170	2	US-09-107-433-3057	Sequence 3057, Ap	521	29	53.7	325	2	US-09-940-308A-8	Sequence 8, Appli
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450	29	53.7	174	2	US-09-107-433-3442	Sequence 3442, Ap	523	29	53.7	328	1	US-08-793-410-7	Sequence 7, Appli
451	29	53.7	180	2	US-09-612-0338-10	Sequence 10, Appli	524	29	53.7	339	2	US-09-463-962-2	Sequence 2, Appli
452	29	53.7	185	2	US-09-583-110-5249	Sequence 5249, Ap	525	29	53.7	339	2	US-09-252-991A-26841	Sequence 26841, A
453	29	53.7	190	2	US-09-107-433-4319	Sequence 4319, Ap	526	29	53.7	345	2	US-09-248-796A-18454	Sequence 18454, A
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457	29	53.7	199	2	US-09-066-330-9	Sequence 9, Appli	530	29	53.7	380	2	US-09-710-279-1402	Sequence 1402, Ap
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459	29	53.7	200	2	US-08-545-573A-23	Sequence 23, Appli	532	29	53.7	392	2	US-09-990-444-205	Sequence 205, App
460	29	53.7	201	1	US-08-377-309-5	Sequence 5, Appli	533	29	53.7	392	2	US-09-997-333-205	Sequence 205, App
461	29	53.7	201	2	US-09-186-723-5	Sequence 5, Appli	534	29	53.7	393	1	US-09-992-598-205	Sequence 205, App
462	29	53.7	201	2	US-08-505-012-8	Sequence 8, Appli	535	29	53.7	393	2	US-08-377-309-7	Sequence 7, Appli
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465	29	53.7	201	2	US-09-187-978-5	Sequence 5, Appli	538	29	53.7	393	2	US-09-186-949A-8	Sequence 8, Appli



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541	29	53.7	393	2	US-09-187-978-7	Sequence 7, Appl1	614	29	53.7	702	2	US-10-197-220-170	Sequence 170, App
542	29	53.7	393	2	US-10-115-701A-7	Sequence 7, Appl1	615	29	53.7	704	2	US-09-543-681A-1274	Sequence 727A, App
543	29	53.7	393	2	US-09-940-308A-7	Sequence 7, Appl1	616	29	53.7	707	2	US-10-104-047-3162	Sequence 3162, Ap
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546	29	53.7	394	2	US-09-134-000C-6314	Sequence 6314, Ap	619	29	53.7	746	2	US-09-589-892B-2	Sequence 2, Appl1
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563	29	53.7	451	2	US-09-543-681A-7311	Sequence 7311, Ap	636	29	53.7	968	2	US-09-688-188B-155	Sequence 155, App
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565	29	53.7	464	2	US-09-134-001C-3488	Sequence 3488, Ap	638	29	53.7	968	2	US-09-291-417D-155	Sequence 155, App
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576	29	53.7	554	2	US-09-321-276-4	Sequence 4, Appl1	649	29	53.7	2972	2	US-08-488-446-387	Sequence 387, App
577	29	53.7	554	2	US-08-916-481-2	Sequence 2, Appl1	650	29	53.7	2972	2	US-08-467-344A-387	Sequence 387, App
578	29	53.7	557	2	US-09-902-540-14087	Sequence 14087, A	651	29	53.7	2972	2	US-08-424-550B-387	Sequence 387, App
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586	29	53.7	590	2	US-09-186-723-2	Sequence 2, Appl1	659	28	51.9	12	2	US-09-795-798-12	Sequence 12, Appl1
587	29	53.7	590	2	US-08-505-012-5	Sequence 5, Appl1	660	28	51.9	13	1	US-08-054-860-15	Sequence 15, Appl1
588	29	53.7	590	2	US-09-186-949A-3	Sequence 3, Appl1	661	28	51.9	13	2	US-08-442-378-15	Sequence 15, Appl1
589	29	53.7	590	2	US-08-758-757-2	Sequence 2, Appl1	662	28	51.9	16	2	US-09-763-848-1	Sequence 1, Appl1
590	29	53.7	590	2	US-09-187-978-2	Sequence 2, Appl1	663	28	51.9	36	1	US-08-487-890A-66	Sequence 66, Appl1
591	29	53.7	590	2	US-10-115-701A-2	Sequence 2, Appl1	664	28	51.9	36	1	US-08-478-435-66	Sequence 66, Appl1
592	29	53.7	590	2	US-09-940-308A-2	Sequence 2, Appl1	665	28	51.9	36	1	US-08-337-483-66	Sequence 66, Appl1
593	29	53.7	590	2	US-09-940-308A-2	Sequence 2, Appl1	666	28	51.9	36	1	US-08-478-373-66	Sequence 66, Appl1
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597	29	53.7	606	2	US-08-070-778-3	Sequence 3, Appl1	670	28	51.9	36	2	US-08-637-654-66	Sequence 66, Appl1
598	29	53.7	608	2	US-08-976-063E-40	Sequence 40, Appl1	671	28	51.9	36	2	US-08-649-518-66	Sequence 66, Appl1
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604	29	53.7	611	2	US-09-543-681A-5447	Sequence 5447, Ap	677	28	51.9	61	2	US-09-234-873A-138	Sequence 138, App
605	29	53.7	612	2	US-09-949-016-11201	Sequence 11201, A	678	28	51.9	61	2	US-10-076-604-138	Sequence 138, App
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686	28	51.9	65	2	US-09-248-796A-25101	Sequence 25101, A	759	28	51.9	251	2	US-09-992-598-511	Sequence 511, App
687	28	51.9	87	2	US-09-344-624-15	Sequence 15, Appl	760	28	51.9	252	2	US-09-489-039A-7755	Sequence 7755, Ap
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690	28	51.9	102	2	US-09-270-767-58325	Sequence 58325, A	763	28	51.9	260	2	US-08-742-693-31	Sequence 31, Appl
691	28	51.9	107	2	US-09-344-624-7	Sequence 7, Appl	764	28	51.9	260	2	US-09-949-016-10927	Sequence 32, Appl
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698	28	51.9	116	2	US-09-026-985-50	Sequence 50, Appl	771	28	51.9	291	2	US-09-489-039A-12107	Sequence 4, Appl
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702	28	51.9	118	2	US-10-012-819-128	Sequence 128, App	775	28	51.9	299	2	US-09-902-540-9859	Sequence 9859, Ap
703	28	51.9	119	4	PCT-US94-07659-6	Sequence 6, Appl	776	28	51.9	306	2	US-09-820-924-4	Sequence 4, Appl
704	28	51.9	120	2	US-09-270-767-32065	Sequence 32065, A	777	28	51.9	308	2	US-10-369-626-4	Sequence 4, Appl
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716	28	51.9	131	2	US-09-107-532A-5741	Sequence 5741, Ap	789	28	51.9	349	2	US-09-270-767-36315	Sequence 36315, A
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719	28	51.9	134	2	US-09-621-976-4031	Sequence 4031, Ap	792	28	51.9	358	2	US-09-328-352-7543	Sequence 7543, Ap
720	28	51.9	136	2	US-09-833-017B-25	Sequence 25, Appl	793	28	51.9	359	2	US-09-248-796A-18247	Sequence 18247, A
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722	28	51.9	138	2	US-09-328-352-4588	Sequence 4588, Ap	795	28	51.9	362	2	US-09-820-924-2	Sequence 2, Appl
723	28	51.9	140	2	US-09-583-110-2720	Sequence 2720, Ap	796	28	51.9	363	2	US-10-369-626-2	Sequence 2, Appl
724	28	51.9	143	2	US-09-068-628-7	Sequence 7, Appl	797	28	51.9	376	2	US-09-499-016-6868	Sequence 6868, Ap
725	28	51.9	150	2	US-09-582-337-14	Sequence 14, Appl	798	28	51.9	376	2	US-09-328-352-5219	Sequence 5219, Ap
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## ALIGNMENTS

RESULT 1  
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 ; Sequence 8, Application US/09225322B  
 ; Patent No. 6437098  
 ; GENERAL INFORMATION:  
 ; APPLICANT: SHITARA, KENYA  
 ; APPLICANT: HANNAI, NOBUO  
 ; APPLICANT: HASEGAWA, MAMORU  
 ; APPLICANT: MIYAJI, HIROMASA  
 ; APPLICANT: KUWANA, YOSHIIASA  
 ; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY  
 ; FILE REFERENCE: 249-101

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Query Match      100.0%; Score 54; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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## RESULT 2

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; Patent No. 6437098
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUWANA, YOSHITISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/09/225,322B
; CURRENT FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: US 08/454,680
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
; PRIOR APPLICATION NUMBER: US07/947,674
; PRIOR FILING DATE: 1992-09-17
; PRIOR APPLICATION NUMBER: JP 3-238375
; PRIOR FILING DATE: 1991-09-18
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; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUWANA, YOSHIIISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
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; SOFTWARE: Patentin ver. 2.0
; SEQ ID NO 8
; LENGTH: 130
; TYPE: PRT

```

```

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: cDNA KM-641
US-09-764-304-8

Query Match      100.0%; Score 54; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VKLGTYFYDS 10
Db 109 VKLGTYFYDS 118

RESULT 4
US-09-764-304-18
; Sequence 18, Application US/09764304
; Patent No. 6495666
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KIWANA, YOSHIHISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/09/764,304
; CURRENT FILING DATE: 2001-01-19
; EARLIER APPLICATION NUMBER: 09/225,322
; EARLIER FILING DATE: 1999-01-05
; EARLIER APPLICATION NUMBER: US 08/454,680
; EARLIER FILING DATE: 1995-05-31
; EARLIER APPLICATION NUMBER: US 08/408,133
; EARLIER FILING DATE: 1995-03-21
; EARLIER APPLICATION NUMBER: US 08/292,178
; EARLIER FILING DATE: 1994-08-17
; EARLIER APPLICATION NUMBER: US07/947,674
; EARLIER FILING DATE: 1992-09-17
; EARLIER APPLICATION NUMBER: JP 3-238375
; EARLIER FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: cDNA KM-641
US-09-764-304-18

Query Match      100.0%; Score 54; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VKLGTYFYDS 10
Db 109 VKLGTYFYDS 118

RESULT 5
US-08-211-202-135
; Sequence 135, Application US/08211202
; Patent No. 5565332
; GENERAL INFORMATION:
; APPLICANT: HOOGENBOOM, Hendricus Renerus Jacobus Matteus
; APPLICANT: BAIER, Michael
; APPLICANT: JESPEERS, Laurent Stephane Anne Therese
; APPLICANT: WINTER, Gregory Paul
; TITLE OF INVENTION: Production of chimeric antibodies - a
; TITLE OF INVENTION: combinatorial approach
; NUMBER OF SEQUENCES: 144
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David W. Clough, Marshall O'Toole Gerstein Murray &

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; ADDRESSEE: Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/211.202
; FILING DATE: 23-SEP-1992
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9120252.3
; FILING DATE: 23-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9120377.8
; FILING DATE: 25-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9206318.9
; FILING DATE: 24-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9206372.6
; FILING DATE: 24-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB92/00883
; FILING DATE: 15-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: David W. Clough
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 28111/31960
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 135:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 120 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-211-202-135

Query Match      77.8%; Score 42; DB 1; Length 120;
Best Local Similarity 87.5%; Pred. No. 2.1;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LGTYFYDS 10
Db 101 LGTYFYDS 108

RESULT 6
US-09-604-957-3
; Sequence 3, Application US/09604957
; Patent No. 6486314
; GENERAL INFORMATION:
; APPLICANT: VAN GEEL-SCHUTTEN, GERRITDINA HENDRIKA
; APPLICANT: DIJKHUIZEN, LUBBERT
; APPLICANT: RAHAOUI, HAKIM
; APPLICANT: LEER, ROBERT-JAN
; TITLE OF INVENTION: NOVEL GLUCOSYLTRANSFERASE AND NOVEL GLUCAN
; FILE REFERENCE: BO 4388
; CURRENT APPLICATION NUMBER: US/09/604,957
; CURRENT FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 00201871.1
; PRIOR FILING DATE: 2000-05-25
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3

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; LENGTH: 1278  
; TYPE: PRT  
; ORGANISM: Lactobacillus reuteri  
US-09-604-957-3

Query Match 70.4%; Score 38; DB 2; Length 1278;  
Best Local Similarity 85.7%; Pred. No. 1.4e+02;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 GTYYFDS 10  
DB 1221 GTYYFDN 1227

RESULT 7  
US-09-995-749A-2  
; Sequence 2, Application US/09995749A  
; Patent No. 6867026  
; GENERAL INFORMATION:  
; APPLICANT: VAN GEEL-SCHUTTEN, GERRITDINA HENDRIKA  
; APPLICANT: DIJKHUIZEN, LUBBERT  
; APPLICANT: RAHAOUI, HAKIM  
; APPLICANT: LEER, ROBERT-JAN  
; TITLE OF INVENTION: NOVEL GLUCOSYLTRANSFERASES  
; FILE REFERENCE: BO43388-CIP  
; CURRENT APPLICATION NUMBER: US/09/995,749A  
; CURRENT FILING DATE: 2001-11-29  
; PRIOR APPLICATION NUMBER: 09/604,957  
; PRIOR FILING DATE: 2000-06-28  
; PRIOR APPLICATION NUMBER: EPO 00201871.1  
; PRIOR FILING DATE: 2000-05-25  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 1781  
; TYPE: PRT  
; ORGANISM: Lactobacillus reuteri  
US-09-995-749A-2

Query Match 70.4%; Score 38; DB 2; Length 1781;  
Best Local Similarity 85.7%; Pred. No. 1.9e+02;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 GTYYFDS 10  
DB 1724 GTYYFDN 1730

RESULT 8  
US-09-543-681A-6788  
; Sequence 6788, Application US/09543681A  
; Patent No. 6605709  
; GENERAL INFORMATION:  
; APPLICANT: GARY BRETON  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS  
; FILE REFERENCE: 2709.1002-001  
; CURRENT APPLICATION NUMBER: US/09/543,681A  
; CURRENT FILING DATE: 2000-04-05  
; PRIOR APPLICATION NUMBER: US 60/128,706  
; PRIOR FILING DATE: 1999-04-09  
; NUMBER OF SEQ ID NOS: 8344  
; SEQ ID NO 6788  
; LENGTH: 94  
; TYPE: PRT  
; ORGANISM: Proteus mirabilis  
US-09-543-681A-6788

Query Match 68.5%; Score 37; DB 2; Length 94;  
Best Local Similarity 75.0%; Pred. No. 13;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 LGTYFDS 10

DB 21 LGTYYS 28

RESULT 9  
US-09-107-532A-6082  
; Sequence 6082, Application US/09107532A  
; Patent No. 6583275  
; GENERAL INFORMATION:  
; APPLICANT: Lynn A Doucette-Stamm and David Bush  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS  
; NUMBER OF SEQUENCES: 7310  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION  
; STREET: 100 Beaver Street  
; CITY: Waltham  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02354  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: CD-ROM ISO9660  
; COMPUTER: PC  
; OPERATING SYSTEM: <Unknown>  
; SOFTWARE: ASCII  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/107,532A  
; FILING DATE: 30-Jun-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/085,598  
; FILING DATE: 14 May 1998  
; APPLICATION NUMBER: 60/051571  
; FILING DATE: July 2, 1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ariniello, Pamela Deneke  
; REGISTRATION NUMBER: 40,489  
; REFERENCE/DOCKET NUMBER: GTC-012  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (781)893-5007  
; TELEFAX: (781)893-8277  
; INFORMATION FOR SEQ ID NO: 6082:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 137 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: YES  
; ORIGINAL SOURCE:  
; ORGANISM: Enterococcus faecium  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (B) LOCATION 1...137  
; SEQUENCE DESCRIPTION: SEQ ID NO: 6082:  
US-09-107-532A-6082

Query Match 68.5%; Score 37; DB 2; Length 137;  
Best Local Similarity 75.0%; Pred. No. 20;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 KLGTYFDD 9  
DB 124 KIGTYVHD 131

RESULT 10  
US-09-134-001C-4951  
; Sequence 4951, Application US/09134001C  
; Patent No. 6380370  
; GENERAL INFORMATION:  
; APPLICANT: Lynn Doucette-Stamm et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: GTC-007

```
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 4951
; LENGTH: 388
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-4951

Query Match      68.5%; Score 37; DB 2; Length 388;
Best Local Similarity 66.7%; Pred. No. 59;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      2 KLGTYTFDS 10
      :|||||
Db      250 RVGTYFGS 258

RESULT 11
US-09-489-039A-11090
; Sequence 11090, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breston et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 11090
; LENGTH: 685
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-11090

Query Match      68.5%; Score 37; DB 2; Length 685;
Best Local Similarity 85.7%; Pred. No. 11e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      4 GTTYFDS 10
      :|||||
Db      577 GTTYFDS 583

RESULT 12
US-08-379-057-30
; Sequence 30, Application US/08379057
; Patent No. 5876950
; GENERAL INFORMATION:
; APPLICANT: Siadak, Anthony W.
; APPLICANT: Hollenbaugh, Diane L.
; APPLICANT: Gilliland, Lisa K.
; APPLICANT: Gordon, Marcia L.
; APPLICANT: Bajorath, Jurgen
; APPLICANT: Aruffo, Alejandro A.
; TITLE OF INVENTION: Monoclonal Antibodies Specific For
; TITLE OF INVENTION: Different Epitopes of Human gp39 and Methods for Their Use
; TITLE OF INVENTION: In Diagnosis and Therapy
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bristol-Myers Squibb Company
; STREET: 3005 First Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98121
```

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/379,057
; FILING DATE: 26-JAN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Poor, Brian W.
; REGISTRATION NUMBER: 32,928
; REFERENCE/DOCKET NUMBER: ON0133-
; TELEPHONE: (206) 727-3670
; TELEFAX: (206) 727-3601
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 118 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-379-057-30

Query Match      64.8%; Score 35; DB 1; Length 118;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 TYTFDS 10
      :|||||
Db      57 TYTFDS 62

RESULT 13
US-09-710-279-1932
; Sequence 1932, Application US/09710279
; Patent No. 6703492
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/09/710,279
; CURRENT FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1932
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-09-710-279-1932

Query Match      64.8%; Score 35; DB 2; Length 226;
Best Local Similarity 75.0%; Pred. No. 79;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      2 KLGTYTFD 9
      :|||||
Db      211 KIGTYCFD 218

RESULT 14
US-09-134-001C-4963
; Sequence 4963, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
```

; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: GTC-007  
; CURRENT APPLICATION NUMBER: US/09/134,001C  
; CURRENT FILING DATE: 1998-08-13  
; PRIOR APPLICATION NUMBER: US 60/064,964  
; PRIOR FILING DATE: 1997-11-08  
; PRIOR APPLICATION NUMBER: US 60/055,779  
; PRIOR FILING DATE: 1997-08-14  
; NUMBER OF SEQ ID NOS: 5674  
; SEQ ID NO 4963  
; LENGTH: 288  
; TYPE: PRT  
; ORGANISM: Staphylococcus epidermidis  
US-09-134-001C-4963

Query Match 64.8%; Score 35; DB 2; Length 288;  
Best Local Similarity 75.0%; Pred. No. 1.8e+02;  
Matches 6; Conservative 1; Mismatches 0; Indels 1; Gaps 0;

QY 2 KLGTYTFFD 9  
|:|||||  
Db 273 KIGTYCFD 280

RESULT 15  
US-09-491-577-96  
; Sequence 96, Application US/09491577  
; Patent No. 6610511  
; GENERAL INFORMATION:  
; APPLICANT: Yale University  
; APPLICANT: Carlson, John R.  
; APPLICANT: Kim, Hunhyong  
; APPLICANT: Clyne, Peter J.  
; APPLICANT: Warr, Coral G.  
; TITLE OF INVENTION: No. 6610511el Family of Odorant Receptor Genes in Drosophila  
; FILE REFERENCE: 44574-5061-US  
; CURRENT APPLICATION NUMBER: US/09/491,577  
; CURRENT FILING DATE: 2000-01-25  
; EARLIER APPLICATION NUMBER: US 60/117,132  
; EARLIER FILING DATE: 1999-01-25  
; NUMBER OF SEQ ID NOS: 112  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 96  
; LENGTH: 349  
; TYPE: PRT  
; ORGANISM: Drosophila melanogaster  
US-09-491-577-96

Query Match 64.8%; Score 35; DB 2; Length 349;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LGTYTFF 8  
|||||  
Db 61 LGTYTFF 66

RESULT 16  
US-09-902-540-12035  
; Sequence 12035, Application US/09902540  
; Patent No. 6833447  
; GENERAL INFORMATION:  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Wiegand, Roger C.  
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof  
; FILE REFERENCE: 38-10(115849)B  
; CURRENT APPLICATION NUMBER: US/09/902,540  
; CURRENT FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: 60/217,883  
; PRIOR FILING DATE: 2000-07-10  
; NUMBER OF SEQ ID NOS: 16825

; SEQ ID NO 12035  
; LENGTH: 1110  
; TYPE: PRT  
; ORGANISM: Myxococcus xanthus  
US-09-902-540-12035

Query Match 64.8%; Score 35; DB 2; Length 1110;  
Best Local Similarity 50.0%; Pred. No. 4.2e+02;  
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 VKLGTYTFFDS 10  
|:|||||  
Db 230 VRIGEYWFDN 239

RESULT 17  
US-08-525-539A-41  
; Sequence 41, Application US/08525539A  
; Patent No. 6309636  
; GENERAL INFORMATION:  
; APPLICANT: DO COUTO, FERNANDO J.R.  
; APPLICANT: CERIANI, ROBERTO L.  
; APPLICANT: PETERSON, JERRY A.  
; TITLE OF INVENTION: RECOMBINANT PEPTIDES DERIVED FROM THE  
; TITLE OF INVENTION: MC3 ANTI-BA46 ANTIBODY, METHODS OF USE THEREOF, AND  
; NUMBER OF SEQUENCES: 81  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 755 Page Mill Road  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/525,539A  
; FILING DATE: 14-SEP-1995  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: DYLAN, TYLER  
; REGISTRATION NUMBER: 37,612  
; REFERENCE/DOCKET NUMBER: 27633-20001.21  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 813-5600  
; TELEFAX: (415) 494-0792  
; TELEX: 706141  
; INFORMATION FOR SEQ ID NO: 41:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 19 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-525-539A-41

Query Match 63.0%; Score 34; DB 2; Length 19;  
Best Local Similarity 75.0%; Pred. No. 8.8;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 LGTYTFFDS 10  
|:|||||  
Db 8 LAVTYFDS 15

RESULT 18  
US-07-942-245-22  
; Sequence 22, Application US/07942245  
; Patent No. 5639641  
; GENERAL INFORMATION:



```

; APPLICANT: PEDERSEN, Jan T.
; APPLICANT: SEARLE, Stephen M.J.
; APPLICANT: REES, Anthony R.
; APPLICANT: ROGUSKA, Michael A.
; APPLICANT: GUILD, Braydon C.
; TITLE OF INVENTION: SURFACE RESIDUE VENERING OF RODENT
; TITLE OF INVENTION: ANTIBODIES
; NUMBER OF SEQUENCES: 522
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sughrue, Mion, Zinn, Macpeak & Seas
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: United States
; ZIP: 20037-3202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: HP 9000/700 Workstation
; OPERATING SYSTEM: UNIX
; SOFTWARE: In house
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/942,245
; FILING DATE: 09-SEP-1992
; CLASSIFICATION: 530
; TELEPHONE: (202) 293-7060
; TELEFAX: (202) 293-7860
; TELEX: 6491103
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 115 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-07-942-245-22

Query Match 63.0%; Score 34; DB 1; Length 115;
Best Local Similarity 75.0%; Pred. No. 59;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 LGTYFDS 10
Db 106 LAVYFDS 113

RESULT 19
US-09-232-290-51
; Sequence 51, Application US/09232290A
; Patent No. 6815540
; GENERAL INFORMATION:
; APPLICANT: PLUCKTHUN, ANDREAS
; APPLICANT: NIEBA, LARS
; APPLICANT: HONEGER, ANNEMARIE
; TITLE OF INVENTION: IMMUNOGLOBULIN SUPER FAMILY DOMAINS AND FRAGMENTS WITH
; TITLE OF INVENTION: INCREASED SOLUBILITY
; FILE REFERENCE: MOREHO/7
; CURRENT APPLICATION NUMBER: US/09/232,290A
; CURRENT FILING DATE: 1999-01-15
; EARLIER APPLICATION NUMBER: PCT/EP96/02230
; EARLIER FILING DATE: 1996-05-23
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 51
; LENGTH: 124
; TYPE: PRT
; ORGANISM: Murine
US-09-232-290-51

Query Match 63.0%; Score 34; DB 2; Length 124;
Best Local Similarity 75.0%; Pred. No. 64;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 LGTYFDS 10

; APPLICANT: LYNN DOUCETTE-STAMM ET AL
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 4879
; LENGTH: 271
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-4879

Query Match 63.0%; Score 34; DB 2; Length 271;
Best Local Similarity 62.5%; Pred. No. 1.5e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 VKLGTYYF 8
Db 47 IQLGVYF 54

RESULT 21
US-08-252-995D-13
; Sequence 13, Application US/08252995D
; Patent No. 5650501
; GENERAL INFORMATION:
; APPLICANT: DENNIS, JAMES W
; APPLICANT: HEFFERNAN, MIKE
; APPLICANT: FODE, CAROL
; TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BERESKIN & PARR
; STREET: 40 King Street West
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5H 3Y2
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/252,995D
; FILING DATE: 02-JUN-1994
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: KURDYDYK, LINDA M
; REGISTRATION NUMBER: 34,971
; REFERENCE/DOCKET NUMBER: 3153-96
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 364-7311
; TELEFAX: (416) 361-1398
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 275 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
```

```
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Saccharomyces cerevisiae
US-08-252-995D-13

Query Match 63.0%; Score 34; DB 1; Length 275;
Best Local Similarity 60.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 VKLGTYYFDS 10
   :|||:|
Db 131 LKLGNIFFDS 140

RESULT 22
US-08-834-108-13
; Sequence 13, Application US/08834108
; Patent No. 5976893
; GENERAL INFORMATION:
; APPLICANT: Dennis, James W
; APPLICANT: Heffernan, Mike
; APPLICANT: Fode, Carol
; TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BERESKIN & PARR
; STREET: 40 King Street West
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5H 3Y2
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/834,108
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Kurdydyk, Linda M
; REGISTRATION NUMBER: 34,971
; REFERENCE/DOCKET NUMBER: 3153-210
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 364-7311
; TELEFAX: (416) 361-1398
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; TYPE: amino acid
; LENGTH: 275 amino acids
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Saccharomyces cerevisiae
US-08-834-108-13

Query Match 63.0%; Score 34; DB 1; Length 275;
Best Local Similarity 60.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 VKLGTYYFDS 10
   :|||:|
Db 131 LKLGNIFFDS 140

RESULT 23
US-09-107-532A-6410
; Sequence 6410, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 6410:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 319 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...319
; SEQUENCE DESCRIPTION: SEQ ID NO: 6410:
US-09-107-532A-6410

Query Match 63.0%; Score 34; DB 2; Length 319;
Best Local Similarity 55.6%; Pred. No. 1.7e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 KLGTYYFDS 10
   :|||:|
Db 87 RLGTYYMET 95

RESULT 24
US-10-012-819-60
; Sequence 60, Application US/10012819
; Patent No. 6916615
; GENERAL INFORMATION:
; APPLICANT: Legrain, Pierre
; APPLICANT: Selig, Luc
; APPLICANT: Rain, Jean-Christophe
; TITLE OF INVENTION: Collection of Prokaryotic DNA for Two-Hybrid System, Helicobacter
; TITLE OF INVENTION: pylori Protein-Protein Interactions and Applications thereof
; FILE REFERENCE: B5053
; CURRENT APPLICATION NUMBER: US/10/012,819
; CURRENT FILING DATE: 2001-10-30
; PRIOR APPLICATION NUMBER: EP 99401066.8
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 278
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 60
; LENGTH: 329
```

```
; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-10-012-819-60

Query Match      63.0%; Score 34; DB 2; Length 329;
Best Local Similarity 66.7%; Pred. No. 1.8e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      2 KLGTYFDS 10
       |:|||||
Db      268 KVGTYLTS 276

RESULT 25
US-09-134-000C-4931
; Sequence 4931, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 4931
; LENGTH: 365
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-4931

Query Match      63.0%; Score 34; DB 2; Length 365;
Best Local Similarity 55.6%; Pred. No. 2e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      2 KLGTYFDS 10
       |:|||||
Db      115 RLGTYYLET 123

RESULT 26
US-09-248-796A-14832
; Sequence 14832, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 14832
; LENGTH: 373
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-14832

Query Match      63.0%; Score 34; DB 2; Length 373;
Best Local Similarity 71.4%; Pred. No. 2e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      4 GTTYFDS 10
       |:|||||
Db      137 GSYFYFDN 143

RESULT 27
US-09-543-681A-6460
; Sequence 6460, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRTON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 6460
; LENGTH: 790
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-6460

Query Match      63.0%; Score 34; DB 2; Length 790;
Best Local Similarity 62.5%; Pred. No. 4.5e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      3 LGTYFYFDS 10
       |:|||||
Db      708 VGAYFYFDT 715

RESULT 28
US-09-248-796A-26385
; Sequence 26385, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 26385
; LENGTH: 979
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-26385

Query Match      63.0%; Score 34; DB 2; Length 979;
Best Local Similarity 75.0%; Pred. No. 5.7e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      3 LGTYFYFDS 10
       |:|||||
Db      918 LGNYFYFSS 925

RESULT 29
US-09-471-276-1040
; Sequence 1040, Application US/09471276
; Patent No. 6822072
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6822072
; FILE REFERENCE: GENSET.025CPI
; CURRENT APPLICATION NUMBER: US/09/471,276
```

; CURRENT FILING DATE: 1999-12-21  
; EARLIER APPLICATION NUMBER: 09/057,719  
; EARLIER FILING DATE: 1998-04-09  
; EARLIER APPLICATION NUMBER: 09/069,047  
; EARLIER FILING DATE: 1998-04-28  
; EARLIER APPLICATION NUMBER: PCT/IB99/00712  
; EARLIER FILING DATE: 1999-04-09  
; NUMBER OF SEQ ID NOS: 1622  
; SOFTWARE: Patent.pm  
; SEQ ID NO 1040  
; LENGTH: 51  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SIGNAL  
; LOCATION: -39...-1  
US-09-471-276-1040

Query Match 61.1%; Score 33; DB 2; Length 51;  
Best Local Similarity 71.4%; Pred. No. 38;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 LGTYTFD 9  
|||:|:  
Db 18 LGTYFFE 24

RESULT 30  
US-09-248-796A-19774  
; Sequence 19774, Application US/09248796A  
; Patent No. 6747137  
; GENERAL INFORMATION:  
; APPLICANT: Keith Weinstock et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS  
; FILE REFERENCE: 107196.132  
; CURRENT APPLICATION NUMBER: US/09/248,796A  
; CURRENT FILING DATE: 1999-02-12  
; PRIOR APPLICATION NUMBER: US 60/074,725  
; PRIOR FILING DATE: 1998-02-13  
; PRIOR APPLICATION NUMBER: US 60/096,409  
; PRIOR FILING DATE: 1998-08-13  
; NUMBER OF SEQ ID NOS: 28208  
; SEQ ID NO 19774  
; LENGTH: 81  
; TYPE: PRT  
; ORGANISM: Candida albicans  
US-09-248-796A-19774

Query Match 61.1%; Score 33; DB 2; Length 81;  
Best Local Similarity 55.6%; Pred. No. 62;  
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 VKLGTYTFD 9  
:|:|  
Db 17 IKMSTVFD 25

RESULT 31  
US-10-194-975-48  
; Sequence 48, Application US/10194975  
; Patent No. 6881557  
; GENERAL INFORMATION:  
; APPLICANT: Foote, Jefferson  
; TITLE OF INVENTION: Super Humanized Antibodies  
; FILE REFERENCE: 501231.01  
; CURRENT APPLICATION NUMBER: US/10/194,975  
; CURRENT FILING DATE: 2002-10-10  
; PRIOR APPLICATION NUMBER: US 60/305,111  
; PRIOR FILING DATE: 2001-07-12  
; NUMBER OF SEQ ID NOS: 122  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 48

; LENGTH: 97  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-194-975-48

Query Match 61.1%; Score 33; DB 2; Length 97;  
Best Local Similarity 85.7%; Pred. No. 75;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GTYYFDS 10  
|||||  
Db 56 GTYYADS 62

RESULT 32  
US-09-534-717-617  
; Sequence 617, Application US/09534717  
; Patent No. 6914128  
; GENERAL INFORMATION:  
; APPLICANT: Jochen, Salfeld et al.  
; TITLE OF INVENTION: Human Antibodies That Bind Human IL-12 And Methods For Producing  
; FILE REFERENCE: BBI-093CP  
; CURRENT APPLICATION NUMBER: US/09/534,717  
; CURRENT FILING DATE: 2000-03-24  
; EARLIER APPLICATION NUMBER: 60/126,603  
; EARLIER FILING DATE: March 25, 1999  
; NUMBER OF SEQ ID NOS: 675  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 617  
; LENGTH: 97  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-534-717-617

Query Match 61.1%; Score 33; DB 2; Length 97;  
Best Local Similarity 85.7%; Pred. No. 75;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GTYYFDS 10  
|||||  
Db 56 GTYYADS 62

RESULT 33  
US-09-534-717-618  
; Sequence 618, Application US/09534717  
; Patent No. 6914128  
; GENERAL INFORMATION:  
; APPLICANT: Jochen, Salfeld et al.  
; TITLE OF INVENTION: Human Antibodies That Bind Human IL-12 And Methods For Producing  
; FILE REFERENCE: BBI-093CP  
; CURRENT APPLICATION NUMBER: US/09/534,717  
; CURRENT FILING DATE: 2000-03-24  
; EARLIER APPLICATION NUMBER: 60/126,603  
; EARLIER FILING DATE: March 25, 1999  
; NUMBER OF SEQ ID NOS: 675  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 618  
; LENGTH: 97  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-534-717-618

Query Match 61.1%; Score 33; DB 2; Length 97;  
Best Local Similarity 85.7%; Pred. No. 75;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GTYYFDS 10  
|||||  
Db 56 GTYYADS 62

RESULT 34

US-09-530-139-58  
; Sequence 58, Application US/09530139  
; Patent No. 6670453  
; GENERAL INFORMATION:  
; APPLICANT: FRENKEN, LEON GERARDUS  
; APPLICANT: HOWELL, STEVEN  
; APPLICANT: LEDEBOER, ADRIANUS MARINUS  
; APPLICANT: VAN DER LOOT, CORNELIS PAUL  
; TITLE OF INVENTION: MULTIVALENT ANTIGEN-BINDING PROTEINS  
; FILE REFERENCE: 60113/268075/ASH  
; CURRENT APPLICATION NUMBER: US/09/530,139  
; CURRENT FILING DATE: 2000-04-27  
; PRIOR FILING DATE: 1998-10-27  
; PRIOR APPLICATION NUMBER: EP 97308538.4  
; PRIOR FILING DATE: 1997-10-27  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 58  
; LENGTH: 124  
; TYPE: PRT  
; ORGANISM: Unknown Organism  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: Anti-LAB-phage  
; OTHER INFORMATION: fragment  
US-09-530-139-58  
Query Match 61.1%; Score 33; DB 2; Length 124;  
Best Local Similarity 85.7%; Pred. No. 98;  
Matches 6; Conservative 0; Mismatches 0; Gaps 0;  
Indels 0;  
QY 4 GTTYFDS 10  
DB 57 GTTYADS 63  
RESULT 35  
US-09-107-532A-5809  
; Sequence 5809, Application US/09107532A  
; Patent No. 6583275  
; GENERAL INFORMATION:  
; APPLICANT: LYNN A Doucette-Stamm and David Bush  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: GENOME THERAPEUTICS CORPORATION  
; STREET: 100 Beaver Street  
; CITY: Waltham  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02354  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: CD-ROM ISO9660  
; COMPUTER: PC  
; OPERATING SYSTEM: <Unknown>  
; SOFTWARE: ASCII  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/107,532A  
; FILING DATE: 30-Jun-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/085,598  
; FILING DATE: 14 May 1998  
; APPLICATION NUMBER: 60/051571  
; FILING DATE: July 2, 1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ariniello, Pamela Deneka  
; REGISTRATION NUMBER: 40,489  
; REFERENCE/DOCKET NUMBER: GTC-012  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (781)893-5007  
; TELEFAX: (781)893-8277  
; INFORMATION FOR SEQ ID NO: 5809:

SEQUENCE CHARACTERISTICS:  
; LENGTH: 196 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: YES  
; ORIGINAL SOURCE:  
; ORGANISM: Enterococcus faecium  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (B) LOCATION 1...196  
; SEQUENCE DESCRIPTION: SEQ ID NO: 5809:  
US-09-107-532A-5809  
Query Match 61.1%; Score 33; DB 2; Length 196;  
Best Local Similarity 83.3%; Pred. No. 1.6e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 4 GTTYFD 9  
DB 65 GTTYFE 70  
RESULT 36  
US-08-976-063E-14  
; Sequence 14, Application US/08976063E  
; Patent No. 6524831  
; GENERAL INFORMATION:  
; APPLICANT: Steinbuechel, Alexander  
; APPLICANT: Priefert, Horst  
; APPLICANT: Rabenhorst, Jurgen  
; TITLE OF INVENTION: SYNTHETIC ENZYMES FOR THE PRODUCTION OF CONIFERYL  
; TITLE OF INVENTION: ALCOHOL, CONIFERYLALDEHYDE, FERULIC ACID, VANILLIN AND  
; FILE REFERENCE: BAYER-9998-CAO  
; CURRENT APPLICATION NUMBER: US/08/976,063E  
; CURRENT FILING DATE: 1997-11-21  
; PRIOR APPLICATION NUMBER: 196 49 655.1 GERMANY  
; PRIOR FILING DATE: 1996-11-29  
; NUMBER OF SEQ ID NOS: 45  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 14  
; LENGTH: 228  
; TYPE: PRT  
; ORGANISM: not required under old rule  
US-08-976-063E-14  
Query Match 61.1%; Score 33; DB 2; Length 228;  
Best Local Similarity 85.7%; Pred. No. 1.9e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 3 LGTYTFD 9  
DB 186 LGTYAD 192  
RESULT 37  
US-09-270-767-56999  
; Sequence 56999, Application US/09270767  
; Patent No. 6703491  
; GENERAL INFORMATION:  
; APPLICANT: Homburger et al.  
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
; FILE REFERENCE: File Reference: 7326-094  
; CURRENT APPLICATION NUMBER: US/09/270,767  
; CURRENT FILING DATE: 1999-03-17  
; NUMBER OF SEQ ID NOS: 62517  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 56999  
; LENGTH: 229  
; TYPE: PRT  
; ORGANISM: Drosophila melanogaster  
US-09-270-767-56999

Query Match 61.1%; Score 33; DB 2; Length 229;  
Best Local Similarity 62.5%; Pred. No. 1.9e+02;  
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VKLGTYFF 8  
: : : : :  
DB 97 LELGTYFF 104

RESULT 38  
US-09-248-796A-15824  
; Sequence 15824, Application US/09248796A  
; Patent No. 6747137  
; GENERAL INFORMATION:  
; APPLICANT: Keith Weinstock et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS  
; FILE REFERENCE: 107196.132  
; CURRENT APPLICATION NUMBER: US/09/248,796A  
; CURRENT FILING DATE: 1999-02-12  
; PRIOR FILING DATE: 1998-02-13  
; PRIOR APPLICATION NUMBER: US 60/074,725  
; PRIOR FILING DATE: 1998-02-13  
; PRIOR APPLICATION NUMBER: US 60/096,409  
; PRIOR FILING DATE: 1998-08-13  
; NUMBER OF SEQ ID NOS: 28208  
; SEQ ID NO 15824  
; LENGTH: 265  
; TYPE: PRT  
; ORGANISM: Candida albicans  
US-09-248-796A-15824

Query Match 61.1%; Score 33; DB 2; Length 265;  
Best Local Similarity 62.5%; Pred. No. 2.2e+02;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 LGTYFFDS 10  
: : : : :  
DB 68 VGAYFFDS 75

RESULT 39  
US-09-248-796A-18015  
; Sequence 18015, Application US/09248796A  
; Patent No. 6747137  
; GENERAL INFORMATION:  
; APPLICANT: Keith Weinstock et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS  
; FILE REFERENCE: 107196.132  
; CURRENT APPLICATION NUMBER: US/09/248,796A  
; CURRENT FILING DATE: 1999-02-12  
; PRIOR FILING DATE: 1998-02-13  
; PRIOR APPLICATION NUMBER: US 60/074,725  
; PRIOR FILING DATE: 1998-02-13  
; PRIOR APPLICATION NUMBER: US 60/096,409  
; PRIOR FILING DATE: 1998-08-13  
; NUMBER OF SEQ ID NOS: 28208  
; SEQ ID NO 18015  
; LENGTH: 357  
; TYPE: PRT  
; ORGANISM: Candida albicans  
US-09-248-796A-18015

Query Match 61.1%; Score 33; DB 2; Length 357;  
Best Local Similarity 75.0%; Pred. No. 3e+02;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 KLGTYYFD 9  
: : : : :  
DB 265 KPSTYYFD 272

RESULT 40

US-09-489-039A-7783  
; Sequence 7783, Application US/09489039A  
; Patent No. 6610836  
; GENERAL INFORMATION:  
; APPLICANT: Gary Breton et. al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA  
; FILE REFERENCE: 2709.2004001  
; CURRENT APPLICATION NUMBER: US/09/489,039A  
; CURRENT FILING DATE: 2000-01-27  
; PRIOR APPLICATION NUMBER: US 60/117,747  
; PRIOR FILING DATE: 1999-01-29  
; NUMBER OF SEQ ID NOS: 14342  
; SEQ ID NO 7783  
; LENGTH: 368  
; TYPE: PRT  
; ORGANISM: Klebsiella pneumoniae  
US-09-489-039A-7783

Query Match 61.1%; Score 33; DB 2; Length 368;  
Best Local Similarity 71.4%; Pred. No. 3.1e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 KLGTYYF 8  
: : : : :  
DB 305 QLGTYYF 311

RESULT 41  
US-09-653-755A-4  
; Sequence 4, Application US/09653755A  
; Patent No. 6824989  
; GENERAL INFORMATION:  
; APPLICANT: Eisinger, Dominic P.  
; APPLICANT: Stiles, Lynn  
; APPLICANT: LaMarche, Arthur  
; APPLICANT: Jelinek, Thomas  
; TITLE OF INVENTION: Recombinant Monoclonal Antibody Specific for  
; FILE REFERENCE: 724650-3  
; CURRENT APPLICATION NUMBER: US/09/653,755A  
; CURRENT FILING DATE: 2000-09-01  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 454  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:Amino acid  
; OTHER INFORMATION: sequence for heavy chain of recombinant antibody  
US-09-653-755A-4

Query Match 61.1%; Score 33; DB 2; Length 454;  
Best Local Similarity 62.5%; Pred. No. 3.8e+02;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 KLGTYYFD 9  
: : : : :  
DB 99 RAGATYYFD 106

RESULT 42  
US-09-653-755A-6  
; Sequence 6, Application US/09653755A  
; Patent No. 6824989  
; GENERAL INFORMATION:  
; APPLICANT: Eisinger, Dominic P.  
; APPLICANT: Stiles, Lynn  
; APPLICANT: LaMarche, Arthur  
; APPLICANT: Jelinek, Thomas  
; TITLE OF INVENTION: Recombinant Monoclonal Antibody Specific for  
; FILE REFERENCE: 724650-3  
; CURRENT APPLICATION NUMBER: US/09/653,755A  
; CURRENT FILING DATE: 2000-09-01  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 6  
; LENGTH: 454  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:Amino acid  
; OTHER INFORMATION: sequence for heavy chain of recombinant antibody  
US-09-653-755A-6

RESULT 40

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; FILE REFERENCE: 724650-3
; CURRENT APPLICATION NUMBER: US/09/653,755A
; CURRENT FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Amino acid
; OTHER INFORMATION: sequence for heavy chain of recombinant antibody
; OTHER INFORMATION: with C-terminal histidine tag sequence
US-09-653-755A-6

Query Match 61.1%; Score 33; DB 2; Length 462;
Best Local Similarity 62.5%; Pred. No. 3.9e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 KLGTYTFD 9
   :|||||
Db 99 RAGATTFD 106

RESULT 43
US-09-543-681A-4720
; Sequence 4720, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE REFERENCE: 2709-1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 4720
; LENGTH: 549
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-4720

Query Match 61.1%; Score 33; DB 2; Length 549;
Best Local Similarity 71.4%; Pred. No. 4.7e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 KLGTYTF 8
   :|||||
Db 301 QLGTYTFY 307

RESULT 44
US-09-328-352-8230
; Sequence 8230, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 8230
; LENGTH: 766
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-8230

Query Match 61.1%; Score 33; DB 2; Length 766;
Best Local Similarity 85.7%; Pred. No. 6.7e+02;

; FILE REFERENCE: 038602-0329
; CURRENT APPLICATION NUMBER: US/09/291,417D
; CURRENT FILING DATE: 1999-04-13
; PRIOR APPLICATION NUMBER: 60/081,784
; PRIOR FILING DATE: 1998-04-14
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 92
; LENGTH: 911
; TYPE: PRT
; ORGANISM: Murine sp.
US-09-291-417D-92

Query Match 61.1%; Score 33; DB 2; Length 911;
Best Local Similarity 71.4%; Pred. No. 8e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 LGTYTFD 9
   :|||||
Db 97 LGATTFD 103

RESULT 45
US-09-688-188B-92
; Sequence 92, Application US/09688188B
; Patent No. 6656716
; GENERAL INFORMATION:
; APPLICANT: PLOWMAN, GREGORY
; APPLICANT: MARTINEZ, RICARDO
; APPLICANT: WHYTE, DAVID
; TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES
; FILE REFERENCE: 038602/0328
; CURRENT APPLICATION NUMBER: US/09/688,188B
; CURRENT FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 09/291,417
; PRIOR FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: 60/081,784
; PRIOR FILING DATE: 1998-04-14
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 92
; LENGTH: 911
; TYPE: PRT
; ORGANISM: Murine sp.
US-09-688-188B-92

Query Match 61.1%; Score 33; DB 2; Length 911;
Best Local Similarity 71.4%; Pred. No. 8e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 LGTYTFD 9
   :|||||
Db 97 LGATTFD 103

RESULT 46
US-09-291-417D-92
; Sequence 92, Application US/09291417D
; Patent No. 6680170
; GENERAL INFORMATION:
; APPLICANT: PLOWMAN, GREGORY
; APPLICANT: MARTINEZ, RICARDO
; APPLICANT: WHYTE, DAVID
; TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES
; FILE REFERENCE: 038602/0329
; CURRENT APPLICATION NUMBER: US/09/291,417D
; CURRENT FILING DATE: 1999-04-13
; PRIOR APPLICATION NUMBER: 60/081,784
; PRIOR FILING DATE: 1998-04-14
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 92
; LENGTH: 911
; TYPE: PRT
; ORGANISM: Murine sp.
US-09-291-417D-92

Query Match 61.1%; Score 33; DB 2; Length 911;
Best Local Similarity 71.4%; Pred. No. 8e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 LGTYTFD 9
   :|||||
Db 97 LGATTFD 103

RESULT 47
US-09-688-188B-154
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; Sequence 154, Application US/09688188B  
; Patent No. 6656716  
; GENERAL INFORMATION:  
; APPLICANT: PLOWMAN, GREGORY  
; APPLICANT: MARTINEZ, RICARDO  
; APPLICANT: WHYTE, DAVID  
; TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES  
; FILE REFERENCE: 038602/0328  
; CURRENT APPLICATION NUMBER: US/09/688,188B  
; CURRENT FILING DATE: 2000-10-16  
; PRIOR APPLICATION NUMBER: 09/291,417  
; PRIOR FILING DATE: 1999-04-14  
; PRIOR APPLICATION NUMBER: 60/081,784  
; PRIOR FILING DATE: 1998-04-14  
; NUMBER OF SEQ ID NOS: 155  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 154  
; LENGTH: 966  
; TYPE: PRT  
; ORGANISM: Murine sp.  
US-09-688-188B-154

Query Match 61.1%; Score 33; DB 2; Length 966;  
Best Local Similarity 71.4%; Pred. No. 8.5e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 LGTYTFD 9  
||| |||:  
Db 97 LGAYTYD 103

## RESULT 48

US-09-291-417D-154  
; Sequence 154, Application US/09291417D  
; Patent No. 6680170  
; GENERAL INFORMATION:  
; APPLICANT: PLOWMAN, GREGORY  
; APPLICANT: MARTINEZ, RICARDO  
; APPLICANT: WHYTE, DAVID  
; TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES  
; FILE REFERENCE: 038602/0329  
; CURRENT APPLICATION NUMBER: US/09/291,417D  
; CURRENT FILING DATE: 1999-04-13  
; PRIOR APPLICATION NUMBER: 60/081,784  
; PRIOR FILING DATE: 1998-04-14  
; NUMBER OF SEQ ID NOS: 155  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 154  
; LENGTH: 966  
; TYPE: PRT  
; ORGANISM: Murine sp.  
US-09-291-417D-154

Query Match 61.1%; Score 33; DB 2; Length 966;  
Best Local Similarity 71.4%; Pred. No. 8.5e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 LGTYTFD 9  
||| |||:  
Db 97 LGAYTYD 103

## RESULT 49

US-09-995-749A-5  
; Sequence 5, Application US/09995749A  
; Patent No. 6867026  
; GENERAL INFORMATION:  
; APPLICANT: VAN GEEL-SCHUTTEN, GERRITINA HENDRIKA  
; APPLICANT: DIJKHUIZEN, LUBBERT  
; APPLICANT: RAHAOUI, HAKIM  
; APPLICANT: LEER, ROBERT-JAN  
; TITLE OF INVENTION: NOVEL GLUCOSYLTRANSFERASES  
; FILE REFERENCE: B043388-CIP

; CURRENT APPLICATION NUMBER: US/09/995.749A  
; CURRENT FILING DATE: 2001-11-29  
; PRIOR APPLICATION NUMBER: 09/604,957  
; PRIOR FILING DATE: 2000-06-28  
; PRIOR APPLICATION NUMBER: EPO 00201871.1  
; PRIOR FILING DATE: 2000-05-25  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 5  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: Lactobacillus reuteri  
US-09-995-749A-5

Query Match 59.3%; Score 32; DB 2; Length 13;  
Best Local Similarity 83.3%; Pred. No. 14;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 TTYFDS 10  
||||:  
Db 1 TTYFDN 6

## RESULT 50

US-09-471-276-1304  
; Sequence 1304, Application US/09471276  
; Patent No. 6822072  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Duclert A.  
; APPLICANT: Giordano, J.Y.  
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
; Patent No. 6822072  
; FILE REFERENCE: GENSET. 025CPI  
; CURRENT APPLICATION NUMBER: US/09/471,276  
; CURRENT FILING DATE: 1999-12-21  
; EARLIER APPLICATION NUMBER: 09/057,719  
; EARLIER FILING DATE: 1998-04-09  
; EARLIER APPLICATION NUMBER: 09/069,047  
; EARLIER FILING DATE: 1998-04-28  
; EARLIER APPLICATION NUMBER: PCT/IB99/00712  
; EARLIER FILING DATE: 1999-04-09  
; NUMBER OF SEQ ID NOS: 1622  
; SOFTWARE: Patent.pm  
; SEQ ID NO 1304  
; LENGTH: 55  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SIGNAL  
; LOCATION: -47..-1  
US-09-471-276-1304

Query Match 59.3%; Score 32; DB 2; Length 55;  
Best Local Similarity 62.5%; Pred. No. 63;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 VKLGTTFYF 8  
:||||:  
Db 27 LKLGNYFYF 34

Search completed: April 6, 2006, 09:00:53  
Job time : 20.3898 secs



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OM protein - protein search, using sw model

Run on: April 6, 2006, 09:13:24 ; Search time 80.8475 Seconds

(without alignments)

51.681 Million cell updates/sec

Title: US-10-089-500-5

Perfect score: 54

Sequence: 1 VKLGTYYFDS 10

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Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Published Applications\_AA\_Main:\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	54	100.0	130	3	US-09-764-304-8
2	54	100.0	130	3	US-09-764-304-18
3	54	100.0	130	4	US-10-265-713-8
4	54	100.0	130	4	US-10-265-713-18
5	54	100.0	130	4	US-10-166-626-8
6	54	100.0	130	4	US-10-166-626-18
7	41	75.9	368	5	US-10-831-070-102
8	40	74.1	446	5	US-10-739-930-10028
9	39	72.2	195	4	US-10-425-115-365506
10	39	72.2	206	4	US-10-425-115-204796
11	39	72.2	341	4	US-10-425-115-311275
12	39	72.2	424	4	US-10-425-115-204801
13	39	72.2	427	4	US-10-425-114-46787
14	39	72.2	435	4	US-10-437-963-139528
15	39	72.2	572	4	US-10-425-115-204798
16	38	70.4	48	4	US-10-424-599-145556
17	38	70.4	1781	3	US-09-995-749A-2
18	37	68.5	179	4	US-10-243-552-339
19	37	68.5	254	6	US-11-090-847-130
20	37	68.5	380	3	US-09-833-245-1319
21	37	68.5	388	4	US-10-724-972A-4330
22	37	68.5	1771	5	US-10-484-218-14
23	36	66.7	73	4	US-10-424-599-250992
24	36	66.7	361	4	US-10-081-816-35
25	36	66.7	361	4	US-10-447-328-42
26	36	66.7	361	6	US-11-097-143-29412
27	36	66.7	387	4	US-10-320-797-3156

36	66.7	433	4	US-10-369-493-11075	Sequence 11075, A
36	66.7	440	4	US-10-424-599-154451	Sequence 154451, A
36	66.7	675	4	US-10-782-141-21	Sequence 21, Appl
36	66.7	675	4	US-10-782-096-22	Sequence 22, Appl
36	66.7	675	5	US-10-781-979-23	Sequence 23, Appl
36	66.7	859	4	US-10-425-115-270359	Sequence 270359, A
36	66.7	931	4	US-10-437-963-106243	Sequence 106243, A
35	64.8	23	3	US-09-880-748-2132	Sequence 2132, Ap
35	64.8	23	3	US-09-880-748-3076	Sequence 3076, Ap
35	64.8	23	3	US-10-293-418-2132	Sequence 2132, Ap
35	64.8	118	4	US-10-437-963-168775	Sequence 168775, A
35	64.8	123	5	US-10-638-265-38	Sequence 38, Appl
35	64.8	123	5	US-10-638-265-46	Sequence 46, Appl
35	64.8	123	5	US-10-638-265-54	Sequence 50, Appl
35	64.8	123	5	US-10-638-265-54	Sequence 54, Appl
35	64.8	138	4	US-10-425-115-263537	Sequence 263537, A
35	64.8	139	4	US-10-424-599-178546	Sequence 178546, A
35	64.8	139	4	US-10-424-599-179462	Sequence 179462, A
35	64.8	172	4	US-10-424-599-242803	Sequence 242803, A
35	64.8	255	3	US-09-880-748-4	Sequence 4, Appl
35	64.8	255	3	US-09-880-748-1054	Sequence 1054, Ap
35	64.8	255	3	US-09-880-748-1056	Sequence 1056, Ap
35	64.8	255	3	US-09-880-748-1065	Sequence 1065, Ap
35	64.8	255	3	US-09-880-748-1786	Sequence 1786, Ap
35	64.8	255	4	US-10-293-418-4	Sequence 4, Appl
35	64.8	255	4	US-10-293-418-1054	Sequence 1054, Ap
35	64.8	255	4	US-10-293-418-1056	Sequence 1056, Ap
35	64.8	255	4	US-10-293-418-1786	Sequence 1786, Ap
35	64.8	258	3	US-09-880-748-1773	Sequence 1773, Ap
35	64.8	258	4	US-10-293-418-1773	Sequence 1773, Ap
35	64.8	287	4	US-10-282-122A-70928	Sequence 70928, A
35	64.8	288	4	US-10-724-972A-4373	Sequence 4373, Ap
35	64.8	294	4	US-10-282-122A-71558	Sequence 71558, A
35	64.8	349	4	US-10-601-309-96	Sequence 96, Appl
35	64.8	376	6	US-11-097-143-17001	Sequence 17001, A
35	64.8	459	5	US-10-501-282-1130	Sequence 1130, Ap
35	64.8	569	4	US-10-437-963-131723	Sequence 131723, A
35	64.8	661	4	US-10-282-122A-48472	Sequence 48472, A
35	64.8	686	4	US-10-369-493-12863	Sequence 12863, A
35	64.8	696	4	US-10-369-493-6196	Sequence 6196, Ap
35	64.8	819	6	US-11-097-143-21624	Sequence 21624, A
34	63.0	19	3	US-09-956-206A-41	Sequence 41, Appl
34	63.0	19	5	US-10-965-616-41	Sequence 41, Appl
34	63.0	56	4	US-10-264-049-4243	Sequence 4243, Ap
34	63.0	64	4	US-10-424-599-215116	Sequence 215116, A
34	63.0	88	4	US-10-424-599-151462	Sequence 151462, A
34	63.0	106	4	US-10-424-599-220082	Sequence 220082, A
34	63.0	123	5	US-10-700-632-83	Sequence 83, Appl
34	63.0	124	5	US-10-895-135-61	Sequence 61, Appl
34	63.0	128	4	US-10-292-486-44	Sequence 44, Appl
34	63.0	230	4	US-10-282-122A-42963	Sequence 42963, A
34	63.0	245	5	US-10-450-763-46903	Sequence 46903, A
34	63.0	256	3	US-09-898-837A-32	Sequence 32, Appl
34	63.0	277	4	US-10-335-977-5088	Sequence 5088, Ap
34	63.0	284	4	US-10-335-977-5089	Sequence 5089, Ap
34	63.0	285	3	US-09-895-913A-138	Sequence 138, App
34	63.0	329	4	US-10-012-819-60	Sequence 60, Appl
34	63.0	329	4	US-10-425-115-205795	Sequence 205795, A
34	63.0	463	4	US-10-156-761-14792	Sequence 14792, A
34	63.0	498	5	US-10-450-763-53878	Sequence 53878, A
34	63.0	510	3	US-09-815-242-10157	Sequence 10157, A
34	63.0	510	4	US-10-282-122A-42962	Sequence 42962, A
34	63.0	626	4	US-10-425-115-366836	Sequence 366836, A
34	63.0	705	4	US-10-363-493-1864	Sequence 1864, Ap
34	63.0	787	5	US-10-946-647-1382	Sequence 1382, Ap
34	63.0	1776	5	US-10-484-218-12	Sequence 12, Appl
34	63.0	1943	4	US-10-282-122A-58750	Sequence 58750, A
34	63.0	1974	3	US-09-895-913A-12	Sequence 12, Appl
33	61.1	12	4	US-10-688-925-39	Sequence 39, Appl
33	61.1	12	4	US-10-688-925-39	Sequence 39, Appl
33	61.1	15	5	US-10-911-838-8	Sequence 8, Appl
33	61.1	17	4	US-10-031-874A-47	Sequence 47, Appl

101	33	61.1	17	4	US-10-031-874A-112	Sequence 112, App	174	33	61.1	538	5	US-10-501-282-6170	Sequence 6170, Ap
102	33	61.1	51	4	US-10-450-036A-47	Sequence 47, Appl	175	33	61.1	569	4	US-10-437-963-197645	Sequence 197645,
103	33	61.1	17	5	US-10-926-683-1040	Sequence 1040, Ap	176	33	61.1	575	4	US-10-120-801-60	Sequence 60, Appl
104	33	61.1	52	3	US-09-764-877-1941	Sequence 1941, Ap	177	33	61.1	575	4	US-10-312-352-8	Sequence 8, Appl
105	33	61.1	52	4	US-10-242-513-1941	Sequence 1941, Ap	178	33	61.1	575	4	US-10-408-765A-1901	Sequence 1901, Ap
106	33	61.1	63	4	US-10-424-599-261398	Sequence 261398,	179	33	61.1	618	4	US-10-282-122A-74768	Sequence 74768, A
107	33	61.1	65	4	US-10-425-115-32118	Sequence 32118,	180	33	61.1	618	4	US-10-424-599-147053	Sequence 147053,
108	33	61.1	87	4	US-10-425-115-289685	Sequence 289685,	181	33	61.1	620	4	US-10-408-765A-1812	Sequence 1812, Ap
109	33	61.1	95	3	US-09-864-761-47118	Sequence 47118, A	182	33	61.1	676	4	US-10-282-122A-74789	Sequence 74789, A
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111	33	61.1	97	4	US-10-032-037B-70	Sequence 48, Appl	184	33	61.1	698	4	US-10-437-963-109740	Sequence 109740,
112	33	61.1	97	4	US-10-032-037B-70	Sequence 70, Appl	185	33	61.1	826	4	US-10-282-122A-78345	Sequence 78345, A
113	33	61.1	97	4	US-10-029-988B-71	Sequence 71, Appl	186	33	61.1	850	5	US-10-450-763-34993	Sequence 34993, A
114	33	61.1	97	4	US-10-029-988B-71	Sequence 71, Appl	187	33	61.1	869	5	US-10-450-763-50017	Sequence 50017, A
115	33	61.1	97	4	US-10-032-423A-71	Sequence 71, Appl	188	33	61.1	911	3	US-09-291-417-92	Sequence 92, Appl
116	33	61.1	97	4	US-10-032-423A-71	Sequence 71, Appl	189	33	61.1	911	5	US-10-725-329-92	Sequence 92, Appl
117	33	61.1	97	4	US-10-029-926B-70	Sequence 70, Appl	190	33	61.1	911	5	US-10-725-329-92	Sequence 92, Appl
118	33	61.1	97	4	US-10-029-926B-71	Sequence 71, Appl	191	33	61.1	966	5	US-10-725-329-154	Sequence 154, App
119	33	61.1	97	5	US-10-884-830-617	Sequence 617, App	192	33	61.1	966	5	US-10-725-121-154	Sequence 154, App
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123	33	61.1	105	3	US-09-864-761-38933	Sequence 38933, A	196	33	61.1	3194	4	US-10-282-122A-59046	Sequence 59046, A
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125	33	61.1	115	4	US-10-408-901-10	Sequence 10, Appl	198	33	61.1	3871	4	US-10-369-493-6539	Sequence 6539, Ap
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127	33	61.1	116	4	US-10-408-901-6	Sequence 6, Appl	200	32	59.3	19	3	US-09-880-748-3113	Sequence 3113, Ap
128	33	61.1	116	4	US-10-408-901-14	Sequence 14, Appl	201	32	59.3	19	4	US-10-293-418-3113	Sequence 3113, Ap
129	33	61.1	116	4	US-10-408-901-22	Sequence 22, Appl	202	32	59.3	21	4	US-10-062-710-179	Sequence 179, App
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134	33	61.1	119	5	US-10-815-449-3	Sequence 3, Appl	207	32	59.3	76	4	US-10-425-115-261791	Sequence 261791,
135	33	61.1	119	5	US-10-815-449-5	Sequence 5, Appl	208	32	59.3	76	4	US-10-425-115-283587	Sequence 283587,
136	33	61.1	121	4	US-10-309-762-130	Sequence 130, App	209	32	59.3	82	4	US-10-425-115-288662	Sequence 288662,
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138	33	61.1	121	4	US-10-688-925-22	Sequence 22, Appl	211	32	59.3	97	4	US-10-424-599-285242	Sequence 285242,
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141	33	61.1	127	4	US-10-425-115-325515	Sequence 325515, A	214	32	59.3	126	4	US-10-264-237-1589	Sequence 1589, Ap
142	33	61.1	178	4	US-10-767-701-42656	Sequence 42656, A	215	32	59.3	136	5	US-10-910-901-24	Sequence 24, Appl
143	33	61.1	182	4	US-10-309-763-246	Sequence 246, App	216	32	59.3	145	4	US-10-029-386-32010	Sequence 32010, A
144	33	61.1	202	3	US-09-801-944B-159	Sequence 159, App	217	32	59.3	155	4	US-10-425-114-51611	Sequence 51611, A
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168	33	61.1	446	4	US-10-408-901-50	Sequence 50, Appl	241	32	59.3	381	4	US-10-335-977-7592	Sequence 7592, Ap
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249	32	59.3	446	6	US-11-097-143-19902	Sequence 19902, A	322	32	59.3	802	3	US-09-978-643A-169	Sequence 169, App
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251	32	59.3	459	4	US-10-259-165-74	Sequence 74, Appl	324	32	59.3	802	3	US-09-978-375A-169	Sequence 169, App
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253	32	59.3	460	4	US-10-282-122A-74419	Sequence 74419, A	326	32	59.3	802	3	US-09-978-188A-169	Sequence 169, App
254	32	59.3	460	5	US-10-474-792-500	Sequence 500, App	327	32	59.3	802	3	US-09-978-681A-169	Sequence 169, App
255	32	59.3	460	6	US-11-096-190-35	Sequence 35, Appl	328	32	59.3	802	3	US-09-978-194A-169	Sequence 169, App
256	32	59.3	466	4	US-10-282-122A-74240	Sequence 74240, A	329	32	59.3	802	3	US-09-999-829A-169	Sequence 169, App
257	32	59.3	470	3	US-09-859-053-28	Sequence 28, App	330	32	59.3	802	3	US-09-978-299A-169	Sequence 169, App
258	32	59.3	470	4	US-10-800-250-28	Sequence 28, Appl	331	32	59.3	802	3	US-09-978-544A-169	Sequence 169, App
259	32	59.3	470	4	US-10-625-105-28	Sequence 28, Appl	332	32	59.3	802	3	US-09-978-665A-169	Sequence 169, App
260	32	59.3	472	3	US-09-815-242-13542	Sequence 13542, A	333	32	59.3	802	3	US-09-978-802A-169	Sequence 169, App
261	32	59.3	474	6	US-11-097-143-4329	Sequence 4329, App	334	32	59.3	802	3	US-09-999-831A-169	Sequence 169, App
262	32	59.3	479	3	US-09-815-242-13307	Sequence 13307, A	335	32	59.3	802	3	US-09-978-824-169	Sequence 169, App
263	32	59.3	479	4	US-10-282-122A-73937	Sequence 73937, A	336	32	59.3	802	3	US-10-017-081A-169	Sequence 169, App
264	32	59.3	479	5	US-10-472-928-1952	Sequence 1952, App	337	32	59.3	802	4	US-10-167-749-169	Sequence 169, App
265	32	59.3	488	4	US-10-408-765A-2601	Sequence 2601, App	338	32	59.3	802	4	US-10-013-921A-169	Sequence 169, App
266	32	59.3	496	3	US-09-815-242-5321	Sequence 5321, App	339	32	59.3	802	4	US-10-013-929A-169	Sequence 169, App
267	32	59.3	497	4	US-10-369-493-17660	Sequence 17660, A	340	32	59.3	802	4	US-10-016-177A-169	Sequence 169, App
268	32	59.3	497	4	US-10-369-493-17182	Sequence 17182, A	341	32	59.3	802	4	US-10-166-709A-169	Sequence 169, App
269	32	59.3	498	3	US-09-815-242-12335	Sequence 12335, A	342	32	59.3	802	4	US-10-143-031A-169	Sequence 169, App
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272	32	59.3	499	4	US-10-282-122A-71359	Sequence 71359, A	345	32	59.3	802	4	US-10-017-083A-169	Sequence 169, App
273	32	59.3	504	4	US-10-724-972A-4347	Sequence 4347, App	346	32	59.3	802	4	US-10-145-128A-169	Sequence 169, App
274	32	59.3	516	4	US-10-437-963-199612	Sequence 199612, A	347	32	59.3	802	4	US-10-017-191A-169	Sequence 169, App
275	32	59.3	520	4	US-10-282-122A-67146	Sequence 67146, A	348	32	59.3	802	4	US-10-143-028A-169	Sequence 169, App
276	32	59.3	521	4	US-10-282-122A-58397	Sequence 58397, A	349	32	59.3	802	4	US-10-143-029A-169	Sequence 169, App
277	32	59.3	522	4	US-10-425-115-24411	Sequence 24411, A	350	32	59.3	802	4	US-10-145-089A-169	Sequence 169, App
278	32	59.3	556	4	US-10-425-115-212022	Sequence 212022, A	351	32	59.3	802	4	US-10-165-067A-169	Sequence 169, App
279	32	59.3	560	3	US-09-071-035-220	Sequence 220, App	352	32	59.3	802	4	US-10-145-128A-169	Sequence 169, App
280	32	59.3	560	4	US-10-206-576-220	Sequence 220, App	353	32	59.3	802	4	US-10-164-728A-169	Sequence 169, App
281	32	59.3	560	5	US-10-912-362-220	Sequence 220, App	354	32	59.3	802	4	US-10-013-926A-169	Sequence 169, App
282	32	59.3	587	4	US-10-424-599-179849	Sequence 179849, A	355	32	59.3	802	4	US-10-165-247A-169	Sequence 169, App
283	32	59.3	625	4	US-10-661-809-19	Sequence 19, Appl	356	32	59.3	802	4	US-10-145-124A-169	Sequence 169, App
284	32	59.3	627	3	US-09-071-035-218	Sequence 218, App	357	32	59.3	802	4	US-10-160-502A-169	Sequence 169, App
285	32	59.3	627	3	US-10-206-576-218	Sequence 218, App	358	32	59.3	802	4	US-10-145-087A-169	Sequence 169, App
286	32	59.3	627	4	US-10-661-809-13	Sequence 13, App	359	32	59.3	802	4	US-10-017-086A-169	Sequence 169, App
287	32	59.3	627	5	US-10-912-362-218	Sequence 218, App	360	32	59.3	802	4	US-10-164-829A-169	Sequence 169, App
288	32	59.3	630	4	US-10-043-344-113	Sequence 113, App	361	32	59.3	802	4	US-10-164-929A-169	Sequence 169, App
289	32	59.3	630	4	US-10-437-963-162796	Sequence 162796, A	362	32	59.3	802	4	US-10-013-922A-169	Sequence 169, App
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291	32	59.3	658	4	US-10-156-214A-10	Sequence 10, Appl	364	32	59.3	802	4	US-10-013-924A-169	Sequence 169, App
292	32	59.3	677	6	US-11-097-143-22341	Sequence 22341, A	365	32	59.3	802	4	US-10-017-084A-169	Sequence 169, App
293	32	59.3	700	4	US-10-282-122A-52271	Sequence 52271, A	366	32	59.3	802	4	US-10-145-016A-169	Sequence 169, App
294	32	59.3	708	5	US-10-501-282-1740	Sequence 1740, App	367	32	59.3	802	4	US-10-145-088A-169	Sequence 169, App
295	32	59.3	715	5	US-10-501-282-1742	Sequence 1742, App	368	32	59.3	802	4	US-10-145-092A-169	Sequence 169, App
296	32	59.3	726	4	US-10-282-122A-74417	Sequence 74417, A	369	32	59.3	802	4	US-10-145-129A-169	Sequence 169, App
297	32	59.3	742	4	US-10-282-122A-53523	Sequence 53523, A	370	32	59.3	802	4	US-10-165-038A-169	Sequence 169, App
298	32	59.3	794	4	US-10-800-911-1	Sequence 1, Appl	371	32	59.3	802	4	US-10-165-353A-169	Sequence 169, App
299	32	59.3	799	4	US-10-072-012-410	Sequence 410, App	372	32	59.3	802	4	US-10-167-600-169	Sequence 169, App
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302	32	59.3	802	3	US-09-978-295A-169	Sequence 169, App	375	32	59.3	802	4	US-10-210-028-169	Sequence 169, App
303	32	59.3	802	3	US-09-978-697-169	Sequence 169, App	376	32	59.3	802	4	US-10-017-085A-169	Sequence 169, App
304	32	59.3	802	3	US-09-978-192A-169	Sequence 169, App	377	32	59.3	802	4	US-10-013-916A-169	Sequence 169, App
305	32	59.3	802	3	US-09-999-832A-169	Sequence 169, App	378	32	59.3	802	4	US-10-143-026B-169	Sequence 169, App
306	32	59.3	802	3	US-09-978-189-169	Sequence 169, App	379	32	59.3	802	4	US-10-013-918A-169	Sequence 169, App
307	32	59.3	802	3	US-09-978-608A-169	Sequence 169, App	380	32	59.3	802	4	US-10-162-521A-169	Sequence 169, App
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316	32	59.3	802	3	US-09-999-834A-169	Sequence 169, App	389	32	59.3	802	4	US-10-013-920A-169	Sequence 169, App
317	32	59.3	802	3	US-09-978-423A-169	Sequence 169, App	390	32	59.3	802	4	US-10-164-749A-169	Sequence 169, App
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393	32	59.3	802	5	US-10-918-851-169	Sequence 169, App	466	31	57.4	74	4	US-10-424-599-192345	Sequence 192345,
394	32	59.3	802	5	US-10-805-667-169	Sequence 169, App	467	31	57.4	75	4	US-10-767-701-54415	Sequence 54415, A
395	32	59.3	802	5	US-10-897-359-169	Sequence 169, App	468	31	57.4	79	4	US-10-424-599-219575	Sequence 219575,
396	32	59.3	802	5	US-10-893-802-169	Sequence 169, App	469	31	57.4	80	5	US-10-688-255-8	Sequence 8, Appli
397	32	59.3	802	5	US-10-897-360-169	Sequence 169, App	470	31	57.4	81	4	US-10-424-599-278055	Sequence 278055,
398	32	59.3	802	5	US-10-165-036A-169	Sequence 169, App	471	31	57.4	86	4	US-10-424-599-220800	Sequence 220800,
399	32	59.3	802	6	US-11-129-762-169	Sequence 169, App	472	31	57.4	89	4	US-10-424-599-230390	Sequence 230390,
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401	32	59.3	815	5	US-10-450-763-46268	Sequence 46268, A	474	31	57.4	93	4	US-10-425-115-368300	Sequence 368300,
402	32	59.3	926	5	US-10-732-923-7110	Sequence 7110, App	475	31	57.4	95	4	US-10-424-599-219861	Sequence 219861,
403	32	59.3	970	4	US-10-149-310-126	Sequence 126, App	476	31	57.4	97	3	US-09-187-693-47	Sequence 47, Appl
404	32	59.3	1284	5	US-10-732-923-22580	Sequence 22580, App	477	31	57.4	97	6	US-11-021-735-47	Sequence 47, Appl
405	32	59.3	1373	4	US-10-734-564-123	Sequence 123, App	478	31	57.4	98	4	US-10-101-464A-88	Sequence 88, Appl
406	32	59.3	1497	5	US-10-484-218-18	Sequence 18, Appl	479	31	57.4	98	5	US-10-864-252-88	Sequence 88, Appl
407	32	59.3	1518	4	US-10-383-930-40	Sequence 40, Appl	480	31	57.4	104	4	US-10-276-774-1529	Sequence 1529, Ap
408	32	59.3	1518	5	US-10-797-821-40	Sequence 40, Appl	481	31	57.4	106	4	US-10-424-599-219243	Sequence 219243,
409	32	59.3	1554	4	US-10-383-930-38	Sequence 38, Appl	482	31	57.4	107	3	US-09-899-896-11	Sequence 11, Appl
410	32	59.3	1554	5	US-10-797-821-38	Sequence 38, Appl	483	31	57.4	112	4	US-10-437-963-154932	Sequence 154932,
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412	31.5	58.3	52	4	US-10-424-599-242309	Sequence 242309,	485	31	57.4	115	5	US-10-982-359-16	Sequence 16, Appl
413	31.5	58.3	208	4	US-10-221-625-68	Sequence 68, Appl	486	31	57.4	115	5	US-10-982-359-44	Sequence 44, Appl
414	31.5	58.3	208	4	US-10-408-765A-718	Sequence 718, App	487	31	57.4	116	4	US-10-269-711-19	Sequence 19, Appl
415	31.5	58.3	616	4	US-10-437-963-133917	Sequence 133917,	488	31	57.4	116	4	US-10-684-109-19	Sequence 19, Appl
416	31.5	58.3	1882	4	US-10-437-963-182883	Sequence 182883,	489	31	57.4	116	5	US-10-982-359-84	Sequence 84, Appl
417	31	57.4	8	4	US-10-160-232-17	Sequence 17, Appl	490	31	57.4	119	3	US-09-864-408A-880	Sequence 880, App
418	31	57.4	11	3	US-09-423-800-64	Sequence 64, Appl	491	31	57.4	119	4	US-10-269-010-1	Sequence 1, Appli
419	31	57.4	11	3	US-09-269-921-8	Sequence 8, Appl	492	31	57.4	119	4	US-10-268-883-3	Sequence 3, Appli
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422	31	57.4	11	4	US-10-169-003-64	Sequence 64, Appl	495	31	57.4	120	3	US-09-509-098-201	Sequence 201, App
423	31	57.4	11	4	US-10-218-253-8	Sequence 8, Appli	496	31	57.4	120	3	US-09-509-098-202	Sequence 202, App
424	31	57.4	11	4	US-10-337-981-64	Sequence 64, Appl	497	31	57.4	120	5	US-10-688-255-2	Sequence 2, Appli
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427	31	57.4	12	3	US-09-880-748-2194	Sequence 2194, App	500	31	57.4	125	5	US-10-763-539-70	Sequence 70, Appl
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429	31	57.4	12	5	US-10-683-451-11	Sequence 11, Appl	502	31	57.4	132	5	US-10-783-311-87	Sequence 87, Appl
430	31	57.4	13	5	US-10-745-775-48	Sequence 48, Appl	503	31	57.4	133	4	US-10-160-232-88	Sequence 88, Appl
431	31	57.4	13	5	US-10-783-311-93	Sequence 93, Appl	504	31	57.4	136	4	US-10-160-232-91	Sequence 91, Appl
432	31	57.4	15	5	US-10-946-647-1255	Sequence 1255, App	505	31	57.4	136	4	US-10-160-232-95	Sequence 95, Appl
433	31	57.4	18	3	US-09-880-748-2331	Sequence 2331, App	506	31	57.4	136	4	US-10-268-883-2	Sequence 2, Appli
434	31	57.4	18	4	US-10-293-418-2331	Sequence 2331, App	507	31	57.4	138	4	US-10-364-743-102	Sequence 102, App
435	31	57.4	22	3	US-09-509-098-177	Sequence 177, App	508	31	57.4	138	4	US-10-425-114-45199	Sequence 45199, A
436	31	57.4	22	3	US-09-509-098-180	Sequence 180, App	509	31	57.4	138	5	US-10-452-593-102	Sequence 102, App
437	31	57.4	22	3	US-09-509-098-181	Sequence 181, App	510	31	57.4	139	3	US-09-760-723-7	Sequence 7, Appli
438	31	57.4	22	3	US-09-509-098-182	Sequence 182, App	511	31	57.4	139	3	US-09-760-723-8	Sequence 8, Appli
439	31	57.4	22	3	US-09-509-098-183	Sequence 183, App	512	31	57.4	139	3	US-09-355-925-7	Sequence 7, Appli
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442	31	57.4	22	3	US-09-509-098-186	Sequence 186, App	515	31	57.4	139	3	US-09-269-921-108	Sequence 108, App
443	31	57.4	22	3	US-09-509-098-187	Sequence 187, App	516	31	57.4	139	3	US-09-269-921-109	Sequence 109, App
444	31	57.4	22	3	US-09-509-098-188	Sequence 188, App	517	31	57.4	139	3	US-09-269-921-110	Sequence 110, App
445	31	57.4	22	3	US-09-509-098-189	Sequence 189, App	518	31	57.4	139	3	US-09-269-921-111	Sequence 111, App
446	31	57.4	22	3	US-09-509-098-190	Sequence 190, App	519	31	57.4	139	3	US-09-269-921-112	Sequence 112, App
447	31	57.4	22	3	US-09-509-098-191	Sequence 191, App	520	31	57.4	139	3	US-09-269-921-113	Sequence 113, App
448	31	57.4	22	3	US-09-509-098-192	Sequence 192, App	521	31	57.4	139	3	US-09-269-921-114	Sequence 114, App
449	31	57.4	22	3	US-09-509-098-193	Sequence 193, App	522	31	57.4	139	3	US-09-269-921-115	Sequence 115, App
450	31	57.4	22	3	US-09-509-098-194	Sequence 194, App	523	31	57.4	139	3	US-09-269-921-116	Sequence 116, App
451	31	57.4	22	3	US-09-509-098-195	Sequence 195, App	524	31	57.4	139	3	US-09-269-921-117	Sequence 117, App
452	31	57.4	22	3	US-09-509-098-196	Sequence 196, App	525	31	57.4	139	3	US-09-269-921-118	Sequence 118, App
453	31	57.4	22	3	US-09-509-098-197	Sequence 197, App	526	31	57.4	139	3	US-09-269-921-119	Sequence 119, App
454	31	57.4	35	3	US-09-864-761-43354	Sequence 43354, A	527	31	57.4	139	3	US-09-269-921-120	Sequence 120, App
455	31	57.4	45	3	US-09-939-980-480	Sequence 480, App	528	31	57.4	139	3	US-09-269-921-121	Sequence 121, App
456	31	57.4	56	4	US-10-424-599-276514	Sequence 276514,	529	31	57.4	139	3	US-09-269-921-122	Sequence 122, App
457	31	57.4	59	4	US-10-424-599-154002	Sequence 154002,	530	31	57.4	139	3	US-09-269-921-123	Sequence 123, App
458	31	57.4	59	4	US-10-425-115-219186	Sequence 219186,	531	31	57.4	139	3	US-09-269-921-124	Sequence 124, App
459	31	57.4	60	4	US-10-424-599-279836	Sequence 279836,	532	31	57.4	139	3	US-09-269-921-125	Sequence 125, App
460	31	57.4	62	4	US-10-424-599-176492	Sequence 176492,	533	31	57.4	139	3	US-09-269-921-126	Sequence 126, App
461	31	57.4	67	4	US-10-425-115-367020	Sequence 367020,	534	31	57.4	139	3	US-09-269-921-127	Sequence 127, App
462	31	57.4	69	4	US-10-282-122A-59063	Sequence 59063, A	535	31	57.4	139	3	US-09-269-921-128	Sequence 128, App
463	31	57.4	69	4	US-10-424-599-210687	Sequence 210687,	536	31	57.4	139	3	US-09-509-098-4	Sequence 4, Appli
464	31	57.4	71	4	US-10-437-963-120167	Sequence 201667,	537	31	57.4	139	3	US-09-509-098-16	Sequence 16, Appli
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543	31	57.4	139	3	US-09-509-098-26	Sequence 26, Appl	616	31	57.4	256	4	US-10-293-418-1285	Sequence 1285, Ap
544	31	57.4	139	3	US-09-509-098-28	Sequence 28, Appl	617	31	57.4	268	4	US-10-425-114-49612	Sequence 49612, A
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552	31	57.4	139	3	US-09-509-098-44	Sequence 44, Appl	625	31	57.4	293	4	US-10-353-690-4	Sequence 4, Appl1
553	31	57.4	139	3	US-09-509-098-46	Sequence 46, Appl	626	31	57.4	293	4	US-10-684-978-6	Sequence 6, Appl1
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556	31	57.4	139	3	US-09-509-098-98	Sequence 98, Appl	629	31	57.4	317	3	US-09-393-634-60	Sequence 60, Appl
557	31	57.4	139	3	US-09-509-098-100	Sequence 100, Appl	630	31	57.4	317	3	US-09-510-332-26	Sequence 26, Appl
558	31	57.4	139	3	US-09-509-098-127	Sequence 127, Appl	631	31	57.4	317	4	US-10-383-982-60	Sequence 60, Appl
559	31	57.4	139	4	US-10-315-125-7	Sequence 7, Appl1	632	31	57.4	317	4	US-10-364-861-60	Sequence 60, Appl
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562	31	57.4	139	4	US-10-218-253-108	Sequence 108, Appl	635	31	57.4	320	4	US-10-424-599-207974	Sequence 207974, A
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565	31	57.4	139	4	US-10-218-253-111	Sequence 111, Appl	638	31	57.4	323	4	US-10-413-699B-114	Sequence 114, App
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571	31	57.4	139	4	US-10-218-253-117	Sequence 117, Appl	644	31	57.4	367	4	US-10-289-762-562	Sequence 562, App
572	31	57.4	139	4	US-10-218-253-118	Sequence 118, Appl	645	31	57.4	368	4	US-10-369-493-21307	Sequence 21307, A
573	31	57.4	139	4	US-10-218-253-119	Sequence 119, Appl	646	31	57.4	383	5	US-10-493-759-2	Sequence 2, Appl1
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575	31	57.4	139	4	US-10-218-253-121	Sequence 121, Appl	648	31	57.4	386	5	US-10-631-467-1497	Sequence 1497, Ap
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577	31	57.4	139	4	US-10-218-253-123	Sequence 123, Appl	650	31	57.4	392	6	US-11-097-143-10095	Sequence 10095, A
578	31	57.4	139	4	US-10-218-253-124	Sequence 124, Appl	651	31	57.4	396	4	US-10-193-616-14	Sequence 14, Appl
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601	31	57.4	184	4	US-10-424-599-150592	Sequence 150592, A	674	31	57.4	466	4	US-10-032-585-7878	Sequence 7878, Ap
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605	31	57.4	210	4	US-10-767-701-39411	Sequence 39411, A	678	31	57.4	490	2	US-08-781-986A-5212	Sequence 5212, Ap
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607	31	57.4	236	4	US-10-425-115-201663	Sequence 201663, A	680	31	57.4	491	4	US-10-437-963-102565	Sequence 102565, A
608	31	57.4	239	4	US-10-437-963-116524	Sequence 116524, A	681	31	57.4	491	4	US-10-425-115-333659	Sequence 333659, A
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610	31	57.4	244	3	US-09-880-748-1881	Sequence 1881, Ap	683	31	57.4	494	4	US-10-369-493-8951	Sequence 8951, Ap
611	31	57.4	244	4	US-10-293-418-1881	Sequence 1881, Ap	684	31	57.4	503	3	US-09-071-035-360	Sequence 360, App

685	31	57.4	503	4	US-10-206-576-360	Sequence 360, App	758	31	57.4	871	4	US-10-425-115-222052	Sequence 222052,
686	31	57.4	503	4	US-10-289-762-784	Sequence 784, App	759	31	57.4	884	6	US-11-013-314-44	Sequence 44, Appl
687	31	57.4	503	5	US-10-912-362-360	Sequence 360, App	760	31	57.4	909	4	US-10-424-599-259000	Sequence 259000,
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693	31	57.4	540	3	US-09-984-245-134	Sequence 134, App	766	31	57.4	948	5	US-10-872-155-194	Sequence 194, App
694	31	57.4	540	3	US-09-966-262-134	Sequence 134, App	767	31	57.4	949	4	US-10-437-963-118800	Sequence 118800,
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696	31	57.4	540	4	US-10-059-395-134	Sequence 134, App	769	31	57.4	981	4	US-10-424-599-150591	Sequence 150591,
697	31	57.4	540	4	US-10-143-090-134	Sequence 134, App	770	31	57.4	996	4	US-10-335-977-9519	Sequence 9519, Ap
698	31	57.4	540	5	US-10-960-251-134	Sequence 134, App	771	31	57.4	1014	4	US-10-101-464A-807	Sequence 807, App
699	31	57.4	540	5	US-10-472-533-348	Sequence 348, App	772	31	57.4	1014	5	US-10-864-252-807	Sequence 807, App
700	31	57.4	543	5	US-10-501-282-4464	Sequence 4464, Ap	773	31	57.4	1024	4	US-10-211-962-86	Sequence 86, Appl
701	31	57.4	547	4	US-10-043-344-149	Sequence 149, App	774	31	57.4	1045	4	US-10-369-493-1836	Sequence 1836, Ap
702	31	57.4	550	6	US-11-097-143-26679	Sequence 26679, A	775	31	57.4	1045	4	US-10-041-018-199	Sequence 199, App
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704	31	57.4	553	4	US-10-369-493-14320	Sequence 14320, A	777	31	57.4	1045	4	US-10-041-018-264	Sequence 264, App
705	31	57.4	556	3	US-09-819-266-28	Sequence 28, Appl	778	31	57.4	1045	4	US-10-041-018-309	Sequence 309, App
706	31	57.4	561	5	US-10-781-979-7	Sequence 7, Appli	779	31	57.4	1045	4	US-10-041-018-336	Sequence 336, App
707	31	57.4	568	5	US-10-501-282-4466	Sequence 4466, Ap	780	31	57.4	1074	3	US-09-071-035-358	Sequence 358, App
708	31	57.4	571	5	US-10-501-282-4468	Sequence 4468, Ap	781	31	57.4	1074	3	US-09-071-035-394	Sequence 394, App
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710	31	57.4	576	4	US-10-369-493-11697	Sequence 11697, A	783	31	57.4	1074	5	US-10-206-576-394	Sequence 394, App
711	31	57.4	576	4	US-10-369-493-14740	Sequence 14740, A	784	31	57.4	1074	5	US-10-912-362-358	Sequence 358, App
712	31	57.4	576	4	US-10-369-493-15216	Sequence 15216, A	785	31	57.4	1081	4	US-10-912-362-394	Sequence 394, App
713	31	57.4	578	4	US-10-600-070-123	Sequence 123, App	786	31	57.4	1081	4	US-10-369-493-3989	Sequence 3989, Ap
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715	31	57.4	583	4	US-10-282-122A-74149	Sequence 74149, A	788	31	57.4	1150	6	US-11-018-615-18	Sequence 18, Appl
716	31	57.4	583	4	US-10-474-776-714	Sequence 714, App	789	31	57.4	1150	6	US-11-018-615-19	Sequence 19, Appl
717	31	57.4	583	5	US-10-472-928-3804	Sequence 3804, Ap	790	31	57.4	1187	3	US-10-282-122A-44786	Sequence 44786, A
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719	31	57.4	589	3	US-09-750-986D-30	Sequence 30, Appl	792	31	57.4	1252	3	US-09-137-531-9	Sequence 9, Appli
720	31	57.4	619	5	US-09-738-626-5308	Sequence 5308, Ap	793	31	57.4	1308	5	US-10-719-993-754	Sequence 754, App
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722	31	57.4	631	4	US-10-043-344-111	Sequence 111, App	795	31	57.4	1332	4	US-10-041-856-3	Sequence 3, Appli
723	31	57.4	631	4	US-10-043-344-115	Sequence 115, App	796	31	57.4	1332	4	US-10-041-856-5	Sequence 5, Appli
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725	31	57.4	654	4	US-10-043-344-12	Sequence 12, Appl	798	31	57.4	1332	6	US-11-073-203-3	Sequence 3, Appli
726	31	57.4	660	4	US-10-043-344-8	Sequence 8, Appli	799	31	57.4	1332	6	US-11-073-203-5	Sequence 5, Appli
727	31	57.4	660	4	US-10-043-344-10	Sequence 10, Appl	800	31	57.4	1365	5	US-10-383-930-39	Sequence 39, Appl
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729	31	57.4	683	3	US-09-841-132-357	Sequence 357, App	802	31	57.4	1413	5	US-10-719-993-755	Sequence 755, App
730	31	57.4	683	5	US-10-872-155-357	Sequence 357, App	803	31	57.4	1419	5	US-10-197-220-173	Sequence 173, App
731	31	57.4	700	4	US-10-437-963-180018	Sequence 180018,	804	31	57.4	1419	6	US-11-109-468-173	Sequence 173, App
732	31	57.4	713	4	US-10-282-122A-46856	Sequence 46856, A	805	31	57.4	1420	5	US-10-450-763-50282	Sequence 50282, A
733	31	57.4	721	4	US-10-094-749-3065	Sequence 3065, Ap	806	31	57.4	1435	4	US-10-238-075-941	Sequence 941, App
734	31	57.4	735	4	US-10-156-761-13908	Sequence 13908, A	807	31	57.4	1452	5	US-10-719-993-753	Sequence 753, App
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737	31	57.4	762	4	US-10-437-963-141715	Sequence 141715,	810	31	57.4	1655	5	US-10-450-763-45314	Sequence 45314, A
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741	31	57.4	782	4	US-10-270-710-29	Sequence 29, Appl	814	31	57.4	1770	4	US-10-467-534-21	Sequence 21, Appl
742	31	57.4	782	4	US-10-270-859-29	Sequence 29, Appl	815	31	57.4	1770	5	US-10-872-155-444	Sequence 444, App
743	31	57.4	782	4	US-10-270-846-29	Sequence 29, Appl	816	31	57.4	1776	3	US-09-841-132-179	Sequence 179, App
744	31	57.4	784	5	US-10-946-647-1415	Sequence 1415, Ap	817	31	57.4	1776	6	US-10-872-155-179	Sequence 179, App
745	31	57.4	784	5	US-10-946-647-1442	Sequence 1442, Ap	818	31	57.4	1809	6	US-11-097-143-10836	Sequence 10836, A
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748	31	57.4	801	4	US-10-600-070-127	Sequence 127, App	821	31	57.4	2158	5	US-10-739-930-5650	Sequence 5650, Ap
749	31	57.4	801	4	US-10-600-070-129	Sequence 129, App	822	31	57.4	2399	4	US-10-282-122A-59054	Sequence 59054, A
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751	31	57.4	801	5	US-10-739-930-5771	Sequence 5771, Ap	824	31	57.4	2504	4	US-10-262-794A-12	Sequence 12, Appl
752	31	57.4	822	4	US-10-425-115-323759	Sequence 323759,	825	31	57.4	2504	4	US-10-754-115-59	Sequence 59, Appl
753	31	57.4	824	3	US-09-866-582-34	Sequence 34, Appl	826	31	57.4	2504	4	US-10-282-122A-76865	Sequence 76865, A
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755	31	57.4	848	4	US-10-284-084-58	Sequence 58, Appl	828	30.5	56.5	239	4	US-10-000-903-12	Sequence 12, Appl
756	31	57.4	857	4	US-10-282-122A-76365	Sequence 76365, A	829	30.5	56.5	239	5	US-10-899-771-12	Sequence 12, Appl
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832	30.5	56.5	318	3	US-09-769-787-192	Sequence 192, App	905	30	55.6	129	4	US-10-364-743-117	Sequence 117, App
833	30.5	56.5	318	4	US-10-702-305A-14	Sequence 14, Appl	906	30	55.6	129	5	US-10-452-593-117	Sequence 117, App
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843	30	55.6	13	3	US-09-909-460-10	Sequence 10, Appl	916	30	55.6	156	5	US-10-197-816-20	Sequence 20, Appl
844	30	55.6	13	3	US-09-872-836-10	Sequence 10, Appl	917	30	55.6	160	4	US-10-425-115-315605	Sequence 315605, A
845	30	55.6	13	3	US-09-906-206A-16	Sequence 16, Appl	918	30	55.6	161	5	US-10-994-726-494	Sequence 494, App
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852	30	55.6	18	5	US-10-734-661A-20	Sequence 20, Appl	925	30	55.6	179	4	US-10-104-047-2630	Sequence 2630, Ap
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857	30	55.6	38	3	US-09-378-638-7	Sequence 7, Appl	930	30	55.6	189	5	US-10-491-823-111	Sequence 111, App
858	30	55.6	38	5	US-10-785-819-143	Sequence 143, App	931	30	55.6	191	5	US-10-732-923-7778	Sequence 7778, Ap
859	30	55.6	38	5	US-10-785-819-157	Sequence 157, App	932	30	55.6	198	4	US-10-425-115-305260	Sequence 305260, A
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871	30	55.6	78	4	US-10-291-265-442	Sequence 442, App	944	30	55.6	222	4	US-10-282-122A-55455	Sequence 55455, A
872	30	55.6	78	4	US-10-291-265-914	Sequence 914, App	945	30	55.6	230	3	US-09-820-339A-43	Sequence 8, Appl
873	30	55.6	80	4	US-10-424-599-205296	Sequence 205296, A	946	30	55.6	231	3	US-09-898-837A-43	Sequence 43, Appl
874	30	55.6	80	4	US-10-335-977-7163	Sequence 7163, Ap	947	30	55.6	233	5	US-10-512-004-1	Sequence 1, Appl
875	30	55.6	80	4	US-10-425-115-219781	Sequence 219781, A	948	30	55.6	234	3	US-09-898-837A-48	Sequence 48, Appl
876	30	55.6	87	4	US-10-425-115-23273	Sequence 23273, A	949	30	55.6	235	3	US-09-820-339A-6	Sequence 6, Appl
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882	30	55.6	100	4	US-10-767-701-49678	Sequence 49678, A	955	30	55.6	250	4	US-10-293-418-1484	Sequence 1484, Ap
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884	30	55.6	112	4	US-10-424-599-259538	Sequence 259538, A	957	30	55.6	252	6	US-11-090-847-118	Sequence 118, App
885	30	55.6	114	5	US-10-472-928-3456	Sequence 3456, Ap	958	30	55.6	258	4	US-10-425-114-41180	Sequence 41180, A
886	30	55.6	117	4	US-10-424-599-215403	Sequence 215403, A	959	30	55.6	258	4	US-10-425-114-67960	Sequence 67960, A
887	30	55.6	118	4	US-10-160-506-74	Sequence 74, Appl	960	30	55.6	268	6	US-11-090-847-126	Sequence 126, App
888	30	55.6	118	4	US-10-449-379-74	Sequence 74, Appl	961	30	55.6	268	4	US-10-282-122A-50288	Sequence 50288, A
889	30	55.6	118	4	US-10-688-015-74	Sequence 74, Appl	962	30	55.6	278	4	US-10-424-599-154207	Sequence 154207, A
890	30	55.6	118	4	US-10-160-505-74	Sequence 74, Appl	963	30	55.6	278	4	US-10-660-236-22	Sequence 22, Appl
891	30	55.6	118	5	US-10-617-320-2670	Sequence 2670, Ap	964	30	55.6	279	3	US-09-815-242-5308	Sequence 5308, Ap
892	30	55.6	120	4	US-10-292-486-42	Sequence 42, Appl	965	30	55.6	280	4	US-10-424-599-154203	Sequence 154203, A
893	30	55.6	120	4	US-10-425-115-232814	Sequence 232814, A	966	30	55.6	282	4	US-10-758-979-47	Sequence 47, Appl
894	30	55.6	124	4	US-10-437-963-116681	Sequence 116681, A	967	30	55.6	285	4	US-10-051-874-89	Sequence 89, Appl
895	30	55.6	125	4	US-10-041-860-42	Sequence 42, Appl	968	30	55.6	288	3	US-09-895-913A-42	Sequence 42, Appl
896	30	55.6	125	4	US-10-041-860-207	Sequence 207, App	969	30	55.6	289	5	US-10-938-370-8	Sequence 8, Appl
897	30	55.6	125	4	US-10-665-383-62	Sequence 62, Appl	970	30	55.6	293	4	US-10-451-467A-524	Sequence 524, App
898	30	55.6	126	3	US-09-840-459-74	Sequence 74, Appl	971	30	55.6	293	5	US-10-741-849-7156	Sequence 7156, Ap
899	30	55.6	126	4	US-10-766-773-74	Sequence 74, Appl	972	30	55.6	294	3	US-09-815-242-12323	Sequence 12323, A
900	30	55.6	126	4	US-10-766-610-74	Sequence 74, Appl	973	30	55.6	294	4	US-10-282-122A-44364	Sequence 44364, A
901	30	55.6	126	4	US-10-733-563-74	Sequence 74, Appl	974	30	55.6	294	5	US-10-857-625-633	Sequence 633, App
902	30	55.6	127	4	US-10-424-599-172106	Sequence 172106, A	975	30	55.6	295	4	US-10-282-122A-51507	Sequence 51507, A
903	30	55.6	127	4	US-10-425-115-285987	Sequence 285987, A	976	30	55.6	299	3	US-09-789-210-66	Sequence 66, Appl

977 30 55.6 300 4 US-10-282-122A-52772 Sequence 52772, A  
978 30 55.6 305 4 US-10-282-122A-60078 Sequence 60078, A  
979 30 55.6 306 4 US-10-767-701-43963 Sequence 43963, A  
980 30 55.6 307 3 US-09-825-882-18 Sequence 18, Appl  
981 30 55.6 307 4 US-10-017-161-1786 Sequence 1786, Ap  
982 30 55.6 307 4 US-10-292-798-1442 Sequence 1442, Ap  
983 30 55.6 307 4 US-10-343-650A-680 Sequence 680, App  
984 30 55.6 307 4 US-10-724-208-18 Sequence 18, Appl  
985 30 55.6 307 4 US-10-770-127-189 Sequence 189, App  
986 30 55.6 307 5 US-10-724-209-18 Sequence 18, Appl  
987 30 55.6 307 5 US-10-986-871-18 Sequence 18, Appl  
988 30 55.6 310 4 US-10-408-692-16 Sequence 16, Appl  
989 30 55.6 310 4 US-10-424-599-172105 Sequence 172105,  
990 30 55.6 316 4 US-10-156-761-11745 Sequence 11745, A  
991 30 55.6 319 5 US-10-015-989A-12 Sequence 12, Appl  
992 30 55.6 322 4 US-10-424-599-252016 Sequence 252016,  
993 30 55.6 325 4 US-10-282-122A-43629 Sequence 43629, A  
994 30 55.6 328 4 US-10-282-122A-67144 Sequence 67144, A  
995 30 55.6 328 5 US-10-015-989A-11 Sequence 11, Appl  
996 30 55.6 331 5 US-10-450-763-32305 Sequence 32305, A  
997 30 55.6 332 3 US-09-769-787-190 Sequence 190, App  
998 30 55.6 332 4 US-10-421-654-10 Sequence 10, Appl  
999 30 55.6 332 5 US-10-472-928-592 Sequence 592, App  
1000 30 55.6 332 5 US-10-796-907-10 Sequence 10, Appl

## ALIGNMENTS

RESULT 1  
US-09-764-304-8  
; Sequence 8, Application US/09764304  
; Patent No. US20020026036A1  
; GENERAL INFORMATION:  
; APPLICANT: SHITARA, KENYA  
; APPLICANT: HANAI, NOBUO  
; APPLICANT: HASEGAWA, MAMORU  
; APPLICANT: MIYAJI, HIROMASA  
; APPLICANT: KUWANA, YOSHIHISA  
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY  
; FILE REFERENCE: 249-101  
; CURRENT APPLICATION NUMBER: US/09/764,304  
; EARLIER FILING DATE: 2001-01-19  
; EARLIER APPLICATION NUMBER: 09/225,322  
; EARLIER FILING DATE: 1999-01-05  
; EARLIER FILING DATE: 1995-05-31  
; EARLIER FILING DATE: 1994-08-17  
; EARLIER APPLICATION NUMBER: US07/947,674  
; EARLIER FILING DATE: 1992-09-17  
; EARLIER APPLICATION NUMBER: JP 3-238375  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 8  
; LENGTH: 130  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: CDNA KM-641  
US-09-764-304-8

Query Match 100.0%; Score 54; DB 3; Length 130;  
Best Local Similarity 100.0%; Pred. No. 0.16;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 VKLGTGYFDS 10  
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Db 109 VKLGTGYFDS 118

RESULT 2  
US-09-764-304-18  
; Sequence 18, Application US/09764304  
; Patent No. US20020026036A1  
; GENERAL INFORMATION:  
; APPLICANT: SHITARA, KENYA  
; APPLICANT: HANAI, NOBUO  
; APPLICANT: HASEGAWA, MAMORU  
; APPLICANT: MIYAJI, HIROMASA  
; APPLICANT: KUWANA, YOSHIHISA  
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY  
; FILE REFERENCE: 249-101  
; CURRENT APPLICATION NUMBER: US/09/764,304  
; EARLIER FILING DATE: 2001-01-19  
; EARLIER APPLICATION NUMBER: 09/225,322  
; EARLIER FILING DATE: 1999-01-05  
; EARLIER FILING DATE: 1995-05-31  
; EARLIER FILING DATE: 1994-08-17  
; EARLIER APPLICATION NUMBER: US07/947,674  
; EARLIER FILING DATE: 1992-09-17  
; EARLIER APPLICATION NUMBER: JP 3-238375  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 18  
; LENGTH: 130  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: CDNA KM-641  
US-09-764-304-18

Query Match 100.0%; Score 54; DB 3; Length 130;  
Best Local Similarity 100.0%; Pred. No. 0.16;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 VKLGTGYFDS 10  
|||  
Db 109 VKLGTGYFDS 118

RESULT 3  
US-10-265-713-8  
; Sequence 8, Application US/10265713  
; Publication No. US20030095964A1  
; GENERAL INFORMATION:  
; APPLICANT: SHITARA, KENYA  
; APPLICANT: HANAI, NOBUO  
; APPLICANT: HASEGAWA, MAMORU  
; APPLICANT: MIYAJI, HIROMASA  
; APPLICANT: KUWANA, YOSHIHISA  
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY  
; FILE REFERENCE: 249-101  
; CURRENT APPLICATION NUMBER: US/10/265,713  
; CURRENT FILING DATE: 2002-10-08  
; PRIOR APPLICATION NUMBER: US/09/225,322  
; PRIOR FILING DATE: 1999-01-05  
; PRIOR APPLICATION NUMBER: US 08/454,680  
; PRIOR FILING DATE: 1995-05-31  
; PRIOR APPLICATION NUMBER: US 08/408,133  
; PRIOR FILING DATE: 1995-03-21  
; PRIOR APPLICATION NUMBER: US 08/292,178  
; PRIOR FILING DATE: 1994-08-17  
; PRIOR APPLICATION NUMBER: US07/947,674  
; PRIOR FILING DATE: 1992-09-17  
; PRIOR APPLICATION NUMBER: JP 3-238375  
; PRIOR FILING DATE: 1991-09-18  
; NUMBER OF SEQ ID NOS: 19



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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: cDNA KM-641
US-10-265-713-8

Query Match      100.0%; Score 54; DB 4; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VKLGTYFYFDS 10
Db      109 VKLGTYFYFDS 118

RESULT 4
US-10-265-713-18
; Sequence 18, Application US/10265713
; Publication No. US20030095964A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KIWANA, YOSHIHISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/10/265,713
; CURRENT FILING DATE: 2002-10-08
; PRIOR APPLICATION NUMBER: US/09/225,322
; PRIOR FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: US 08/454,680
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
; PRIOR APPLICATION NUMBER: US07/947,674
; PRIOR FILING DATE: 1992-09-17
; PRIOR APPLICATION NUMBER: JP 3-238375
; PRIOR FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: cDNA KM-641
US-10-265-713-18

Query Match      100.0%; Score 54; DB 4; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VKLGTYFYFDS 10
Db      109 VKLGTYFYFDS 118

RESULT 5
US-10-166-626-8
; Sequence 8, Application US/10166626
; Publication No. US20030166876A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KIWANA, YOSHIHISA
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; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/10/166,626
; CURRENT FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: US/09/225,322B
; PRIOR FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: US 08/454,680
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
; PRIOR APPLICATION NUMBER: US07/947,674
; PRIOR FILING DATE: 1992-09-17
; PRIOR APPLICATION NUMBER: JP 3-238375
; PRIOR FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: cDNA KM-641
US-10-166-626-8

Query Match      100.0%; Score 54; DB 4; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VKLGTYFYFDS 10
Db      109 VKLGTYFYFDS 118

RESULT 6
US-10-166-626-18
; Sequence 18, Application US/10166626
; Publication No. US20030166876A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KIWANA, YOSHIHISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/10/166,626
; CURRENT FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: US/09/225,322B
; PRIOR FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: US 08/454,680
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
; PRIOR APPLICATION NUMBER: US07/947,674
; PRIOR FILING DATE: 1992-09-17
; PRIOR APPLICATION NUMBER: JP 3-238375
; PRIOR FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: cDNA KM-641
US-10-166-626-18

Query Match      100.0%; Score 54; DB 4; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.16;
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Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 VKLGTYYFDS 10  
Db 109 VKLGTYYFDS 118

RESULT 7  
US-10-831-070-102  
; Sequence 102, Application US/10831070  
; Publication No. US20050112612A1  
; GENERAL INFORMATION:  
; APPLICANT: Kladenhammer, Todd R.  
; APPLICANT: Russell, William M.  
; APPLICANT: Alterman, Eric  
; APPLICANT: Cano, Raul J.  
; APPLICANT: Hamrick, Alice  
; TITLE OF INVENTION: Lactobacillus Acidophilus Nucleic Acid  
; TITLE OF INVENTION: Sequences Encoding Cell Surface Homologues and Uses  
; TITLE OF INVENTION: Therefore  
; FILE REFERENCE: 5051,690  
; CURRENT APPLICATION NUMBER: US/10/831,070  
; CURRENT FILING DATE: 2004-04-23  
; NUMBER OF SEQ ID NOS: 308  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 102  
; LENGTH: 368  
; TYPE: PRT  
; ORGANISM: Lactobacillus acidophilus  
US-10-831-070-102

Query Match 75.9%; Score 41; DB 5; Length 368;  
Best Local Similarity 100.0%; Pred. No. 74;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GTYYFDS 10  
Db 229 GTYYFDS 235  
RESULT 8  
US-10-739-930-10028  
; Sequence 10028, Application US/10739930  
; Publication No. US20040216190A1  
; GENERAL INFORMATION:  
; APPLICANT: Kovalic, David K.  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH  
; TITLE OF INVENTION: PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT  
; FILE REFERENCE: 38-21(53377)B  
; CURRENT APPLICATION NUMBER: US/10/739,930  
; CURRENT FILING DATE: 2003-12-18  
; NUMBER OF SEQ ID NOS: 11088  
; SEQ ID NO 10028  
; LENGTH: 446  
; TYPE: PRT  
; ORGANISM: Triticum aestivum  
; FEATURE:  
; OTHER INFORMATION: Clone ID: TRIAE-23APR03-C244\_147.p  
US-10-739-930-10028

Query Match 74.1%; Score 40; DB 5; Length 446;  
Best Local Similarity 80.0%; Pred. No. 1.3e+02;  
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 VKLGTYYFDS 10  
Db 195 VILGQYYFDS 204

RESULT 9  
US-10-425-115-365506  
; Sequence 365506, Application US/10425115  
; Publication No. US20040214272A1

; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants  
; FILE REFERENCE: 38-21(53222)B  
; CURRENT APPLICATION NUMBER: US/10/425,115  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 369326  
; SEQ ID NO 365506  
; LENGTH: 195  
; TYPE: PRT  
; ORGANISM: Zea mays  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)..(195)  
; OTHER INFORMATION: unsure at all Xaa locations  
; FEATURE:  
; OTHER INFORMATION: Clone ID: MET4577\_96506C.1.pep  
US-10-425-115-365506

Query Match 72.2%; Score 39; DB 4; Length 195;  
Best Local Similarity 87.5%; Pred. No. 87;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 LGTYFYFDS 10  
Db 145 LGQYYFDS 152

RESULT 10  
US-10-425-115-204796  
; Sequence 204796, Application US/10425115  
; Publication No. US20040214272A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants  
; FILE REFERENCE: 38-21(53222)B  
; CURRENT APPLICATION NUMBER: US/10/425,115  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 369326  
; SEQ ID NO 204796  
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; TYPE: PRT  
; ORGANISM: Zea mays  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)..(206)  
; OTHER INFORMATION: unsure at all Xaa locations  
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; OTHER INFORMATION: Clone ID: MET4577\_118363C.1.pep  
US-10-425-115-204796

Query Match 72.2%; Score 39; DB 4; Length 206;  
Best Local Similarity 87.5%; Pred. No. 92;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 LGTYFYFDS 10  
Db 169 LGQYYFDS 176

RESULT 11  
US-10-425-115-311275  
; Sequence 311275, Application US/10425115  
; Publication No. US20040214272A1  
; GENERAL INFORMATION:

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; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 311275
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_46938C.1.pep
US-10-425-115-311275

Query Match          72.2%; Score 39; DB 4; Length 341;
Best Local Similarity 87.5%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 LGTYFYDS 10
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Db 159 LGQYFYDS 166

RESULT 12
US-10-425-115-204801
; Sequence 204801, Application US/10425115
; Publication No. US2004021427A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 204801
; LENGTH: 424
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(424)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_118368C.1.pep
US-10-425-115-204801

Query Match          72.2%; Score 39; DB 4; Length 424;
Best Local Similarity 87.5%; Pred. No. 1.9e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 LGTYFYDS 10
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Db 150 LGQYFYDS 157

RESULT 13
US-10-425-114-46787
; Sequence 46787, Application US/10425114
; Publication No. US2004003488A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
```

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; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 46787
; LENGTH: 427
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700799057_FLI.pep
US-10-425-114-46787

Query Match          72.2%; Score 39; DB 4; Length 427;
Best Local Similarity 87.5%; Pred. No. 1.9e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 LGTYFYDS 10
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Db 150 LGQYFYDS 157

RESULT 14
US-10-437-963-139528
; Sequence 139528, Application US/10437963
; Publication No. US2004012343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 139528
; LENGTH: 435
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_40810C.1.pep
US-10-437-963-139528

Query Match          72.2%; Score 39; DB 4; Length 435;
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Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 LGTYFYDS 10
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Db 146 LGQYFYDS 153

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; Sequence 204798, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
```

```
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 204798
; LENGTH: 572
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)-(572)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_118365C.1.pep
US-10-425-115-204798

Query Match          72.2%; Score 39; DB 4; Length 572;
Best Local Similarity 87.5%; Pred. No. 2.5e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 LGTYFFDS 10
Db 355 LGQYFFDS 362

RESULT 16
US-10-424-599-145556
; Sequence 145556, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 145556
; LENGTH: 48
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_102456C.1.pep
US-10-424-599-145556

Query Match          70.4%; Score 38; DB 4; Length 48;
Best Local Similarity 87.5%; Pred. No. 32;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 KLQTYFFD 9
Db 12 KLQTYLFD 19

RESULT 17
US-09-995-749A-2
; Sequence 2, Application US/09995749A
; Patent No. US2002015568A1
; GENERAL INFORMATION:
; APPLICANT: VAN GEEL-SCHUTTEN, GERRITDINA HENDRIKA
; APPLICANT: DIJKHUIZEN LUBBERT
; APPLICANT: RAHAQUI, HAKIM
; APPLICANT: LEER, ROBERT-JAN
; TITLE OF INVENTION: NOVEL GLUCOSYLTRANSFERASES
; FILE REFERENCE: B043388-CIP
; CURRENT APPLICATION NUMBER: US/09/995,749A
; CURRENT FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: 09/604,957
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: EPO 00201871.1
; PRIOR FILING DATE: 2000-05-25
; NUMBER OF SEQ ID NOS: 19
```

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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 1781
; TYPE: PRT
; ORGANISM: Lactobacillus reuteri
US-09-995-749A-2

Query Match          70.4%; Score 38; DB 3; Length 1781;
Best Local Similarity 85.7%; Pred. No. 1.2e+03;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 GTYYFDS 10
Db 1724 GTYYFDN 1730

RESULT 18
US-10-243-552-339
; Sequence 339, Application US/10243552
; Publication No. US20030224379A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Zhiwei
; APPLICANT: Weng, Gezhi
; APPLICANT: Ma, Yunqing
; TITLE OF INVENTION: Novel Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 807A
; CURRENT APPLICATION NUMBER: US/10/243,552
; CURRENT FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 60/322,511
; PRIOR FILING DATE: 2001-09-13
; PRIOR APPLICATION NUMBER: PCT/US00/35017
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: US 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: PCT/US01/03800
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: US 09/496,914
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: US 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: PCT/US01/04927
; PRIOR FILING DATE: 2001-02-26
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 998
; SOFTWARE: pt_FL_genes Version 5.0
; SEQ ID NO 339
; LENGTH: 179
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-243-552-339

Query Match          68.5%; Score 37; DB 4; Length 179;
Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 LGTYFFDS 10
Db 150 LGTYSDS 157

RESULT 19
US-11-090-847-130
; Sequence 130, Application US/11090847
; Publication No. US20050215770A1
```

; GENERAL INFORMATION:  
; APPLICANT: Bell, et al.  
; TITLE OF INVENTION: Antibodies Against Nogo Receptor  
; FILE REFERENCE: PF609  
; CURRENT APPLICATION NUMBER: US/11/090,847  
; CURRENT FILING DATE: 2005-03-25  
; PRIOR APPLICATION NUMBER: US 60/556,386  
; PRIOR FILING DATE: 2004-03-26  
; NUMBER OF SEQ ID NOS: 249  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 130  
; LENGTH: 254  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: scFv protein NGF2G02  
US-11-090-847-130

Query Match 68.5%; Score 37; DB 6; Length 254;  
Best Local Similarity 85.7%; Pred. No. 2.5e+02;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 GTYTFDS 10  
|:|||||  
DB 101 GSYTFDS 107

RESULT 20  
US-09-833-245-1319  
; Sequence 1319, Application US/09833245  
; Publication No. US20040010134A1  
; GENERAL INFORMATION:  
; APPLICANT: Human Genome Sciences, Inc.  
; TITLE OF INVENTION: Albumin Fusion Proteins  
; FILE REFERENCE: PF546PCT  
; CURRENT APPLICATION NUMBER: US/09/833,245  
; CURRENT FILING DATE: 2001-04-12  
; PRIOR APPLICATION NUMBER: 60/229, 358  
; PRIOR FILING DATE: 2000-04-12  
; PRIOR APPLICATION NUMBER: 60/256, 931  
; PRIOR FILING DATE: 2000-12-21  
; PRIOR APPLICATION NUMBER: 60/199, 384  
; PRIOR FILING DATE: 2000-04-25  
; NUMBER OF SEQ ID NOS: 2267  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1319  
; LENGTH: 380  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-833-245-1319

Query Match 68.5%; Score 37; DB 3; Length 380;  
Best Local Similarity 87.5%; Pred. No. 3.7e+02;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 LGTYTFDS 10  
|||||  
DB 183 LGTYFSDS 190

RESULT 21  
US-10-724-972A-4330  
; Sequence 4330, Application US/10724972A  
; Publication No. US20040147734A1  
; GENERAL INFORMATION:  
; APPLICANT: Doucette-Stamm, Lynn  
; APPLICANT: Bush, David  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS  
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: PATH03-16  
; CURRENT APPLICATION NUMBER: US/10/724,972A  
; CURRENT FILING DATE: 2003-12-01  
; PRIOR APPLICATION NUMBER: 09/450,969

; PRIOR FILING DATE: 1999-11-29  
; PRIOR APPLICATION NUMBER: 09/134,001  
; PRIOR FILING DATE: 1998-08-13  
; PRIOR APPLICATION NUMBER: 60/064,964  
; PRIOR FILING DATE: 1997-11-08  
; PRIOR APPLICATION NUMBER: 60/055,779  
; PRIOR FILING DATE: 1997-08-14  
; NUMBER OF SEQ ID NOS: 7544  
; SEQ ID NO 4330  
; LENGTH: 388  
; TYPE: PRT  
; ORGANISM: S.epidermidis  
US-10-724-972A-4330

Query Match 68.5%; Score 37; DB 4; Length 388;  
Best Local Similarity 66.7%; Pred. No. 3.8e+02;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 KLGTYTFDS 10  
::|||||  
DB 250 RVGTYFDS 258

RESULT 22  
US-10-484-218-14  
; Sequence 14, Application US/10484218  
; Publication No. US20050059633A1  
; GENERAL INFORMATION:  
; APPLICANT: VAN GEEL-SCHUTTEN, GERRITDINA HENDRIKA  
; TITLE OF INVENTION: GLUCANS AND GLUCANSUCRASES DERIVED FROM  
; TITLE OF INVENTION: LACTIC ACID BACTERIA  
; FILE REFERENCE: 2001-1316  
; CURRENT APPLICATION NUMBER: US/10/484,218  
; CURRENT FILING DATE: 2004-01-20  
; PRIOR APPLICATION NUMBER: PCT/NL02/00495  
; PRIOR FILING DATE: 2002-07-22  
; PRIOR APPLICATION NUMBER: EP 01202752.0  
; PRIOR FILING DATE: 2001-07-20  
; PRIOR APPLICATION NUMBER: EP 01202841.1  
; PRIOR FILING DATE: 2001-07-25  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 14  
; LENGTH: 1771  
; TYPE: PRT  
; ORGANISM: Lactobacillus reuteri  
US-10-484-218-14

Query Match 68.5%; Score 37; DB 5; Length 1771;  
Best Local Similarity 72.7%; Pred. No. 1.7e+03;  
Matches 8; Conservative 1; Mismatches 0; Indels 2; Gaps 1;

QY 1 VKLG--TYTFD 9  
||:|||||  
DB 1710 VKIGNDTYTFD 1720

RESULT 23  
US-10-424-599-250992  
; Sequence 250992, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa Thomas J  
; APPLICANT: Kovalic David K  
; APPLICANT: Zhou Yihua  
; APPLICANT: Cao Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 250992

```

; LENGTH: 73
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_68675C.1.pcp
US-10-424-599-250992

Query Match          66.7%; Score 36; DB 4; Length 73;
Best Local Similarity 60.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 VKLGTYYFDS 10
Db 42 IYFSTYYFDS 51

RESULT 24
US-10-081-816-35
; Sequence 35, Application US/10081816
; Publication No. US20030045472A1
; GENERAL INFORMATION:
; APPLICANT: Axel, Richard
; APPLICANT: Scott, Kristin
; TITLE OF INVENTION: Chemosensory Gene Family Encoding Gustatory And Olfactory Receptors
; FILE OF INVENTION: Uses Thereof
; FILE REFERENCE: 0575/64019-A/JPM/ADM
; CURRENT APPLICATION NUMBER: US/10/081,816
; CURRENT FILING DATE: 2002-02-22
; PRIOR APPLICATION NUMBER: 60/271,319
; PRIOR FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 35
; LENGTH: 361
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-10-081-816-35

Query Match          66.7%; Score 36; DB 4; Length 361;
Best Local Similarity 75.0%; Pred. No. 5.2e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 LGTYTFDS 10
Db 21 LNTYTFDT 28

RESULT 25
US-10-447-328-42
; Sequence 42, Application US/10447328
; Publication No. US20040003419A1
; GENERAL INFORMATION:
; APPLICANT: Carlson, John R.
; APPLICANT: Clyne, Peter J.
; APPLICANT: Warr, Coral G.
; APPLICANT: Yale University
; TITLE OF INVENTION: No. US20040003419A1el Taste Receptors in Drosophila
; FILE REFERENCE: 44574-5072
; CURRENT APPLICATION NUMBER: US/10/447,328
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: US/09/593,519
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/138,668
; PRIOR FILING DATE: 1999-06-14
; PRIOR APPLICATION NUMBER: US 60/181,704
; PRIOR FILING DATE: 2000-02-10
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 42
; LENGTH: 361
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-10-447-328-42

```

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Query Match          66.7%; Score 36; DB 4; Length 361;
Best Local Similarity 75.0%; Pred. No. 5.2e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 LGTYTFDS 10
Db 21 LNTYTFDT 28

RESULT 26
US-11-097-143-29412
; Sequence 29412, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; TITLE OF INVENTION: DROSOPHILA GENES.
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-26
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29412
; LENGTH: 361
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-11-097-143-29412

Query Match          66.7%; Score 36; DB 6; Length 361;
Best Local Similarity 75.0%; Pred. No. 5.2e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 LGTYTFDS 10
Db 21 LNTYTFDT 28

RESULT 27
US-10-320-797-3156
; Sequence 3156, Application US/10320797
; Publication No. US20040014955A1
; GENERAL INFORMATION:
; APPLICANT: Eroshkin, Alexey M.
; APPLICANT: Zamudio, Carlos
; TITLE OF INVENTION: IDENTIFICATION OF ESSENTIAL GENES OF CRYPTOCOCCUS NEOFORMANS AND
; TITLE OF INVENTION: METHODS OF USE
; FILE REFERENCE: 10182-021-999
; CURRENT APPLICATION NUMBER: US/10/320,797
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: 60/341,261
; PRIOR FILING DATE: 2001-12-17
; NUMBER OF SEQ ID NOS: 3361
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3156

```

```
; LENGTH: 387
; TYPE: PRT
; ORGANISM: Cryptococcus neoformans
US-10-320-797-3156

Query Match          66.7%; Score 36; DB 4; Length 387;
Best Local Similarity 70.0%; Pred. No. 5.6e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 VKLGYTFDS 10
Db 24 IKLGLTYRDS 33

RESULT 28
US-10-369-493-11075
; Sequence 11075, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 11075
; LENGTH: 433
; TYPE: PRT
; ORGANISM: Ferroplasma acidarmanus
US-10-369-493-11075

Query Match          66.7%; Score 36; DB 4; Length 433;
Best Local Similarity 66.7%; Pred. No. 6.3e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 KLGTYTFDS 10
Db 136 KIGTYNYDS 144

RESULT 29
US-10-424-599-154451
; Sequence 154451, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 154451
; LENGTH: 440
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(440)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_110491C.1.pep
US-10-424-599-154451
```

```
Query Match          66.7%; Score 36; DB 4; Length 440;
Best Local Similarity 75.0%; Pred. No. 6.4e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 LGTYTFDS 10
Db 154 LGQYTFDT 161

RESULT 30
US-10-782-141-21
; Sequence 21, Application US/10782141
; Publication No. US20040197917A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Hargiss, Tracy
; APPLICANT: Koziel, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: AXMI-014, A Delta-Endotoxin Gene and
; TITLE OF INVENTION: Methods for Its Use
; FILE REFERENCE: 045600/274143
; CURRENT APPLICATION NUMBER: US/10/782,141
; CURRENT FILING DATE: 2004-02-20
; PRIOR APPLICATION NUMBER: 60/448,632
; PRIOR FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 675
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-782-141-21

Query Match          66.7%; Score 36; DB 4; Length 675;
Best Local Similarity 85.7%; Pred. No. 9.7e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GTTYFDS 10
Db 627 GNYTFDS 633

RESULT 31
US-10-782-096-22
; Sequence 22, Application US/10782096
; Publication No. US20040210564A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Hargiss, Tracy
; APPLICANT: Koziel, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: AXMI-009, A Delta-Endotoxin Gene and
; TITLE OF INVENTION: Methods for Its Use
; FILE REFERENCE: 045600/274148
; CURRENT APPLICATION NUMBER: US/10/782,096
; CURRENT FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: 60/448,633
; PRIOR FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 675
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-782-096-22

Query Match          66.7%; Score 36; DB 4; Length 675;
Best Local Similarity 85.7%; Pred. No. 9.7e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

QY 4 GTYYFDS 10  
|:|:|:|:|  
Db 627 GNYFDS 633

RESULT 32

US-10-781-979-23  
; Sequence 23, Application US/10781979  
; Publication No. US20040250311A1  
; GENERAL INFORMATION:  
; APPLICANT: Carozzi, Nadine  
; APPLICANT: Hargiss, Tracy  
; APPLICANT: Kozziel, Michael G.  
; APPLICANT: Duck, Nicholas B.  
; APPLICANT: Cart, Brian  
; TITLE OF INVENTION: AXMT-008, A Delta-Endotoxin Gene and  
; TITLE OF INVENTION: Methods for Its Use  
; FILE REFERENCE: 045600/274147  
; CURRENT APPLICATION NUMBER: US/10/781,979  
; CURRENT FILING DATE: 2004-02-20  
; PRIOR APPLICATION NUMBER: 60/448,797  
; PRIOR FILING DATE: 2003-02-20  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 23  
; TYPE: PRT  
; LENGTH: 675  
; ORGANISM: Bacillus thuringiensis  
US-10-781-979-23

Query Match 66.7%; Score 36; DB 5; Length 675;  
Best Local Similarity 85.7%; Pred. No. 9.7e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GTYYFDS 10  
|:|:|:|:|  
Db 627 GNYFDS 633

RESULT 33

US-10-425-115-270359  
; Sequence 270359, Application US/10425115  
; Publication No. US20040214272A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants  
; FILE REFERENCE: 38-21(53222)B  
; CURRENT APPLICATION NUMBER: US/10/425,115  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 369326  
; SEQ ID NO 270359  
; LENGTH: 859  
; TYPE: PRT  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: MRT4577\_178164C.1.pap  
US-10-425-115-270359

Query Match 66.7%; Score 36; DB 4; Length 859;  
Best Local Similarity 85.7%; Pred. No. 1.2e+03;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 GTYYFDS 10  
|:|:|:|:|  
Db 430 GTHYFDS 436

RESULT 34

US-10-437-963-106243

; Sequence 106243, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 106243  
; LENGTH: 931  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)..(931)  
; OTHER INFORMATION: unsure at all xaa locations  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_10705C.1.pap  
US-10-437-963-106243

Query Match 66.7%; Score 36; DB 4; Length 931;  
Best Local Similarity 85.7%; Pred. No. 1.3e+03;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 GTYYFDS 10  
|:|:|:|:|  
Db 471 GTHYFDS 477

RESULT 35

US-09-880-748-2132  
; Sequence 2132, Application US/09880748  
; Publication No. US20030059937A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS  
; FILE REFERENCE: PF523  
; CURRENT APPLICATION NUMBER: US/09/880,748  
; CURRENT FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/212,210  
; PRIOR FILING DATE: 2000-06-15  
; PRIOR APPLICATION NUMBER: 60/240,816  
; PRIOR FILING DATE: 2000-10-17  
; PRIOR APPLICATION NUMBER: 60/276,248  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/277,379  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/293,499  
; PRIOR FILING DATE: 2001-05-25  
; NUMBER OF SEQ ID NOS: 3239  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2132  
; LENGTH: 23  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-880-748-2132

Query Match 64.8%; Score 35; DB 3; Length 23;  
Best Local Similarity 55.6%; Pred. No. 51;  
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 VKLGTYYFD 9  
: :|:|:|:|  
Db 14 INVGPYFD 22



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RESULT 36
US-09-880-748-3076
; Sequence 3076, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3076
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-3076

Query Match          64.8%; Score 35; DB 3; Length 23;
Best Local Similarity 55.6%; Pred. No. 51;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      1 VKLGYTFD 9
      : : |||||
DB      14 INVGPFYFD 22

RESULT 37
US-10-293-418-2132
; Sequence 2132, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2132
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-2132

Query Match          64.8%; Score 35; DB 4; Length 23;
Best Local Similarity 55.6%; Pred. No. 51;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      1 VKLGYTFD 9
      : : |||||
DB      14 INVGPFYFD 22
```

```
Best Local Similarity 55.6%; Pred. No. 51;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      1 VKLGYTFD 9
      : : |||||
DB      14 INVGPFYFD 22

RESULT 38
US-10-293-418-3076
; Sequence 3076, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 3076
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-3076

Query Match          64.8%; Score 35; DB 4; Length 23;
Best Local Similarity 55.6%; Pred. No. 51;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      1 VKLGYTFD 9
      : : |||||
DB      14 INVGPFYFD 22

RESULT 39
US-10-437-963-168775
; Sequence 168775, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 168775
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Oryza sativa
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; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1) .. (118)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_67257C.1.pap
US-10-437-963-168775

Query Match          64.8%; Score 35; DB 4; Length 118;
Best Local Similarity 60.0%; Pred. No. 2.7e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 VKLGTYYFDS 10
Db 42 VGVSTYYFDT 51

RESULT 40
US-10-638-265-38
; Sequence 38, Application US/10638265
; Publication No. US20050031614A1
; GENERAL INFORMATION:
; APPLICANT: Roskos, Lorin
; APPLICANT: Foltz, Ian
; APPLICANT: King, Chadwick
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PARATHYROID
; TITLE OF INVENTION: HORMONE (PTH) AND USES THEREOF
; FILE REFERENCE: ABGENIX.092A
; CURRENT APPLICATION NUMBER: US/10/638,265
; CURRENT FILING DATE: 2003-08-08
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Homosapien
US-10-638-265-38

Query Match          64.8%; Score 35; DB 5; Length 123;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TTYFDS 10
Db 100 TTYFDS 105

RESULT 41
US-10-638-265-46
; Sequence 46, Application US/10638265
; Publication No. US20050031614A1
; GENERAL INFORMATION:
; APPLICANT: Roskos, Lorin
; APPLICANT: Foltz, Ian
; APPLICANT: King, Chadwick
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PARATHYROID
; TITLE OF INVENTION: HORMONE (PTH) AND USES THEREOF
; FILE REFERENCE: ABGENIX.092A
; CURRENT APPLICATION NUMBER: US/10/638,265
; CURRENT FILING DATE: 2003-08-08
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 46
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Homosapien
US-10-638-265-46

Query Match          64.8%; Score 35; DB 5; Length 123;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TTYFDS 10
Db 100 TTYFDS 105

RESULT 42
US-10-638-265-50
; Sequence 50, Application US/10638265
; Publication No. US20050031614A1
; GENERAL INFORMATION:
; APPLICANT: Roskos, Lorin
; APPLICANT: Foltz, Ian
; APPLICANT: King, Chadwick
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PARATHYROID
; TITLE OF INVENTION: HORMONE (PTH) AND USES THEREOF
; FILE REFERENCE: ABGENIX.092A
; CURRENT APPLICATION NUMBER: US/10/638,265
; CURRENT FILING DATE: 2003-08-08
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 50
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Homosapien
US-10-638-265-50

Query Match          64.8%; Score 35; DB 5; Length 123;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TTYFDS 10
Db 100 TTYFDS 105

RESULT 43
US-10-638-265-54
; Sequence 54, Application US/10638265
; Publication No. US20050031614A1
; GENERAL INFORMATION:
; APPLICANT: Roskos, Lorin
; APPLICANT: Foltz, Ian
; APPLICANT: King, Chadwick
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PARATHYROID
; TITLE OF INVENTION: HORMONE (PTH) AND USES THEREOF
; FILE REFERENCE: ABGENIX.092A
; CURRENT APPLICATION NUMBER: US/10/638,265
; CURRENT FILING DATE: 2003-08-08
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 54
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Homosapien
US-10-638-265-54

Query Match          64.8%; Score 35; DB 5; Length 123;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TTYFDS 10
Db 100 TTYFDS 105

RESULT 44
US-10-425-115-263537
; Sequence 263537, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
```

```

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 263537
; LENGTH: 138
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(138)
; OTHER INFORMATION: unsure at all xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_171959C.1.pep
US-10-425-115-263537

Query Match 64.8%; Score 35; DB 4; Length 138;
Best Local Similarity 70.0%; Pred. No. 3e+02;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 VKLGTYYFDS 10
Db 107 VNLGTYVESS 116

RESULT 45
US-10-424-599-178546
; Sequence 178546, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 178546
; LENGTH: 139
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_132244C.1.pep
US-10-424-599-178546

Query Match 64.8%; Score 35; DB 4; Length 139;
Best Local Similarity 60.0%; Pred. No. 3e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 VKLGTYYFDS 10
Db 42 VAVGVYWFDS 51

RESULT 46
US-10-424-599-179462
; Sequence 179462, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28

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; LENGTH: 255
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-4

Query Match      64.8%; Score 35; DB 3; Length 255;
Best Local Similarity 55.6%; Pred. No. 5.5e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      1 VKLGTYTFD 9
      : : | |||
Db      112 INVGPYTFD 120

RESULT 49
US-09-880-748-1054
; Sequence 1054, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLYS
; FILE REFERENCE: PFS23
; CURRENT APPLICATION NUMBER: US/09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1054
; LENGTH: 255
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1054

Query Match      64.8%; Score 35; DB 3; Length 255;
Best Local Similarity 55.6%; Pred. No. 5.5e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      1 VKLGTYTFD 9
      : : | |||
Db      112 INVGPYTFD 120

RESULT 50
US-09-880-748-1056
; Sequence 1056, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLYS
; FILE REFERENCE: PFS23
; CURRENT APPLICATION NUMBER: US/09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
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OM protein - protein search, using sw model

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Title: US-10-089-500-5  
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Sequence: 1 VKLGYYFDS 10

Scoring table: BLOSUM62

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Searched: 184161 seqs, 31191982 residues

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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1	54	100.0	10	6	US-10-473-037-5
2	54	100.0	119	6	US-10-473-037-9
3	54	100.0	119	6	US-10-473-037-49
4	54	100.0	130	7	US-11-228-293-8
5	54	100.0	130	7	US-11-228-293-18
6	54	100.0	130	7	US-11-228-319-8
7	54	100.0	130	7	US-11-228-319-18
8	54	100.0	138	6	US-10-473-037-1
9	37	68.5	123	7	US-11-102-512-57
10	35	64.8	23	7	US-11-054-515-2132
11	35	64.8	23	7	US-11-054-515-3076
12	35	64.8	23	7	US-11-266-444-2132
13	35	64.8	23	7	US-11-266-444-3076
14	35	64.8	123	6	US-10-956-008-38
15	35	64.8	123	6	US-10-956-008-46
16	35	64.8	123	6	US-10-956-008-50
17	35	64.8	123	6	US-10-956-008-54
18	35	64.8	124	7	US-11-102-512-61
19	35	64.8	226	6	US-10-793-626-1932
20	35	64.8	255	7	US-11-054-515-4
21	35	64.8	255	7	US-11-054-515-1054
22	35	64.8	255	7	US-11-054-515-1056
23	35	64.8	255	7	US-11-054-515-1065
24	35	64.8	255	7	US-11-054-515-1786
25	35	64.8	255	7	US-11-266-444-4

25	64.8	255	7	US-11-266-444-1054	Sequence 1054, Ap
26	64.8	255	7	US-11-266-444-1056	Sequence 1056, Ap
27	64.8	255	7	US-11-266-444-1065	Sequence 1065, Ap
28	64.8	255	7	US-11-266-444-1065	Sequence 1065, Ap
29	64.8	255	7	US-11-266-444-1786	Sequence 1786, Ap
30	64.8	258	7	US-11-054-515-1773	Sequence 1773, Ap
31	64.8	258	7	US-11-266-444-1773	Sequence 1773, Ap
32	64.8	287	7	US-11-087-099-10597	Sequence 10597, A
33	63.0	128	7	US-11-221-281-44	Sequence 44, Appl
34	63.0	161	7	US-11-096-568A-18183	Sequence 18183, A
35	63.0	208	7	US-11-096-568A-18181	Sequence 18181, A
36	63.0	565	7	US-11-074-176-98	Sequence 98, Appl
37	61.1	12	7	US-11-201-825-41	Sequence 41, Appl
38	61.1	17	6	US-10-473-037-4	Sequence 4, Appl
39	61.1	97	7	US-11-054-669-48	Sequence 48, Appl
40	61.1	97	7	US-11-093-274-32	Sequence 32, Appl
41	61.1	116	7	US-11-102-512-30	Sequence 30, Appl
42	61.1	116	7	US-11-102-512-31	Sequence 31, Appl
43	61.1	116	7	US-11-102-512-64	Sequence 64, Appl
44	61.1	116	7	US-11-102-512-76	Sequence 76, Appl
45	61.1	116	7	US-11-102-512-77	Sequence 77, Appl
46	61.1	118	6	US-10-925-360A-208	Sequence 208, App
47	61.1	119	7	US-11-049-536-524	Sequence 524, App
48	61.1	119	7	US-11-199-739-524	Sequence 524, App
49	61.1	121	7	US-11-201-825-14	Sequence 14, Appl
50	61.1	121	7	US-11-201-825-29	Sequence 29, Appl
51	61.1	123	7	US-11-049-536-238	Sequence 238, App
52	61.1	123	7	US-11-049-536-378	Sequence 378, App
53	61.1	123	7	US-11-049-536-398	Sequence 398, App
54	61.1	123	7	US-11-199-739-238	Sequence 238, App
55	61.1	123	7	US-11-199-739-378	Sequence 378, App
56	61.1	123	7	US-11-199-739-398	Sequence 398, App
57	61.1	123	7	US-11-102-512-15	Sequence 15, Appl
58	61.1	123	7	US-11-102-512-56	Sequence 56, Appl
59	61.1	124	7	US-11-049-536-310	Sequence 310, Appl
60	61.1	124	7	US-11-199-739-310	Sequence 310, Appl
61	61.1	132	7	US-11-096-568A-30044	Sequence 30044, A
62	61.1	208	7	US-11-128-440-4	Sequence 4, Appl
63	61.1	226	7	US-11-096-568A-30043	Sequence 30043, A
64	61.1	247	7	US-11-024-959-440	Sequence 440, App
65	61.1	254	7	US-11-087-099-5469	Sequence 5469, Ap
66	61.1	258	7	US-11-201-825-8	Sequence 8, Appl
67	61.1	258	7	US-11-201-825-25	Sequence 25, Appl
68	61.1	349	7	US-11-087-099-8908	Sequence 8908, Ap
69	61.1	561	7	US-11-096-568A-8968	Sequence 8968, Ap
70	61.1	687	7	US-11-096-568A-8967	Sequence 8967, Ap
71	61.1	707	7	US-11-096-568A-6966	Sequence 6966, Ap
72	61.1	3194	7	US-11-052-554A-90	Sequence 90, Appl
73	59.3	19	7	US-11-054-515-3113	Sequence 3113, Ap
74	59.3	19	7	US-11-266-444-3113	Sequence 3113, Ap
75	59.3	125	7	US-11-049-536-214	Sequence 214, App
76	59.3	125	7	US-11-199-739-214	Sequence 214, App
77	59.3	126	7	US-11-049-536-422	Sequence 422, App
78	59.3	126	7	US-11-199-739-422	Sequence 422, App
79	59.3	127	7	US-11-049-536-454	Sequence 454, App
80	59.3	127	7	US-11-199-739-454	Sequence 454, App
81	59.3	256	7	US-11-054-515-1967	Sequence 1967, Ap
82	59.3	256	7	US-11-266-444-1967	Sequence 1967, Ap
83	59.3	338	7	US-11-052-554A-228	Sequence 228, App
84	59.3	499	6	US-10-793-626-1484	Sequence 1484, Ap
85	59.3	802	7	US-11-037-243-113	Sequence 113, App
86	59.3	815	7	US-11-072-512-2496	Sequence 2496, Ap
87	59.3	967	7	US-11-124-367A-312	Sequence 312, App
88	59.3	1369	7	US-11-124-367A-311	Sequence 311, App
89	57.4	8	7	US-11-250-411-17	Sequence 17, Appl
90	57.4	11	7	US-11-226-325-10	Sequence 10, Appl
91	57.4	12	7	US-11-054-515-2194	Sequence 2194, Ap
92	57.4	12	7	US-11-266-444-2194	Sequence 2194, Ap
93	57.4	18	7	US-11-054-515-2931	Sequence 2931, Ap
94	57.4	18	7	US-11-266-444-2931	Sequence 2931, Ap
95	57.4	22	7	US-11-226-325-177	Sequence 177, App
96	57.4	22	7	US-11-226-325-180	Sequence 180, App
97	57.4	22	7	US-11-226-325-181	Sequence 181, App
98	57.4	22	7	US-11-226-325-182	Sequence 182, App

99	31	57.4	22	7	US-11-226-325-183	Sequence 183, App	172	31	57.4	510	7	US-11-096-568A-28407	Sequence 28407, A
100	31	57.4	22	7	US-11-226-325-184	Sequence 184, App	173	31	57.4	550	7	US-11-096-568A-18027	Sequence 18027, A
101	31	57.4	22	7	US-11-226-325-185	Sequence 185, App	174	31	57.4	577	7	US-11-096-568A-1515	Sequence 1515, Ap
102	31	57.4	22	7	US-11-226-325-186	Sequence 186, App	175	31	57.4	589	7	US-11-087-099-12436	Sequence 12436, A
103	31	57.4	22	7	US-11-226-325-187	Sequence 187, App	176	31	57.4	694	7	US-11-096-568A-26859	Sequence 26859, A
104	31	57.4	22	7	US-11-226-325-188	Sequence 188, App	177	31	57.4	779	7	US-11-096-568A-32052	Sequence 32052, Ap
105	31	57.4	22	7	US-11-226-325-189	Sequence 189, App	178	31	57.4	782	7	US-11-087-099-3299	Sequence 3299, Ap
106	31	57.4	22	7	US-11-226-325-190	Sequence 190, App	179	31	57.4	824	7	US-11-096-568A-26858	Sequence 26858, A
107	31	57.4	22	7	US-11-226-325-191	Sequence 191, App	180	31	57.4	916	7	US-11-096-568A-32061	Sequence 32061, A
108	31	57.4	22	7	US-11-226-325-192	Sequence 192, App	181	31	57.4	939	7	US-11-096-568A-32060	Sequence 32060, A
109	31	57.4	22	7	US-11-226-325-193	Sequence 193, App	182	31	57.4	1308	7	US-11-124-367A-396	Sequence 396, App
110	31	57.4	22	7	US-11-226-325-194	Sequence 194, App	183	31	57.4	1332	7	US-11-124-367A-394	Sequence 394, App
111	31	57.4	22	7	US-11-226-325-195	Sequence 195, App	184	31	57.4	1413	7	US-11-124-367A-395	Sequence 395, App
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113	31	57.4	22	7	US-11-226-325-197	Sequence 197, App	186	31	57.4	1770	7	US-11-103-957-21	Sequence 21, Appl
114	31	57.4	116	6	US-10-925-368A-209	Sequence 209, App	187	31	57.4	1770	7	US-11-018-868-17	Sequence 17, Appl
115	31	57.4	117	7	US-11-250-411-99	Sequence 99, Appl	188	31	57.4	2399	7	US-11-018-868-17	Sequence 92, Appl
116	31	57.4	117	7	US-11-250-411-102	Sequence 102, App	189	31	57.4	2504	6	US-10-647-956A-8	Sequence 8, Appl
117	31	57.4	117	7	US-11-250-411-106	Sequence 106, App	190	30.5	56.5	318	6	US-10-873-528-192	Sequence 192, App
118	31	57.4	120	7	US-11-226-325-198	Sequence 198, App	191	30.5	56.5	318	7	US-11-052-554A-233	Sequence 233, App
119	31	57.4	120	7	US-11-226-325-201	Sequence 201, App	192	30	55.6	9	7	US-11-218-813-95	Sequence 95, Appl
120	31	57.4	120	7	US-11-226-325-202	Sequence 202, App	193	30	55.6	10	7	US-11-157-494-10	Sequence 10, Appl
121	31	57.4	123	7	US-11-102-512-18	Sequence 18, Appl	194	30	55.6	15	7	US-11-054-515-2803	Sequence 2803, Ap
122	31	57.4	124	7	US-11-102-512-68	Sequence 68, Appl	195	30	55.6	15	7	US-11-266-444-2803	Sequence 2803, Ap
123	31	57.4	124	7	US-11-102-513-74	Sequence 74, Appl	196	30	55.6	78	7	US-11-000-463-442	Sequence 442, App
124	31	57.4	125	7	US-11-096-074-57	Sequence 57, Appl	197	30	55.6	78	7	US-11-000-463-914	Sequence 914, App
125	31	57.4	125	7	US-11-095-822-57	Sequence 57, Appl	198	30	55.6	102	6	US-10-467-657-1986	Sequence 1986, Ap
126	31	57.4	127	6	US-10-993-543-164	Sequence 164, App	199	30	55.6	116	7	US-11-102-512-21	Sequence 21, Appl
127	31	57.4	133	6	US-10-993-543-4	Sequence 4, Appl	200	30	55.6	116	7	US-11-102-512-44	Sequence 44, Appl
128	31	57.4	136	7	US-11-250-411-88	Sequence 88, Appl	201	30	55.6	118	7	US-11-157-494-26	Sequence 26, Appl
129	31	57.4	136	7	US-11-250-411-91	Sequence 91, Appl	202	30	55.6	118	7	US-11-218-813-74	Sequence 74, Appl
130	31	57.4	136	7	US-11-250-411-95	Sequence 95, Appl	203	30	55.6	119	6	US-10-834-397-26	Sequence 26, Appl
131	31	57.4	139	7	US-11-226-325-4	Sequence 4, Appl	204	30	55.6	120	7	US-11-102-512-17	Sequence 17, Appl
132	31	57.4	139	7	US-11-226-325-16	Sequence 16, Appl	205	30	55.6	120	7	US-11-221-281-42	Sequence 42, Appl
133	31	57.4	139	7	US-11-226-325-18	Sequence 18, Appl	206	30	55.6	153	6	US-10-793-626-2826	Sequence 2826, Ap
134	31	57.4	139	7	US-11-226-325-20	Sequence 20, Appl	207	30	55.6	163	6	US-10-467-657-52	Sequence 52, Appl
135	31	57.4	139	7	US-11-226-325-22	Sequence 22, Appl	208	30	55.6	163	6	US-10-467-657-208	Sequence 208, App
136	31	57.4	139	7	US-11-226-325-24	Sequence 24, Appl	209	30	55.6	163	6	US-10-467-657-3562	Sequence 3562, Ap
137	31	57.4	139	7	US-11-226-325-26	Sequence 26, Appl	210	30	55.6	163	6	US-10-467-657-6462	Sequence 6462, Ap
138	31	57.4	139	7	US-11-226-325-28	Sequence 28, Appl	211	30	55.6	163	6	US-10-467-657-8396	Sequence 8396, Ap
139	31	57.4	139	7	US-11-226-325-30	Sequence 30, Appl	212	30	55.6	179	6	US-10-467-657-8396	Sequence 8396, Ap
140	31	57.4	139	7	US-11-226-325-32	Sequence 32, Appl	213	30	55.6	250	7	US-11-072-512-2630	Sequence 2630, Ap
141	31	57.4	139	7	US-11-226-325-34	Sequence 34, Appl	214	30	55.6	250	7	US-11-054-515-1484	Sequence 1484, Ap
142	31	57.4	139	7	US-11-226-325-36	Sequence 36, Appl	215	30	55.6	288	7	US-11-096-568A-31161	Sequence 31161, A
143	31	57.4	139	7	US-11-226-325-38	Sequence 38, Appl	216	30	55.6	294	7	US-11-087-099-788	Sequence 788, App
144	31	57.4	139	7	US-11-226-325-40	Sequence 40, Appl	217	30	55.6	294	7	US-11-087-099-5652	Sequence 5652, Ap
145	31	57.4	139	7	US-11-226-325-42	Sequence 42, Appl	218	30	55.6	294	7	US-11-096-568A-31160	Sequence 31160, A
146	31	57.4	139	7	US-11-226-325-44	Sequence 44, Appl	219	30	55.6	305	7	US-11-096-568A-11194	Sequence 11194, A
147	31	57.4	139	7	US-11-226-325-46	Sequence 46, Appl	220	30	55.6	311	7	US-11-096-568A-11193	Sequence 11193, A
148	31	57.4	139	7	US-11-226-325-48	Sequence 48, Appl	221	30	55.6	323	6	US-11-096-568A-31159	Sequence 31159, A
149	31	57.4	139	7	US-11-226-325-50	Sequence 50, Appl	222	30	55.6	323	6	US-10-873-528-190	Sequence 190, App
150	31	57.4	139	7	US-11-226-325-98	Sequence 98, Appl	223	30	55.6	342	7	US-11-013-711-133	Sequence 133, App
151	31	57.4	139	7	US-11-226-325-100	Sequence 100, App	224	30	55.6	342	7	US-11-013-711-134	Sequence 134, App
152	31	57.4	139	7	US-11-226-325-127	Sequence 127, App	225	30	55.6	342	7	US-11-087-099-4274	Sequence 4274, Ap
153	31	57.4	181	7	US-11-098-686-10422	Sequence 10422, A	226	30	55.6	343	7	US-11-080-991-86	Sequence 86, Appl
154	31	57.4	181	7	US-11-096-568A-16565	Sequence 16565, A	227	30	55.6	343	7	US-11-019-711-130	Sequence 130, App
155	31	57.4	195	7	US-11-096-568A-14824	Sequence 14824, A	228	30	55.6	353	7	US-11-096-568A-11192	Sequence 11192, A
156	31	57.4	207	7	US-11-096-568A-16564	Sequence 16564, A	229	30	55.6	357	6	US-10-506-454-1670	Sequence 1670, Ap
157	31	57.4	235	7	US-11-096-568A-16563	Sequence 16563, A	230	30	55.6	393	6	US-10-821-234-1043	Sequence 1043, Ap
158	31	57.4	244	7	US-11-054-515-1881	Sequence 1881, Ap	231	30	55.6	457	6	US-10-467-657-604	Sequence 604, App
159	31	57.4	256	7	US-11-054-515-1285	Sequence 1285, Ap	232	30	55.6	503	6	US-10-873-528-74	Sequence 74, Appl
160	31	57.4	256	7	US-11-266-444-1285	Sequence 1285, Ap	233	30	55.6	546	7	US-11-096-568A-28401	Sequence 28401, A
161	31	57.4	256	7	US-11-087-099-1255	Sequence 1255, A	234	30	55.6	546	7	US-11-096-568A-28400	Sequence 28400, A
162	31	57.4	256	7	US-11-087-099-256	Sequence 256, App	235	30	55.6	572	7	US-11-052-554A-129	Sequence 129, App
163	31	57.4	327	7	US-11-087-099-256	Sequence 256, App	236	30	55.6	614	6	US-11-096-568A-28399	Sequence 28399, A
164	31	57.4	335	7	US-11-096-568A-11912	Sequence 11912, A	237	30	55.6	846	6	US-10-517-939-90	Sequence 90, Appl
165	31	57.4	362	7	US-11-087-099-10906	Sequence 10906, A	238	30	55.6	877	6	US-10-821-234-960	Sequence 960, App
166	31	57.4	382	7	US-11-087-099-3182	Sequence 3182, Ap	239	30	55.6	1750	7	US-11-087-099-12397	Sequence 12397, A
167	31	57.4	395	7	US-11-096-568A-11911	Sequence 11911, A	240	29.5	54.6	319	6	US-10-506-454-445	Sequence 445, App
168	31	57.4	430	7	US-11-096-568A-18028	Sequence 18028, A	241	29.5	54.6	403	7	US-11-146-428-90	Sequence 90, Appl
169	31	57.4	434	7	US-11-096-568A-11910	Sequence 11910, A	242	29.5	54.6	448	7	US-11-052-554A-65	Sequence 65, Appl
170	31	57.4	473	7	US-11-096-568A-28409	Sequence 28409, A	243	29	53.7	12	7	US-11-054-515-2207	Sequence 2207, Ap
171	31	57.4	480	7	US-11-096-568A-28408	Sequence 28408, A	244	29	53.7	12	7	US-11-266-444-2207	Sequence 2207, Ap

245	29	53.7	16	7	US-11-171-567-163	Sequence 163, App	318	29	53.7	590	5	US-09-940-308-2	Sequence 2, Appli
246	29	53.7	102	6	US-10-997-2018-6	Sequence 6, Appli	319	29	53.7	621	7	US-10-793-626-2614	Sequence 2614, Ap
247	29	53.7	116	7	US-11-102-512-7	Sequence 7, Appli	320	29	53.7	700	7	US-11-096-568A-29838	Sequence 29838, A
248	29	53.7	116	7	US-11-102-512-22	Sequence 22, Appli	321	29	53.7	707	7	US-11-072-512-3162	Sequence 3162, Ap
249	29	53.7	116	7	US-11-102-512-25	Sequence 25, Appli	322	29	53.7	745	7	US-11-087-099-5760	Sequence 5760, Ap
250	29	53.7	116	7	US-11-102-512-72	Sequence 72, Appli	323	29	53.7	794	6	US-10-793-626-1050	Sequence 1050, Ap
251	29	53.7	117	7	US-11-102-512-12	Sequence 12, Appli	324	29	53.7	1034	7	US-11-103-957-11	Sequence 11, Appl
252	29	53.7	120	7	US-11-171-567-200	Sequence 200, App	325	29	53.7	1034	7	US-11-018-868-20	Sequence 20, Appl
253	29	53.7	121	7	US-11-102-512-19	Sequence 19, Appli	326	29	53.7	1076	7	US-11-098-686-11338	Sequence 11338, A
254	29	53.7	122	7	US-11-102-512-75	Sequence 75, Appli	327	29	53.7	1190	7	US-11-096-568A-28022	Sequence 28022, A
255	29	53.7	124	7	US-11-102-512-71	Sequence 71, Appli	328	29	53.7	1316	7	US-11-087-099-10229	Sequence 10229, A
256	29	53.7	129	6	US-10-475-075-243	Sequence 743, App	329	29	53.7	1351	7	US-11-129-741-2937	Sequence 2937, Ap
257	29	53.7	129	6	US-10-475-075-513	Sequence 513, App	330	29	53.7	1351	7	US-11-129-741-2947	Sequence 2947, Ap
258	29	53.7	130	7	US-11-049-536-386	Sequence 386, App	331	29	53.7	1355	7	US-11-096-568A-28021	Sequence 28021, A
259	29	53.7	130	7	US-11-096-568A-8386	Sequence 8386, Ap	332	29	53.7	1356	7	US-11-129-741-2939	Sequence 2939, Ap
260	29	53.7	130	7	US-11-199-739-386	Sequence 386, App	333	29	53.7	1356	7	US-11-129-741-2943	Sequence 2943, Ap
261	29	53.7	155	7	US-11-013-592-24	Sequence 24, Appli	334	29	53.7	1356	7	US-11-129-741-2943	Sequence 2943, Ap
262	29	53.7	201	5	US-09-940-308-5	Sequence 5, Appli	335	29	53.7	1356	7	US-11-129-741-2945	Sequence 2945, Ap
263	29	53.7	225	7	US-11-096-568A-17620	Sequence 17620, A	336	29	53.7	1356	7	US-11-129-741-2949	Sequence 2949, Ap
264	29	53.7	227	7	US-11-024-959-316	Sequence 316, App	337	29	53.7	1356	7	US-11-129-741-2951	Sequence 2951, Ap
265	29	53.7	227	6	US-10-793-626-162	Sequence 162, App	338	29	53.7	1356	7	US-11-129-741-4245	Sequence 4245, Ap
266	29	53.7	240	7	US-11-054-515-2013	Sequence 2013, Ap	339	29	53.7	1362	6	US-10-895-064-420	Sequence 420, App
267	29	53.7	240	7	US-11-266-444-2013	Sequence 2013, Ap	340	29	53.7	1362	7	US-11-129-741-420	Sequence 28020, A
268	29	53.7	242	7	US-11-096-568A-17619	Sequence 17619, A	341	29	53.7	1366	7	US-11-096-568A-28020	Sequence 28020, A
269	29	53.7	247	7	US-11-054-515-1899	Sequence 1899, Ap	342	29	53.7	1385	7	US-11-129-741-3655	Sequence 3655, Ap
270	29	53.7	247	7	US-11-266-444-1899	Sequence 1899, Ap	343	29	53.7	1720	7	US-11-182-016-19	Sequence 19, Appl
271	29	53.7	276	7	US-11-087-099-8417	Sequence 8417, Ap	344	29	53.7	3568	6	US-10-453-372-194	Sequence 194, Appl
272	29	53.7	321	7	US-11-096-568A-3008	Sequence 3008, Ap	345	29	53.7	3570	6	US-10-453-372-178	Sequence 178, App
273	29	53.7	321	7	US-11-096-568A-3011	Sequence 3011, Ap	346	29	53.7	3570	6	US-10-453-372-196	Sequence 196, App
274	29	53.7	321	7	US-09-940-308-8	Sequence 8, Appli	347	29	53.7	3570	6	US-10-453-372-198	Sequence 198, App
275	29	53.7	326	7	US-11-098-686-10624	Sequence 10624, A	348	29	53.7	3570	6	US-10-453-372-200	Sequence 200, App
276	29	53.7	327	7	US-11-098-686-10156	Sequence 10156, A	349	29	53.7	3570	6	US-10-453-372-202	Sequence 202, App
277	29	53.7	328	6	US-10-518-752-9	Sequence 9, Appli	350	29	53.7	3570	6	US-10-453-372-204	Sequence 204, App
278	29	53.7	332	6	US-10-895-064-22	Sequence 22, Appli	351	29	53.7	3570	6	US-10-453-372-206	Sequence 206, App
279	29	53.7	332	6	US-10-895-064-23	Sequence 23, Appli	352	29	53.7	4868	7	US-11-044-111-24	Sequence 24, Appl
280	29	53.7	332	7	US-11-129-741-22	Sequence 22, Appli	353	29	51.9	11	6	US-10-665-658-51	Sequence 51, Appl
281	29	53.7	332	7	US-11-129-741-23	Sequence 23, Appli	354	29	51.9	11	6	US-10-665-658-52	Sequence 52, Appl
282	29	53.7	334	6	US-10-895-064-24	Sequence 24, Appli	355	29	51.9	11	6	US-10-665-658-54	Sequence 54, Appl
283	29	53.7	334	6	US-10-895-064-26	Sequence 26, Appli	356	29	51.9	11	6	US-10-665-658-55	Sequence 55, Appl
284	29	53.7	334	7	US-11-129-741-24	Sequence 24, Appli	357	29	51.9	11	6	US-10-665-658-57	Sequence 57, Appl
285	29	53.7	334	7	US-11-129-741-26	Sequence 26, Appli	358	29	51.9	12	6	US-10-665-658-12	Sequence 12, Appl
286	29	53.7	344	6	US-10-895-064-21	Sequence 21, Appli	359	29	51.9	15	7	US-11-054-515-2859	Sequence 2859, Ap
287	29	53.7	344	7	US-11-129-741-21	Sequence 21, Appli	360	29	51.9	103	7	US-11-266-444-2859	Sequence 2859, Ap
288	29	53.7	349	7	US-11-096-568A-3764	Sequence 3764, Ap	361	29	51.9	121	7	US-11-074-176-156	Sequence 156, App
289	29	53.7	350	6	US-10-506-454-1301	Sequence 1301, Ap	362	29	51.9	116	7	US-11-102-512-10	Sequence 10, Appl
290	29	53.7	355	7	US-11-096-568A-3763	Sequence 3763, Ap	363	29	51.9	116	7	US-11-102-512-29	Sequence 29, Appl
291	29	53.7	360	7	US-11-203-526-14	Sequence 14, Appli	364	29	51.9	116	7	US-11-102-512-81	Sequence 81, Appl
292	29	53.7	362	7	US-11-087-099-1797	Sequence 1797, Ap	365	29	51.9	121	6	US-10-665-658-4	Sequence 4, Appli
293	29	53.7	362	7	US-11-096-568A-3762	Sequence 3762, Ap	366	29	51.9	121	6	US-10-665-658-5	Sequence 5, Appli
294	29	53.7	363	7	US-11-203-526-16	Sequence 16, Appli	367	29	51.9	121	6	US-10-665-658-24	Sequence 24, Appl
295	29	53.7	374	7	US-11-096-568A-24539	Sequence 24539, A	368	29	51.9	121	7	US-11-107-028-50	Sequence 50, Appl
296	29	53.7	377	7	US-11-019-711-66	Sequence 66, Appli	369	29	51.9	121	7	US-11-107-028-52	Sequence 52, Appl
297	29	53.7	380	6	US-10-793-626-1402	Sequence 1402, Ap	370	29	51.9	121	7	US-11-149-031-2	Sequence 2, Appli
298	29	53.7	386	7	US-11-096-568A-18911	Sequence 18911, A	371	29	51.9	121	7	US-11-149-031-4	Sequence 4, Appli
299	29	53.7	392	7	US-11-084-458-2	Sequence 2, Appli	372	29	51.9	121	7	US-11-208-422-14	Sequence 14, Appl
300	29	53.7	393	5	US-09-940-308-7	Sequence 7, Appli	373	29	51.9	128	7	US-11-049-536-578	Sequence 578, App
301	29	53.7	395	6	US-10-793-626-664	Sequence 664, App	374	29	51.9	128	7	US-11-199-739-578	Sequence 578, App
302	29	53.7	408	7	US-11-096-568A-24538	Sequence 24538, A	375	29	51.9	130	7	US-11-109-264-51	Sequence 51, Appl
303	29	53.7	413	7	US-11-096-568A-24537	Sequence 24537, A	376	29	51.9	149	7	US-11-087-099-5504	Sequence 5504, Ap
304	29	53.7	415	7	US-11-096-568A-18910	Sequence 18910, A	377	29	51.9	155	6	US-10-720-603A-3	Sequence 3, Appli
305	29	53.7	444	7	US-11-172-320-6	Sequence 6, Appli	378	29	51.9	158	7	US-11-096-568A-4180	Sequence 4180, Ap
306	29	53.7	444	7	US-11-173-969-6	Sequence 6, Appli	379	29	51.9	159	7	US-11-087-099-6515	Sequence 6515, Ap
307	29	53.7	452	7	US-11-096-568A-18909	Sequence 18909, A	380	29	51.9	160	7	US-11-194-052-23	Sequence 23, Appl
308	29	53.7	455	7	US-11-203-526-18	Sequence 18, Appli	381	29	51.9	165	7	US-11-096-568A-4179	Sequence 4179, Ap
309	29	53.7	459	7	US-11-203-526-12	Sequence 12, Appli	382	29	51.9	184	7	US-11-087-099-4739	Sequence 4739, Ap
310	29	53.7	462	7	US-11-203-526-10	Sequence 10, Appli	383	29	51.9	192	7	US-11-096-568A-4178	Sequence 4178, Ap
311	29	53.7	472	7	US-11-087-099-11838	Sequence 11838, A	384	29	51.9	195	7	US-11-087-099-7399	Sequence 7399, Ap
312	29	53.7	521	7	US-11-087-099-8035	Sequence 8035, Ap	385	29	51.9	208	6	US-10-878-556A-133	Sequence 133, App
313	29	53.7	552	7	US-11-096-568A-29840	Sequence 29840, A	386	29	51.9	228	7	US-11-096-568A-16486	Sequence 16486, A
314	29	53.7	563	6	US-10-873-528-27	Sequence 27, Appli	387	29	51.9	230	7	US-11-129-741-4229	Sequence 4229, Ap
315	29	53.7	563	6	US-10-873-528-28	Sequence 28, Appli	388	29	51.9	237	7	US-11-096-568A-19223	Sequence 19223, A
316	29	53.7	567	6	US-10-793-626-3184	Sequence 3184, Ap	389	29	51.9	238	6	US-10-714-887-134	Sequence 124, App
317	29	53.7	579	7	US-11-096-568A-29839	Sequence 29839, A	390	29	51.9	239	6	US-10-895-064-1311	Sequence 1311, App

391	28	51.9	239	7	US-11-129-741-1311	Sequence 1311, Ap	464	28	51.9	445	7	US-11-087-099-10524	Sequence 10524, A
392	28	51.9	241	6	US-10-467-657-4474	Sequence 4474, Ap	465	28	51.9	451	7	US-11-096-568A-6808	Sequence 6808, Ap
393	28	51.9	243	7	US-11-087-099-10090	Sequence 10090, Ap	466	28	51.9	454	7	US-11-087-099-11061	Sequence 11061, A
394	28	51.9	247	7	US-11-054-515-1112	Sequence 1112, Ap	467	28	51.9	454	7	US-11-096-568A-20795	Sequence 20795, A
395	28	51.9	247	7	US-11-266-444-1112	Sequence 1112, Ap	468	28	51.9	456	6	US-10-641-678-55	Sequence 55, Appl
396	28	51.9	250	6	US-10-472-681B-7	Sequence 7, Appl1	468	28	51.9	457	7	US-11-098-686-11046	Sequence 11046, A
397	28	51.9	251	6	US-10-131-826A-266	Sequence 266, Ap	470	28	51.9	462	6	US-10-523-503-80	Sequence 80, Appl
398	28	51.9	251	6	US-10-973-115B-286	Sequence 266, Ap	471	28	51.9	465	7	US-11-072-512-2227	Sequence 2227, Ap
399	28	51.9	251	7	US-11-054-515-3245	Sequence 3245, Ap	472	28	51.9	466	6	US-10-517-939-376	Sequence 276, Ap
400	28	51.9	251	7	US-11-135-855-46	Sequence 46, Appl	473	28	51.9	471	7	US-11-096-568A-6807	Sequence 6807, Ap
401	28	51.9	260	7	US-11-087-099-11521	Sequence 11521, A	474	28	51.9	475	7	US-11-096-568A-21668	Sequence 21668, A
402	28	51.9	261	7	US-11-087-099-12359	Sequence 12359, A	475	28	51.9	478	7	US-11-096-568A-21667	Sequence 21667, A
403	28	51.9	263	6	US-10-821-234-1312	Sequence 1312, Ap	476	28	51.9	479	7	US-11-096-568A-21666	Sequence 21666, A
404	28	51.9	264	7	US-11-096-568A-16485	Sequence 16485, A	477	28	51.9	484	7	US-11-087-099-8314	Sequence 8314, Ap
405	28	51.9	265	7	US-11-096-568A-23105	Sequence 23105, A	478	28	51.9	495	7	US-11-096-568A-15874	Sequence 15874, A
406	28	51.9	272	7	US-11-087-099-10281	Sequence 10281, A	479	28	51.9	526	6	US-10-641-678-46	Sequence 46, Appl
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409	28	51.9	304	7	US-11-087-099-8084	Sequence 8084, Ap	482	28	51.9	560	7	US-11-131-479-16	Sequence 16, Appl
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412	28	51.9	309	7	US-11-087-099-533	Sequence 533, Ap	485	28	51.9	593	7	US-11-087-099-5719	Sequence 5719, Ap
413	28	51.9	317	7	US-11-087-099-6843	Sequence 6843, Ap	486	28	51.9	596	7	US-11-087-099-9309	Sequence 9309, Ap
414	28	51.9	328	7	US-11-096-568A-13515	Sequence 13515, A	487	28	51.9	599	6	US-10-204-639-59	Sequence 59, Appl
415	28	51.9	332	7	US-11-096-568A-5795	Sequence 5795, Ap	488	28	51.9	626	7	US-11-052-554A-127	Sequence 127, Appl
416	28	51.9	332	7	US-11-096-568A-23104	Sequence 23104, A	489	28	51.9	726	6	US-10-131-826A-28	Sequence 28, Appl
417	28	51.9	335	7	US-11-096-568A-19221	Sequence 19221, A	490	28	51.9	765	6	US-10-973-115B-28	Sequence 28, Appl
418	28	51.9	336	7	US-11-087-099-5650	Sequence 5650, Ap	491	28	51.9	765	6	US-10-467-657-5656	Sequence 5656, Ap
419	28	51.9	338	7	US-11-087-099-9488	Sequence 9488, Ap	492	28	51.9	929	6	US-11-046-653-4	Sequence 4, Appl1
420	28	51.9	341	7	US-11-087-099-2283	Sequence 2283, Ap	493	28	51.9	934	7	US-11-046-653-4	Sequence 4, Appl1
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422	28	51.9	342	7	US-11-087-099-1567	Sequence 1567, Ap	495	28	51.9	941	6	US-10-973-115B-464	Sequence 464, Ap
423	28	51.9	342	7	US-11-087-099-9364	Sequence 9364, Ap	496	28	51.9	941	7	US-11-124-368A-191	Sequence 191, Ap
424	28	51.9	342	7	US-11-087-099-4828	Sequence 4828, Ap	497	28	51.9	941	7	US-11-124-368A-193	Sequence 193, Ap
425	28	51.9	342	7	US-11-087-099-8730	Sequence 8730, Ap	498	28	51.9	945	6	US-10-131-826A-146	Sequence 146, Ap
426	28	51.9	342	7	US-11-087-099-10417	Sequence 10417, A	499	28	51.9	945	6	US-10-973-115B-146	Sequence 146, Ap
427	28	51.9	343	7	US-11-087-099-4750	Sequence 4750, Ap	500	28	51.9	945	7	US-11-019-711-38	Sequence 38, Appl
428	28	51.9	343	7	US-11-087-099-6322	Sequence 6322, Ap	501	28	51.9	945	7	US-11-019-711-121	Sequence 121, Ap
429	28	51.9	343	7	US-11-087-099-9364	Sequence 9364, Ap	502	28	51.9	945	7	US-11-183-136-20	Sequence 20, Appl
430	28	51.9	344	7	US-11-087-099-6760	Sequence 6760, Ap	503	28	51.9	948	7	US-11-124-368A-192	Sequence 192, Ap
431	28	51.9	344	7	US-11-096-568A-15192	Sequence 15192, A	504	28	51.9	955	7	US-11-052-554A-179	Sequence 179, Ap
432	28	51.9	346	7	US-11-096-568A-5794	Sequence 5794, Ap	505	28	51.9	1244	6	US-10-330-773-624	Sequence 624, Ap
433	28	51.9	350	6	US-10-467-657-3256	Sequence 3256, Ap	506	28	51.9	1392	6	US-10-330-773-622	Sequence 622, Ap
434	28	51.9	350	7	US-11-087-099-1303	Sequence 1303, Ap	507	28	51.9	1400	6	US-10-821-234-1045	Sequence 1045, Ap
435	28	51.9	350	7	US-11-087-099-5841	Sequence 5841, Ap	508	28	51.9	1627	6	US-10-821-234-1283	Sequence 1283, Ap
436	28	51.9	350	7	US-11-087-099-7982	Sequence 7982, Ap	509	28	51.9	2710	7	US-11-051-453-41	Sequence 41, Appl
437	28	51.9	350	7	US-11-096-568A-20796	Sequence 20796, A	510	28	51.9	2890	7	US-11-115-639-31	Sequence 31, Appl
438	28	51.9	353	6	US-10-506-454-1580	Sequence 1580, Ap	511	28	51.9	2890	7	US-11-115-639-32	Sequence 32, Appl
439	28	51.9	353	7	US-11-087-099-5698	Sequence 5698, Ap	512	28	51.9	2890	7	US-11-115-639-33	Sequence 33, Appl
440	28	51.9	353	7	US-11-087-099-7312	Sequence 7312, Ap	513	28	51.9	2902	7	US-11-052-554A-91	Sequence 91, Appl
441	28	51.9	354	7	US-11-096-568A-13514	Sequence 13514, A	514	27.5	50.9	178	7	US-11-087-099-5168	Sequence 5168, Ap
442	28	51.9	356	7	US-11-087-099-1153	Sequence 1153, Ap	515	27.5	50.9	1005	7	US-11-113-424-63	Sequence 63, Appl
443	28	51.9	357	7	US-11-087-099-10807	Sequence 10807, A	516	27.5	50.9	1015	7	US-11-203-251A-82	Sequence 82, Appl
444	28	51.9	357	7	US-11-096-568A-26092	Sequence 26092, A	517	27.5	50.9	1037	7	US-11-203-251A-81	Sequence 81, Appl
445	28	51.9	358	7	US-11-087-099-9959	Sequence 9959, Ap	518	27	50.0	9	7	US-11-125-837-17	Sequence 17, Appl
446	28	51.9	359	7	US-11-087-099-2495	Sequence 2495, Ap	519	27	50.0	10	7	US-11-004-399-2081	Sequence 2081, Ap
447	28	51.9	366	7	US-11-096-568A-30167	Sequence 30167, A	520	27	50.0	12	7	US-11-054-515-2196	Sequence 2196, Ap
448	28	51.9	370	7	US-11-096-568A-3216	Sequence 3216, Ap	521	27	50.0	12	7	US-11-266-444-2196	Sequence 2196, Ap
449	28	51.9	370	7	US-11-096-568A-3217	Sequence 3217, Ap	522	27	50.0	13	6	US-10-499-773-8	Sequence 8, Appl1
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452	28	51.9	380	7	US-11-096-568A-33299	Sequence 33299, A	525	27	50.0	15	7	US-11-054-515-2909	Sequence 2909, Ap
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454	28	51.9	385	7	US-11-096-568A-26091	Sequence 26091, A	527	27	50.0	16	7	US-11-054-515-2895	Sequence 2895, Ap
455	28	51.9	393	7	US-11-096-568A-3215	Sequence 3215, Ap	528	27	50.0	16	7	US-11-266-444-2895	Sequence 2895, Ap
456	28	51.9	396	7	US-11-022-562-228	Sequence 228, Ap	529	27	50.0	17	6	US-10-982-440-1095	Sequence 105, Ap
457	28	51.9	404	7	US-11-052-554A-344	Sequence 344, Ap	530	27	50.0	17	6	US-10-507-178-2	Sequence 2, Appl1
458	28	51.9	414	7	US-11-087-099-6171	Sequence 6171, Ap	531	27	50.0	17	7	US-11-054-515-2871	Sequence 2871, Ap
459	28	51.9	418	7	US-11-096-568A-33298	Sequence 33298, A	532	27	50.0	17	7	US-11-201-825-39	Sequence 39, Appl
460	28	51.9	422	7	US-11-096-568A-30165	Sequence 30165, A	533	27	50.0	17	7	US-11-266-444-2871	Sequence 2871, Ap
461	28	51.9	422	7	US-11-096-568A-33297	Sequence 33297, A	534	27	50.0	19	7	US-11-108-135-30	Sequence 30, Appl
462	28	51.9	435	7	US-11-087-099-3366	Sequence 3366, Ap	535	27	50.0	19	7	US-11-167-872-62	Sequence 62, Appl
463	28	51.9	441	7	US-11-096-568A-6809	Sequence 6809, Ap	536	27	50.0	19	7	US-11-167-872-68	Sequence 68, Appl



537	27	50.0	19	7	US-11-126-978-30	Sequence 30, Appl	610	27	50.0	116	7	US-11-102-512-33	Sequence 33, Appl
538	27	50.0	20	7	US-11-149-943-28	Sequence 28, Appl	611	27	50.0	116	7	US-11-102-512-34	Sequence 34, Appl
539	27	50.0	20	7	US-11-149-943-38	Sequence 38, Appl	612	27	50.0	116	7	US-11-102-512-43	Sequence 43, Appl
540	27	50.0	21	7	US-11-149-943-32	Sequence 32, Appl	613	27	50.0	116	7	US-11-102-512-45	Sequence 45, Appl
541	27	50.0	21	7	US-11-149-943-34	Sequence 34, Appl	614	27	50.0	116	7	US-11-102-512-59	Sequence 59, Appl
542	27	50.0	22	7	US-11-149-943-23	Sequence 23, Appl	615	27	50.0	116	7	US-11-102-512-60	Sequence 60, Appl
543	27	50.0	22	7	US-11-149-943-29	Sequence 29, Appl	616	27	50.0	116	7	US-11-102-512-63	Sequence 63, Appl
544	27	50.0	33	6	US-10-516-768-19	Sequence 19, Appl	617	27	50.0	116	7	US-11-102-512-65	Sequence 65, Appl
545	27	50.0	37	7	US-11-143-077-12	Sequence 12, Appl	618	27	50.0	116	7	US-11-102-512-66	Sequence 66, Appl
546	27	50.0	37	7	US-11-187-364-12	Sequence 12, Appl	619	27	50.0	116	7	US-11-102-512-67	Sequence 67, Appl
547	27	50.0	85	6	US-10-925-366A-350	Sequence 350, Appl	620	27	50.0	116	7	US-11-102-512-73	Sequence 73, Appl
548	27	50.0	86	6	US-10-925-366A-357	Sequence 357, Appl	621	27	50.0	116	7	US-11-102-512-80	Sequence 80, Appl
549	27	50.0	87	7	US-11-096-568A-8078	Sequence 8078, Appl	622	27	50.0	117	6	US-10-834-397-24	Sequence 24, Appl
550	27	50.0	89	6	US-10-925-366A-367	Sequence 367, Appl	623	27	50.0	117	6	US-10-981-356A-5	Sequence 5, Appl
551	27	50.0	96	6	US-10-993-543-287	Sequence 287, Appl	624	27	50.0	117	7	US-11-075-184A-2	Sequence 2, Appl
552	27	50.0	96	7	US-11-084-554-37	Sequence 37, Appl	625	27	50.0	117	7	US-11-075-184A-8	Sequence 8, Appl
553	27	50.0	96	7	US-11-004-590-38	Sequence 38, Appl	626	27	50.0	117	7	US-11-075-184A-9	Sequence 9, Appl
554	27	50.0	96	7	US-11-136-250-37	Sequence 37, Appl	627	27	50.0	117	7	US-11-075-184A-10	Sequence 10, Appl
555	27	50.0	97	7	US-11-054-669-29	Sequence 29, Appl	628	27	50.0	117	7	US-11-075-184A-11	Sequence 11, Appl
556	27	50.0	97	7	US-11-054-669-31	Sequence 31, Appl	629	27	50.0	117	7	US-11-096-046-6	Sequence 6, Appl
557	27	50.0	97	7	US-11-084-554-41	Sequence 41, Appl	630	27	50.0	117	7	US-11-127-903-29	Sequence 29, Appl
558	27	50.0	97	7	US-11-084-554-43	Sequence 43, Appl	631	27	50.0	117	7	US-11-127-903-30	Sequence 30, Appl
559	27	50.0	97	7	US-11-093-274-34	Sequence 34, Appl	632	27	50.0	117	7	US-11-127-903-32	Sequence 32, Appl
560	27	50.0	97	7	US-11-004-590-28	Sequence 28, Appl	633	27	50.0	117	7	US-11-127-903-34	Sequence 34, Appl
561	27	50.0	97	7	US-11-004-590-32	Sequence 32, Appl	634	27	50.0	117	7	US-11-127-903-36	Sequence 36, Appl
562	27	50.0	97	7	US-11-004-590-34	Sequence 34, Appl	635	27	50.0	117	7	US-11-127-903-37	Sequence 37, Appl
563	27	50.0	97	7	US-11-136-250-41	Sequence 41, Appl	636	27	50.0	117	7	US-11-127-903-44	Sequence 44, Appl
564	27	50.0	97	7	US-11-136-250-43	Sequence 43, Appl	637	27	50.0	117	7	US-11-049-536-190	Sequence 190, Appl
565	27	50.0	98	6	US-10-789-273-10	Sequence 10, Appl	638	27	50.0	117	7	US-11-049-536-274	Sequence 274, Appl
566	27	50.0	98	7	US-11-144-248-32	Sequence 32, Appl	639	27	50.0	117	7	US-11-049-536-354	Sequence 354, Appl
567	27	50.0	98	7	US-11-054-669-22	Sequence 22, Appl	640	27	50.0	117	7	US-11-049-536-390	Sequence 390, Appl
568	27	50.0	98	7	US-11-084-554-33	Sequence 33, Appl	641	27	50.0	117	7	US-11-049-536-414	Sequence 414, Appl
569	27	50.0	98	7	US-11-084-554-42	Sequence 42, Appl	642	27	50.0	117	7	US-11-049-536-458	Sequence 458, Appl
570	27	50.0	98	7	US-11-144-222-32	Sequence 32, Appl	643	27	50.0	117	7	US-11-049-536-462	Sequence 462, Appl
571	27	50.0	98	7	US-11-004-590-23	Sequence 23, Appl	644	27	50.0	117	7	US-11-049-536-530	Sequence 530, Appl
572	27	50.0	98	7	US-11-136-250-33	Sequence 33, Appl	645	27	50.0	117	7	US-11-049-536-558	Sequence 558, Appl
573	27	50.0	98	7	US-11-136-250-42	Sequence 42, Appl	646	27	50.0	117	7	US-11-049-536-602	Sequence 602, Appl
574	27	50.0	98	7	US-11-182-343-32	Sequence 32, Appl	647	27	50.0	117	7	US-11-049-536-610	Sequence 610, Appl
575	27	50.0	98	7	US-11-049-536-721	Sequence 721, Appl	648	27	50.0	117	7	US-11-049-536-642	Sequence 642, Appl
576	27	50.0	99	7	US-11-054-669-27	Sequence 27, Appl	649	27	50.0	117	7	US-11-049-536-686	Sequence 686, Appl
577	27	50.0	99	7	US-11-084-554-38	Sequence 38, Appl	650	27	50.0	117	7	US-11-049-536-698	Sequence 698, Appl
578	27	50.0	99	7	US-11-004-590-29	Sequence 29, Appl	651	27	50.0	117	7	US-11-199-739-190	Sequence 190, Appl
579	27	50.0	99	7	US-11-136-250-38	Sequence 38, Appl	652	27	50.0	117	7	US-11-199-739-274	Sequence 274, Appl
580	27	50.0	109	7	US-11-096-568A-19304	Sequence 19304, A	653	27	50.0	117	7	US-11-199-739-354	Sequence 354, Appl
581	27	50.0	110	6	US-10-771-257-1	Sequence 1, Appl	654	27	50.0	117	7	US-11-199-739-390	Sequence 390, Appl
582	27	50.0	110	7	US-11-127-677-1	Sequence 1, Appl	655	27	50.0	117	7	US-11-199-739-414	Sequence 414, Appl
583	27	50.0	112	6	US-10-771-257-3	Sequence 3, Appl	656	27	50.0	117	7	US-11-199-739-458	Sequence 458, Appl
584	27	50.0	112	7	US-11-127-677-3	Sequence 3, Appl	657	27	50.0	117	7	US-11-199-739-462	Sequence 462, Appl
585	27	50.0	112	7	US-11-127-932-1	Sequence 1, Appl	658	27	50.0	117	7	US-11-199-739-550	Sequence 550, Appl
586	27	50.0	112	7	US-11-127-903-1	Sequence 1, Appl	659	27	50.0	117	7	US-11-199-739-558	Sequence 558, Appl
587	27	50.0	113	6	US-10-665-658-6	Sequence 6, Appl	660	27	50.0	117	7	US-11-199-739-602	Sequence 602, Appl
588	27	50.0	114	7	US-11-217-919-165	Sequence 165, Appl	661	27	50.0	117	7	US-11-199-739-610	Sequence 610, Appl
589	27	50.0	115	7	US-11-108-135-37	Sequence 37, Appl	662	27	50.0	117	7	US-11-199-739-642	Sequence 642, Appl
590	27	50.0	115	7	US-11-127-903-33	Sequence 33, Appl	663	27	50.0	117	7	US-11-199-739-686	Sequence 686, Appl
591	27	50.0	115	7	US-11-127-903-38	Sequence 38, Appl	664	27	50.0	117	7	US-11-199-739-698	Sequence 698, Appl
592	27	50.0	115	7	US-11-126-978-37	Sequence 37, Appl	665	27	50.0	118	6	US-10-771-257-8	Sequence 8, Appl
593	27	50.0	116	6	US-10-925-366A-1	Sequence 1, Appl	666	27	50.0	118	6	US-10-771-257-15	Sequence 15, Appl
594	27	50.0	116	6	US-10-925-366A-213	Sequence 213, Appl	667	27	50.0	118	6	US-10-771-257-17	Sequence 17, Appl
595	27	50.0	116	6	US-10-925-366A-214	Sequence 214, Appl	668	27	50.0	118	6	US-10-886-383-1	Sequence 1, Appl
596	27	50.0	116	6	US-10-925-366A-215	Sequence 215, Appl	669	27	50.0	118	6	US-10-886-383-3	Sequence 3, Appl
597	27	50.0	116	7	US-11-054-669-101	Sequence 101, Appl	670	27	50.0	118	7	US-11-127-677-8	Sequence 8, Appl
598	27	50.0	116	7	US-11-049-536-614	Sequence 614, Appl	671	27	50.0	118	7	US-11-127-677-15	Sequence 15, Appl
599	27	50.0	116	7	US-11-199-739-614	Sequence 614, Appl	672	27	50.0	118	7	US-11-127-677-17	Sequence 17, Appl
600	27	50.0	116	7	US-11-102-512-8	Sequence 1, Appl	673	27	50.0	118	7	US-11-112-240-22	Sequence 22, Appl
601	27	50.0	116	7	US-11-102-512-9	Sequence 8, Appl	674	27	50.0	118	7	US-11-112-304A-22	Sequence 22, Appl
602	27	50.0	116	7	US-11-102-512-13	Sequence 9, Appl	675	27	50.0	118	7	US-11-049-536-198	Sequence 198, Appl
603	27	50.0	116	7	US-11-102-512-16	Sequence 13, Appl	676	27	50.0	118	7	US-11-049-536-334	Sequence 334, Appl
604	27	50.0	116	7	US-11-102-512-16	Sequence 16, Appl	677	27	50.0	118	7	US-11-049-536-338	Sequence 338, Appl
605	27	50.0	116	7	US-11-102-512-24	Sequence 24, Appl	678	27	50.0	118	7	US-11-049-536-546	Sequence 546, Appl
606	27	50.0	116	7	US-11-102-512-26	Sequence 26, Appl	679	27	50.0	118	7	US-11-199-739-198	Sequence 198, Appl
607	27	50.0	116	7	US-11-102-512-27	Sequence 27, Appl	680	27	50.0	118	7	US-11-199-739-334	Sequence 334, Appl
608	27	50.0	116	7	US-11-102-512-28	Sequence 28, Appl	681	27	50.0	118	7	US-11-199-739-338	Sequence 338, Appl
609	27	50.0	116	7	US-11-102-512-32	Sequence 32, Appl	682	27	50.0	118	7	US-11-199-739-546	Sequence 546, Appl

683	27	50.0	118	7	US-11-102-513-14	Sequence 14, Appl	756	27	50.0	121	7	US-11-199-739-622	Sequence 622, App
684	27	50.0	118	7	US-11-217-919-174	Sequence 174, App	757	27	50.0	122	6	US-10-515-241-11	Sequence 11, Appl
685	27	50.0	118	7	US-11-217-919-186	Sequence 186, App	758	27	50.0	122	7	US-11-144-248-24	Sequence 24, Appl
686	27	50.0	119	6	US-10-925-366A-210	Sequence 210, App	759	27	50.0	122	7	US-11-144-232-24	Sequence 24, Appl
687	27	50.0	119	6	US-10-771-257-58	Sequence 58, Appl	760	27	50.0	122	7	US-11-112-240-6	Sequence 6, Appl
688	27	50.0	119	7	US-11-120-338-9	Sequence 9, Appl	761	27	50.0	122	7	US-11-112-304A-6	Sequence 6, Appl
689	27	50.0	119	7	US-11-127-677-56	Sequence 56, Appl	762	27	50.0	122	7	US-11-182-343-24	Sequence 24, Appl
690	27	50.0	119	7	US-11-127-903-31	Sequence 31, Appl	763	27	50.0	122	7	US-11-049-536-186	Sequence 186, App
691	27	50.0	119	7	US-11-127-903-41	Sequence 41, Appl	764	27	50.0	122	7	US-11-049-536-302	Sequence 302, App
692	27	50.0	119	7	US-11-106-820-9	Sequence 9, Appl	765	27	50.0	122	7	US-11-049-536-574	Sequence 574, App
693	27	50.0	119	7	US-11-154-337-6	Sequence 6, Appl	766	27	50.0	122	7	US-11-199-739-186	Sequence 186, App
694	27	50.0	119	7	US-11-182-908-6	Sequence 6, Appl	767	27	50.0	122	7	US-11-199-739-302	Sequence 302, App
695	27	50.0	119	7	US-11-049-536-330	Sequence 330, App	768	27	50.0	122	7	US-11-199-739-574	Sequence 574, App
696	27	50.0	119	7	US-11-049-536-362	Sequence 362, App	769	27	50.0	122	7	US-11-102-512-48	Sequence 48, Appl
697	27	50.0	119	7	US-11-049-536-370	Sequence 370, App	770	27	50.0	123	6	US-10-925-366A-216	Sequence 216, App
698	27	50.0	119	7	US-11-049-536-402	Sequence 402, App	771	27	50.0	123	6	US-10-925-366A-217	Sequence 217, App
699	27	50.0	119	7	US-11-049-536-418	Sequence 418, App	772	27	50.0	123	6	US-10-925-366A-218	Sequence 218, App
700	27	50.0	119	7	US-11-049-536-470	Sequence 470, App	773	27	50.0	123	6	US-10-771-257-47	Sequence 47, Appl
701	27	50.0	119	7	US-11-049-536-534	Sequence 534, App	774	27	50.0	123	6	US-10-771-257-84	Sequence 84, Appl
702	27	50.0	119	7	US-11-049-536-538	Sequence 538, App	775	27	50.0	123	6	US-10-771-257-88	Sequence 88, Appl
703	27	50.0	119	7	US-11-049-536-562	Sequence 562, App	776	27	50.0	123	6	US-10-771-257-90	Sequence 90, Appl
704	27	50.0	119	7	US-11-049-536-638	Sequence 638, App	777	27	50.0	123	6	US-10-771-257-95	Sequence 95, Appl
705	27	50.0	119	7	US-11-049-536-650	Sequence 650, App	778	27	50.0	123	6	US-10-982-440-1	Sequence 1, Appl
706	27	50.0	119	7	US-11-143-077-9	Sequence 9, Appl	779	27	50.0	123	6	US-10-982-440-23	Sequence 23, Appl
707	27	50.0	119	7	US-11-190-364-9	Sequence 9, Appl	780	27	50.0	123	6	US-10-982-440-59	Sequence 59, Appl
708	27	50.0	119	7	US-11-102-120-6	Sequence 6, Appl	781	27	50.0	123	6	US-10-499-246-9	Sequence 9, Appl
709	27	50.0	119	7	US-11-147-780-9	Sequence 9, Appl	782	27	50.0	123	7	US-11-127-677-45	Sequence 45, Appl
710	27	50.0	119	7	US-11-223-361-6	Sequence 6, Appl	783	27	50.0	123	7	US-11-112-240-30	Sequence 30, Appl
711	27	50.0	119	7	US-11-143-386-9	Sequence 9, Appl	784	27	50.0	123	7	US-11-112-304A-30	Sequence 30, Appl
712	27	50.0	119	7	US-11-199-739-330	Sequence 330, App	785	27	50.0	123	7	US-11-049-536-410	Sequence 410, App
713	27	50.0	119	7	US-11-199-739-362	Sequence 362, App	786	27	50.0	123	7	US-11-199-739-410	Sequence 410, App
714	27	50.0	119	7	US-11-199-739-370	Sequence 370, App	787	27	50.0	123	7	US-11-102-512-58	Sequence 58, Appl
715	27	50.0	119	7	US-11-199-739-402	Sequence 402, App	788	27	50.0	123	7	US-11-102-512-69	Sequence 69, Appl
716	27	50.0	119	7	US-11-199-739-418	Sequence 418, App	789	27	50.0	123	7	US-11-102-512-70	Sequence 70, Appl
717	27	50.0	119	7	US-11-199-739-470	Sequence 470, App	790	27	50.0	123	7	US-11-102-512-78	Sequence 78, Appl
718	27	50.0	119	7	US-11-199-739-534	Sequence 534, App	791	27	50.0	123	7	US-11-102-512-79	Sequence 79, Appl
719	27	50.0	119	7	US-11-199-739-538	Sequence 538, App	792	27	50.0	123	7	US-11-102-512-85	Sequence 85, Appl
720	27	50.0	119	7	US-11-199-739-562	Sequence 562, App	793	27	50.0	124	6	US-10-925-366A-211	Sequence 211, App
721	27	50.0	119	7	US-11-199-739-638	Sequence 638, App	794	27	50.0	124	6	US-10-771-257-19	Sequence 19, Appl
722	27	50.0	119	7	US-11-199-739-650	Sequence 650, App	795	27	50.0	124	6	US-10-771-257-22	Sequence 22, Appl
723	27	50.0	119	7	US-11-102-512-20	Sequence 20, Appl	796	27	50.0	124	6	US-10-515-241-8	Sequence 8, Appl
724	27	50.0	119	7	US-11-102-512-42	Sequence 42, Appl	797	27	50.0	124	7	US-11-127-677-19	Sequence 19, Appl
725	27	50.0	119	7	US-11-102-512-46	Sequence 46, Appl	798	27	50.0	124	7	US-11-127-677-22	Sequence 22, Appl
726	27	50.0	119	7	US-11-187-364-9	Sequence 9, Appl	799	27	50.0	124	7	US-11-049-536-298	Sequence 298, App
727	27	50.0	120	6	US-10-925-366A-5	Sequence 5, Appl	800	27	50.0	124	7	US-11-201-825-15	Sequence 15, Appl
728	27	50.0	120	6	US-10-925-366A-235	Sequence 235, App	801	27	50.0	124	7	US-11-199-739-298	Sequence 298, App
729	27	50.0	120	6	US-10-925-366A-280	Sequence 280, App	802	27	50.0	125	6	US-10-771-257-6	Sequence 6, Appl
730	27	50.0	120	6	US-10-925-366A-286	Sequence 286, App	803	27	50.0	125	6	US-10-771-257-43	Sequence 43, Appl
731	27	50.0	120	6	US-10-834-397-38	Sequence 38, Appl	804	27	50.0	125	6	US-10-771-257-52	Sequence 52, Appl
732	27	50.0	120	6	US-10-834-397-63	Sequence 63, Appl	805	27	50.0	125	6	US-10-771-257-52	Sequence 52, Appl
733	27	50.0	120	7	US-11-102-201-1	Sequence 1, Appl	806	27	50.0	125	7	US-11-144-248-16	Sequence 16, Appl
734	27	50.0	120	7	US-11-112-240-2	Sequence 2, Appl	807	27	50.0	125	7	US-11-127-677-6	Sequence 6, Appl
735	27	50.0	120	7	US-11-112-304A-2	Sequence 2, Appl	808	27	50.0	125	7	US-11-127-677-41	Sequence 41, Appl
736	27	50.0	120	7	US-11-049-536-258	Sequence 258, App	809	27	50.0	125	7	US-11-127-677-47	Sequence 47, Appl
737	27	50.0	120	7	US-11-049-536-586	Sequence 586, App	810	27	50.0	125	7	US-11-127-677-50	Sequence 50, Appl
738	27	50.0	120	7	US-11-049-536-590	Sequence 590, App	811	27	50.0	125	7	US-11-144-222-16	Sequence 16, Appl
739	27	50.0	120	7	US-11-049-536-666	Sequence 666, App	812	27	50.0	125	7	US-11-127-903-21	Sequence 21, Appl
740	27	50.0	120	7	US-11-199-739-258	Sequence 258, App	813	27	50.0	125	7	US-11-182-343-16	Sequence 16, Appl
741	27	50.0	120	7	US-11-199-739-586	Sequence 586, App	814	27	50.0	125	7	US-11-049-536-170	Sequence 170, App
742	27	50.0	120	7	US-11-199-739-590	Sequence 590, App	815	27	50.0	125	7	US-11-049-536-286	Sequence 286, App
743	27	50.0	120	7	US-11-199-739-666	Sequence 666, App	816	27	50.0	125	7	US-11-049-536-286	Sequence 286, App
744	27	50.0	120	7	US-11-102-512-5	Sequence 5, Appl	817	27	50.0	125	7	US-11-049-536-366	Sequence 366, App
745	27	50.0	120	7	US-11-102-512-23	Sequence 23, Appl	818	27	50.0	125	7	US-11-049-536-478	Sequence 478, App
746	27	50.0	120	7	US-11-102-512-62	Sequence 62, Appl	819	27	50.0	125	7	US-11-199-739-170	Sequence 170, App
747	27	50.0	120	7	US-11-217-919-85	Sequence 85, Appl	820	27	50.0	125	7	US-11-199-739-242	Sequence 242, App
748	27	50.0	120	7	US-11-217-919-91	Sequence 91, Appl	821	27	50.0	125	7	US-11-199-739-286	Sequence 286, App
749	27	50.0	121	6	US-10-789-273-9	Sequence 9, Appl	822	27	50.0	125	7	US-11-199-739-366	Sequence 366, App
750	27	50.0	121	6	US-10-925-366A-212	Sequence 212, App	823	27	50.0	125	7	US-11-199-739-478	Sequence 478, App
751	27	50.0	121	6	US-10-771-257-7	Sequence 7, Appl	824	27	50.0	126	6	US-10-771-257-13	Sequence 13, Appl
752	27	50.0	121	7	US-11-127-677-7	Sequence 7, Appl	825	27	50.0	126	7	US-11-127-677-13	Sequence 13, Appl
753	27	50.0	121	7	US-11-049-536-346	Sequence 346, App	826	27	50.0	126	7	US-11-127-932-5	Sequence 5, Appl
754	27	50.0	121	7	US-11-049-536-622	Sequence 622, App	827	27	50.0	126	7	US-11-127-903-5	Sequence 5, Appl
755	27	50.0	121	7	US-11-199-739-346	Sequence 346, App	828	27	50.0	126	7	US-11-049-536-342	Sequence 342, App

829	27	50.0	126	7	US-11-049-536-374	Sequence 374, App	902	27	50.0	210	7	US-11-173-740-844	Sequence 844, App
830	27	50.0	126	7	US-11-049-536-430	Sequence 430, App	903	27	50.0	214	6	US-10-993-143-18	Sequence 18, Appl
831	27	50.0	126	7	US-11-199-739-342	Sequence 342, App	904	27	50.0	215	6	US-10-498-246-34	Sequence 34, Appl
832	27	50.0	126	7	US-11-199-739-370	Sequence 374, App	905	27	50.0	217	7	US-11-128-440-11	Sequence 12, Appl
833	27	50.0	126	7	US-11-199-739-430	Sequence 430, App	906	27	50.0	219	7	US-11-128-440-12	Sequence 12, Appl
834	27	50.0	127	6	US-10-771-257-48	Sequence 48, Appl	907	27	50.0	220	7	US-11-096-568A-1823	Sequence 1823, Ap
835	27	50.0	127	7	US-11-127-677-46	Sequence 46, Appl	908	27	50.0	222	6	US-11-096-568A-1823	Sequence 1823, Ap
836	27	50.0	127	7	US-11-049-536-326	Sequence 326, App	909	27	50.0	225	6	US-10-993-143-15	Sequence 15, Appl
837	27	50.0	127	7	US-11-049-536-446	Sequence 446, App	910	27	50.0	225	6	US-10-209-208-1	Sequence 1, Appl
838	27	50.0	127	7	US-11-199-739-326	Sequence 326, App	911	27	50.0	225	6	US-10-209-208-20	Sequence 4, Appl
839	27	50.0	127	7	US-11-199-739-446	Sequence 446, App	912	27	50.0	225	6	US-10-209-208-24	Sequence 20, Appl
840	27	50.0	128	7	US-11-064-174-1	Sequence 1, Appl	913	27	50.0	225	6	US-11-218-880-1	Sequence 24, Appl
841	27	50.0	128	7	US-11-064-174-142	Sequence 142, App	914	27	50.0	225	7	US-11-218-880-4	Sequence 1, Appl
842	27	50.0	128	7	US-11-049-536-76	Sequence 76, App	915	27	50.0	225	7	US-11-218-880-20	Sequence 4, Appl
843	27	50.0	128	7	US-11-049-536-102	Sequence 102, App	916	27	50.0	225	7	US-11-218-880-24	Sequence 20, Appl
844	27	50.0	128	7	US-11-199-739-76	Sequence 76, Appl	917	27	50.0	225	7	US-11-100-988-2	Sequence 24, Appl
845	27	50.0	128	7	US-11-199-739-102	Sequence 102, App	918	27	50.0	225	7	US-11-100-988-3	Sequence 2, Appl
846	27	50.0	129	6	US-10-771-257-61	Sequence 61, Appl	919	27	50.0	225	7	US-11-187-622-8	Sequence 8, Appl
847	27	50.0	129	6	US-10-993-543-160	Sequence 160, App	920	27	50.0	225	7	US-11-187-622-12	Sequence 12, Appl
848	27	50.0	129	7	US-11-127-677-59	Sequence 59, Appl	921	27	50.0	230	7	US-11-082-154A-40	Sequence 40, Appl
849	27	50.0	129	7	US-11-064-174-143	Sequence 143, App	922	27	50.0	237	7	US-11-054-515-1906	Sequence 1906, Ap
850	27	50.0	129	7	US-11-049-536-554	Sequence 554, App	923	27	50.0	237	7	US-11-054-515-1941	Sequence 1941, Ap
851	27	50.0	129	7	US-11-199-739-554	Sequence 554, App	924	27	50.0	237	7	US-11-054-515-2039	Sequence 2039, Ap
852	27	50.0	130	7	US-11-109-264-54	Sequence 54, Appl	925	27	50.0	237	7	US-11-266-444-1906	Sequence 1906, Ap
853	27	50.0	130	7	US-11-049-536-270	Sequence 270, App	926	27	50.0	237	7	US-11-266-444-1941	Sequence 1941, Ap
854	27	50.0	130	7	US-11-199-739-270	Sequence 270, App	927	27	50.0	237	7	US-11-266-444-2039	Sequence 2039, Ap
855	27	50.0	131	7	US-11-049-536-24	Sequence 24, Appl	928	27	50.0	238	7	US-11-193-561-10	Sequence 10, Appl
856	27	50.0	131	7	US-11-049-536-92	Sequence 92, Appl	929	27	50.0	238	7	US-11-193-771-10	Sequence 10, Appl
857	27	50.0	131	7	US-11-199-739-24	Sequence 24, Appl	930	27	50.0	238	7	US-11-193-789-10	Sequence 10, Appl
858	27	50.0	131	7	US-11-199-739-92	Sequence 92, Appl	931	27	50.0	238	7	US-11-193-806-10	Sequence 10, Appl
859	27	50.0	132	6	US-10-993-543-12	Sequence 12, Appl	932	27	50.0	238	7	US-11-193-857-10	Sequence 10, Appl
860	27	50.0	132	7	US-11-049-536-32	Sequence 32, Appl	933	27	50.0	239	7	US-11-054-515-1922	Sequence 1922, Ap
861	27	50.0	132	7	US-11-096-568A-9887	Sequence 9887, Ap	934	27	50.0	239	7	US-11-054-515-2018	Sequence 2018, Ap
862	27	50.0	132	7	US-11-199-739-32	Sequence 32, Appl	935	27	50.0	239	7	US-11-054-515-2022	Sequence 2022, Ap
863	27	50.0	133	7	US-11-188-743-21	Sequence 21, Appl	936	27	50.0	239	7	US-11-054-515-2023	Sequence 2023, Ap
864	27	50.0	133	7	US-11-183-294-24	Sequence 24, Appl	937	27	50.0	239	7	US-11-054-515-2035	Sequence 2035, Ap
865	27	50.0	135	7	US-11-096-568A-14335	Sequence 14335, A	938	27	50.0	239	7	US-11-266-444-1922	Sequence 1922, Ap
866	27	50.0	137	7	US-11-049-536-68	Sequence 68, Appl	939	27	50.0	239	7	US-11-266-444-2018	Sequence 2018, Ap
867	27	50.0	137	7	US-11-049-536-80	Sequence 80, Appl	940	27	50.0	239	7	US-11-266-444-2022	Sequence 2022, Ap
868	27	50.0	137	7	US-11-199-739-68	Sequence 68, Appl	941	27	50.0	239	7	US-11-266-444-2023	Sequence 2023, Ap
869	27	50.0	137	7	US-11-199-739-80	Sequence 80, Appl	942	27	50.0	239	7	US-11-266-444-2035	Sequence 2035, Ap
870	27	50.0	139	7	US-11-125-837-24	Sequence 24, Appl	943	27	50.0	240	6	US-10-925-366A-219	Sequence 219, App
871	27	50.0	143	7	US-11-049-536-48	Sequence 48, Appl	944	27	50.0	240	7	US-11-054-515-1905	Sequence 1905, Ap
872	27	50.0	143	7	US-11-199-739-48	Sequence 48, Appl	945	27	50.0	240	7	US-11-054-515-1930	Sequence 1930, Ap
873	27	50.0	146	7	US-11-096-568A-14334	Sequence 14334, A	946	27	50.0	240	7	US-11-054-515-2047	Sequence 2047, Ap
874	27	50.0	147	7	US-11-049-536-52	Sequence 52, App	947	27	50.0	240	7	US-11-266-444-1905	Sequence 1905, Ap
875	27	50.0	147	7	US-11-234-786-336	Sequence 336, App	948	27	50.0	240	7	US-11-266-444-1930	Sequence 1930, Ap
876	27	50.0	147	7	US-11-199-739-52	Sequence 52, Appl	949	27	50.0	240	7	US-11-266-444-2047	Sequence 2047, Ap
877	27	50.0	150	7	US-11-267-310-9	Sequence 9, Appl	950	27	50.0	241	7	US-11-054-515-2060	Sequence 2060, Ap
878	27	50.0	150	7	US-11-267-191-9	Sequence 9, Appl	951	27	50.0	241	7	US-11-096-568A-16952	Sequence 16952, A
879	27	50.0	153	7	US-11-267-310-11	Sequence 11, Appl	952	27	50.0	241	7	US-11-103-512-88	Sequence 88, Appl
880	27	50.0	153	7	US-11-267-191-11	Sequence 11, Appl	953	27	50.0	241	7	US-11-266-444-1949	Sequence 2060, Ap
881	27	50.0	159	7	US-11-000-463-333	Sequence 333, App	954	27	50.0	242	7	US-11-054-515-1949	Sequence 1949, Ap
882	27	50.0	161	7	US-11-096-568A-25488	Sequence 25488, A	955	27	50.0	242	7	US-11-096-568A-25486	Sequence 25486, A
883	27	50.0	162	6	US-10-516-768-21	Sequence 21, Appl	956	27	50.0	242	7	US-11-239-510-23	Sequence 23, Appl
884	27	50.0	166	7	US-11-096-568A-25939	Sequence 25939, A	957	27	50.0	242	7	US-11-266-444-1949	Sequence 1949, Ap
885	27	50.0	172	6	US-10-714-887-68	Sequence 68, Appl	958	27	50.0	243	7	US-11-054-515-995	Sequence 995, App
886	27	50.0	172	7	US-11-087-099-727	Sequence 727, App	959	27	50.0	243	7	US-11-054-515-1929	Sequence 1929, Ap
887	27	50.0	172	7	US-11-087-099-9945	Sequence 9945, Ap	960	27	50.0	243	7	US-11-054-515-1940	Sequence 1940, Ap
888	27	50.0	177	6	US-10-506-454-1248	Sequence 1248, Ap	961	27	50.0	243	7	US-11-054-515-1942	Sequence 1942, Ap
889	27	50.0	186	6	US-10-873-528-111	Sequence 111, App	962	27	50.0	243	7	US-11-054-515-1944	Sequence 1944, Ap
890	27	50.0	188	6	US-10-485-517-327	Sequence 327, App	963	27	50.0	243	7	US-11-054-515-1945	Sequence 1945, Ap
891	27	50.0	188	6	US-10-485-517-339	Sequence 339, App	964	27	50.0	243	7	US-11-054-515-1969	Sequence 1969, Ap
892	27	50.0	189	7	US-11-096-568A-1824	Sequence 1824, Ap	965	27	50.0	243	7	US-11-054-515-2056	Sequence 2056, Ap
893	27	50.0	193	7	US-11-120-665-21	Sequence 21, Appl	966	27	50.0	243	7	US-11-266-444-995	Sequence 995, App
894	27	50.0	193	7	US-11-096-568A-17711	Sequence 17711, A	967	27	50.0	243	7	US-11-266-444-1929	Sequence 1929, Ap
895	27	50.0	195	7	US-11-096-568A-25487	Sequence 25487, A	968	27	50.0	243	7	US-11-266-444-1940	Sequence 1940, Ap
896	27	50.0	196	6	US-10-454-437-168	Sequence 168, App	969	27	50.0	243	7	US-11-266-444-1942	Sequence 1942, Ap
897	27	50.0	200	7	US-11-096-568A-12151	Sequence 12151, A	970	27	50.0	243	7	US-11-266-444-1944	Sequence 1944, Ap
898	27	50.0	201	7	US-11-096-568A-21390	Sequence 21390, A	971	27	50.0	243	7	US-11-266-444-1945	Sequence 1945, Ap
899	27	50.0	204	7	US-11-128-440-15	Sequence 15, Appl	972	27	50.0	243	7	US-11-266-444-1969	Sequence 1969, Ap
900	27	50.0	205	7	US-11-096-568A-25857	Sequence 25857, A	973	27	50.0	243	7	US-11-266-444-2056	Sequence 2056, Ap
901	27	50.0	210	6	US-10-883-512-86	Sequence 86, Appl	974	27	50.0	244	7	US-11-239-510-13	Sequence 13, Appl

975 27 50.0 245 6 US-10-902-546-13 Sequence 13, Appl  
976 27 50.0 246 7 US-11-054-515-1314 Sequence 1314, Ap  
977 27 50.0 246 7 US-11-054-515-1324 Sequence 1324, Ap  
978 27 50.0 246 7 US-11-054-515-1975 Sequence 1975, Ap  
979 27 50.0 246 7 US-11-054-515-1980 Sequence 1980, Ap  
980 27 50.0 246 7 US-11-266-444-1314 Sequence 1314, Ap  
981 27 50.0 246 7 US-11-266-444-1324 Sequence 1324, Ap  
982 27 50.0 246 7 US-11-266-444-1975 Sequence 1975, Ap  
983 27 50.0 246 7 US-11-266-444-1980 Sequence 1980, Ap  
984 27 50.0 247 7 US-11-054-515-915 Sequence 915, App  
985 27 50.0 247 7 US-11-054-515-923 Sequence 923, App  
986 27 50.0 247 7 US-11-054-515-996 Sequence 996, App  
987 27 50.0 247 7 US-11-054-515-1177 Sequence 1177, App  
988 27 50.0 247 7 US-11-054-515-1652 Sequence 1652, App  
989 27 50.0 247 7 US-11-054-515-1903 Sequence 1903, App  
990 27 50.0 247 7 US-11-054-515-1923 Sequence 1923, App  
991 27 50.0 247 7 US-11-054-515-1953 Sequence 1953, App  
992 27 50.0 247 7 US-11-266-444-915 Sequence 915, App  
993 27 50.0 247 7 US-11-266-444-923 Sequence 923, App  
994 27 50.0 247 7 US-11-266-444-996 Sequence 996, App  
995 27 50.0 247 7 US-11-266-444-1177 Sequence 1177, App  
996 27 50.0 247 7 US-11-266-444-1652 Sequence 1652, App  
997 27 50.0 247 7 US-11-266-444-1903 Sequence 1903, App  
998 27 50.0 247 7 US-11-266-444-1923 Sequence 1923, App  
999 27 50.0 247 7 US-11-266-444-1953 Sequence 1953, App  
1000 27 50.0 248 7 US-11-054-515-921 Sequence 921, App

## ALIGNMENTS

RESULT 1  
US-10-473-037-5  
; Sequence 5, Application US/10473037  
; Publication No. US20050260206A1  
; GENERAL INFORMATION:  
; APPLICANT: KYOWA HAKKO KOGYO CO., LTD.  
; TITLE OF INVENTION: Agents for treatment of cancer using recombinant anti-GD3 antibody  
; TITLE OF INVENTION: the antibody fragments  
; FILE REFERENCE: 11374W01  
; CURRENT APPLICATION NUMBER: US/10/473,037  
; CURRENT FILING DATE: 2003-09-26  
; PRIOR APPLICATION NUMBER: JP2001-097483  
; PRIOR FILING DATE: 2001-03-29  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-473-037-5

Query Match 100.0%; Score 54; DB 6; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.0007;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VKLGTYFYDS 10  
||| ||||| |||

Db 1 VKLGTYFYDS 10

RESULT 2  
US-10-473-037-9  
; Sequence 9, Application US/10473037  
; Publication No. US20050260206A1  
; GENERAL INFORMATION:  
; APPLICANT: KYOWA HAKKO KOGYO CO., LTD.  
; TITLE OF INVENTION: Agents for treatment of cancer using recombinant anti-GD3 antibody  
; TITLE OF INVENTION: the antibody fragments  
; FILE REFERENCE: 11374W01  
; CURRENT APPLICATION NUMBER: US/10/473,037  
; CURRENT FILING DATE: 2003-09-26  
; PRIOR APPLICATION NUMBER: JP2001-097483

; PRIOR FILING DATE: 2001-03-29  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 9  
; LENGTH: 119  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:synthetic protein  
US-10-473-037-9

Query Match 100.0%; Score 54; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 0.0077;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VKLGTYFYDS 10  
||| ||||| |||

Db 99 VKLGTYFYDS 108

## RESULT 3

US-10-473-037-49  
; Sequence 49, Application US/10473037  
; Publication No. US20050260206A1  
; GENERAL INFORMATION:  
; APPLICANT: KYOWA HAKKO KOGYO CO., LTD.  
; TITLE OF INVENTION: Agents for treatment of cancer using recombinant anti-GP3 antibod  
; TITLE OF INVENTION: the antibody fragments  
; FILE REFERENCE: 11374W01  
; CURRENT APPLICATION NUMBER: US/10/473,037  
; CURRENT FILING DATE: 2003-09-26  
; PRIOR APPLICATION NUMBER: JP2001-097483  
; PRIOR FILING DATE: 2001-03-29  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 49  
; LENGTH: 119  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-473-037-49

Query Match 100.0%; Score 54; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 0.0077;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VKLGTYFYDS 10  
||| ||||| |||

Db 99 VKLGTYFYDS 108

## RESULT 4

US-11-228-293-8  
; Sequence 8, Application US/11228293  
; Publication No. US20060057139A1  
; GENERAL INFORMATION:  
; APPLICANT: SHITARA, KENYA  
; APPLICANT: HANAI, NORUO  
; APPLICANT: HASEGAWA, MAMORU  
; APPLICANT: MIYAJI, HIROMASA  
; APPLICANT: KIWANA, YOSHIHISA  
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY  
; FILE REFERENCE: 249-101  
; CURRENT APPLICATION NUMBER: US/11/228,293  
; CURRENT FILING DATE: 2005-09-19  
; PRIOR APPLICATION NUMBER: US/09/225,322  
; PRIOR FILING DATE: 1999-01-05  
; PRIOR APPLICATION NUMBER: US 08/454,680  
; PRIOR FILING DATE: 1995-05-31  
; PRIOR APPLICATION NUMBER: US 08/408,133  
; PRIOR FILING DATE: 1995-03-21  
; PRIOR APPLICATION NUMBER: US 08/292,178  
; PRIOR FILING DATE: 1994-08-17  
; PRIOR APPLICATION NUMBER: US07/947,674

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; PRIOR FILING DATE: 1992-09-17
; PRIOR APPLICATION NUMBER: JP 3-238375
; PRIOR FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 8
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: cDNA KM-641
US-11-228-293-8

Query Match          100.0%; Score 54; DB 7; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.0084;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VKLGTYYFDS 10
        |||||
Db       109 VKLGTYYFDS 118

RESULT 5
US-11-228-293-18
; Sequence 18, Application US/11228293
; Publication No. US20060057139A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUWANA, YOSHIHISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/11/228,293
; CURRENT FILING DATE: 2005-09-19
; PRIOR APPLICATION NUMBER: US/09/225,322
; PRIOR FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: US 08/454,680
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
; PRIOR APPLICATION NUMBER: US07/947,674
; PRIOR FILING DATE: 1992-09-17
; PRIOR APPLICATION NUMBER: JP 3-238375
; PRIOR FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 18
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: cDNA KM-641
US-11-228-293-18

Query Match          100.0%; Score 54; DB 7; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.0084;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VKLGTYYFDS 10
        |||||
Db       109 VKLGTYYFDS 118

RESULT 6
US-11-228-319-8
; Sequence 8, Application US/11228319
; Publication No. US20060058512A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
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; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUWANA, YOSHIHISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/11/228,319
; CURRENT FILING DATE: 2005-09-19
; PRIOR APPLICATION NUMBER: US/09/225,322
; PRIOR FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: US 08/454,680
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
; PRIOR APPLICATION NUMBER: US07/947,674
; PRIOR FILING DATE: 1992-09-17
; PRIOR APPLICATION NUMBER: JP 3-238375
; PRIOR FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 8
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: cDNA KM-641
US-11-228-319-8

Query Match          100.0%; Score 54; DB 7; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.0084;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VKLGTYYFDS 10
        |||||
Db       109 VKLGTYYFDS 118

RESULT 7
US-11-228-319-18
; Sequence 18, Application US/11228319
; Publication No. US20060058512A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUWANA, YOSHIHISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/11/228,319
; CURRENT FILING DATE: 2005-09-19
; PRIOR APPLICATION NUMBER: US/09/225,322
; PRIOR FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: US 08/454,680
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
; PRIOR APPLICATION NUMBER: US07/947,674
; PRIOR FILING DATE: 1992-09-17
; PRIOR APPLICATION NUMBER: JP 3-238375
; PRIOR FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 18
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: cDNA KM-641
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## US-11-228-319-18

Query Match 100.0%; Score 54; DB 7; Length 130;  
Best Local Similarity 100.0%; Pred. No. 0.0084;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VKLGTYYFDS 10  
||| |||||  
Db 109 VKLGTYYFDS 118

## RESULT 8

US-10-473-037-1

; Sequence 1, Application US/10473037

; Publication No. US20050260206A1

; GENERAL INFORMATION:

; APPLICANT: KYOWA HAKKO KOGYO CO., LTD.

; TITLE OF INVENTION: Agents for treatment of cancer using recombinant anti-GD3 antibod

; FILE REFERENCE: 11374WO1

; CURRENT APPLICATION NUMBER: US/10/473,037

; PRIOR FILING DATE: 2003-09-26

; PRIOR APPLICATION NUMBER: JP2001-097483

; PRIOR FILING DATE: 2001-03-29

; NUMBER OF SEQ ID NOS: 50

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 1

; LENGTH: 138

; TYPE: PRT

; ORGANISM: Mus musculus

US-10-473-037-1

Query Match 100.0%; Score 54; DB 6; Length 138;  
Best Local Similarity 100.0%; Pred. No. 0.0088;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VKLGTYYFDS 10  
||| |||||  
Db 118 VKLGTYYFDS 127

## RESULT 9

US-11-102-512-57

; Sequence 57, Application US/11102512

; Publication No. US20060062784A1

; GENERAL INFORMATION:

; APPLICANT: Grant et al., S.

; TITLE OF INVENTION: Compositions monovalent for CD40L binding and methods of use

; FILE REFERENCE: 8039/2132B

; CURRENT APPLICATION NUMBER: US/11/102,512

; CURRENT FILING DATE: 2005-04-08

; PRIOR APPLICATION NUMBER: 60/610,819

; PRIOR FILING DATE: 2004-09-17

; NUMBER OF SEQ ID NOS: 247

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 57

; LENGTH: 123

; TYPE: PRT

; ORGANISM: Homo sapiens

US-11-102-512-57

Query Match 68.5%; Score 37; DB 7; Length 123;  
Best Local Similarity 87.5%; Pred. No. 8.6;  
Matches 7; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 3 LGTYFDS 10  
||| |||||  
Db 56 LGTYFDS 63

## RESULT 10

US-11-054-515-2132

; Sequence 2132, Application US/11054515

; Publication No. US2005025532A1

; GENERAL INFORMATION:

; APPLICANT: Ruben et al.

; TITLE OF INVENTION: Antibodies that Immunoespecifically Bind Blys

; FILE REFERENCE: PF523P3

; CURRENT APPLICATION NUMBER: US/11/054,515

; CURRENT FILING DATE: 2005-02-10

; PRIOR APPLICATION NUMBER: 60/543,296

; PRIOR FILING DATE: 2004-02-11

; PRIOR APPLICATION NUMBER: 60/580,347

; PRIOR FILING DATE: 2004-06-18

; PRIOR APPLICATION NUMBER: 10/293,418

; PRIOR FILING DATE: 2002-11-14

; PRIOR APPLICATION NUMBER: 60/331,469

; PRIOR FILING DATE: 2001-11-16

; PRIOR APPLICATION NUMBER: 60/340,817

; PRIOR FILING DATE: 2001-12-19

; PRIOR APPLICATION NUMBER: 09/880,748

; PRIOR FILING DATE: 2001-06-15

; PRIOR APPLICATION NUMBER: 60/293,499

; PRIOR FILING DATE: 2001-05-25

; PRIOR APPLICATION NUMBER: 60/277,379

; PRIOR FILING DATE: 2001-03-21

; PRIOR APPLICATION NUMBER: 60/276,248

; PRIOR FILING DATE: 2001-03-16

; PRIOR APPLICATION NUMBER: 60/240,816

; PRIOR FILING DATE: 2000-10-17

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 3247

; SEQ ID NO 2132

; LENGTH: 23

; TYPE: PRT

; ORGANISM: Homo sapiens

US-11-054-515-2132

Query Match 64.8%; Score 35; DB 7; Length 23;  
Best Local Similarity 55.6%; Pred. No. 3.9;  
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 VKLGTYYFD 9  
: : |||||  
Db 14 INVGPYFD 22

## RESULT 11

US-11-054-515-3076

; Sequence 3076, Application US/11054515

; Publication No. US2005025532A1

; GENERAL INFORMATION:

; APPLICANT: Ruben et al.

; TITLE OF INVENTION: Antibodies that Immunoespecifically Bind Blys

; FILE REFERENCE: PF523P3

; CURRENT APPLICATION NUMBER: US/11/054,515

; CURRENT FILING DATE: 2005-02-10

; PRIOR APPLICATION NUMBER: 60/543,296

; PRIOR FILING DATE: 2004-02-11

; PRIOR APPLICATION NUMBER: 60/580,347

; PRIOR FILING DATE: 2004-06-18

; PRIOR APPLICATION NUMBER: 10/293,418

; PRIOR FILING DATE: 2002-11-14

; PRIOR APPLICATION NUMBER: 60/331,469

; PRIOR FILING DATE: 2001-11-16

; PRIOR APPLICATION NUMBER: 60/340,817

; PRIOR FILING DATE: 2001-12-19

; PRIOR APPLICATION NUMBER: 09/880,748

; PRIOR FILING DATE: 2001-06-15

; PRIOR APPLICATION NUMBER: 60/293,499

; PRIOR FILING DATE: 2001-05-25

; PRIOR APPLICATION NUMBER: 60/277,379

; PRIOR FILING DATE: 2001-03-21

; PRIOR APPLICATION NUMBER: 60/276,248

; PRIOR FILING DATE: 2001-03-16

; PRIOR APPLICATION NUMBER: 60/240,816

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; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 3076
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-3076

Query Match          64.8%; Score 35; DB 7; Length 23;
Best Local Similarity 55.6%; Pred. No. 3.9;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 VKLGTYYFD 9
Db 14 INVGPIYFD 22

RESULT 12
US-11-266-444-2132
; Sequence 2132, Application US/11266444
; Publication No. US20060062789A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to B Lymphocyte Stimulat
; FILE REFERENCE: PF523P1D1
; CURRENT APPLICATION NUMBER: US/11/266,444
; CURRENT FILING DATE: 2005-11-04
; PRIOR APPLICATION NUMBER: 09/880,746
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2132
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-266-444-2132

Query Match          64.8%; Score 35; DB 7; Length 23;
Best Local Similarity 55.8%; Pred. No. 3.9;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 VKLGTYYFD 9
Db 14 INVGPIYFD 22

RESULT 13
US-11-266-444-3076
; Sequence 3076, Application US/11266444
; Publication No. US20060062789A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to B Lymphocyte Stimulat
; FILE REFERENCE: PF523P1D1
; CURRENT APPLICATION NUMBER: US/11/266,444
; CURRENT FILING DATE: 2005-11-04
; PRIOR APPLICATION NUMBER: 09/880,746
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17

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; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3076
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-266-444-3076

Query Match          64.8%; Score 35; DB 7; Length 23;
Best Local Similarity 55.6%; Pred. No. 3.9;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 VKLGTYYFD 9
Db 14 INVGPIYFD 22

RESULT 14
US-10-956-008-38
; Sequence 38, Application US/10956008
; Publication No. US20060062783A1
; GENERAL INFORMATION:
; APPLICANT: Roskos, Lorin
; APPLICANT: Foltz, Ian
; APPLICANT: King, Chadwick
; APPLICANT: Bell, Gregory
; TITLE OF INVENTION: ANTIBODIES AGAINST PARATHYROID HORMONE
; FILE REFERENCE: ABGENIX.092CP1
; CURRENT APPLICATION NUMBER: US/10/956,008
; CURRENT FILING DATE: 2004-09-30
; PRIOR APPLICATION NUMBER: 10/638,265
; PRIOR FILING DATE: 2003-08-08
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-956-008-38

Query Match          64.8%; Score 35; DB 6; Length 123;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TTYFDS 10
Db 100 TTYFDS 105

RESULT 15
US-10-956-008-46
; Sequence 46, Application US/10956008
; Publication No. US20060062783A1
; GENERAL INFORMATION:
; APPLICANT: Roskos, Lorin
; APPLICANT: Foltz, Ian
; APPLICANT: King, Chadwick
; APPLICANT: Bell, Gregory
; TITLE OF INVENTION: ANTIBODIES AGAINST PARATHYROID HORMONE
; FILE REFERENCE: ABGENIX.092CP1
; CURRENT APPLICATION NUMBER: US/10/956,008
; CURRENT FILING DATE: 2004-09-30
; PRIOR APPLICATION NUMBER: 10/638,265
; PRIOR FILING DATE: 2003-08-08
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 46

```

```
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-956-008-46

Query Match      64.8%; Score 35; DB 6; Length 123;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 TYTFDS 10
Db      100 TYTFDS 105

RESULT 16
US-10-956-008-50
; Sequence 50, Application US/10956008
; Publication No. US20060062783A1
; GENERAL INFORMATION:
; APPLICANT: Roskos, Lorin
; APPLICANT: Poltz, Ian
; APPLICANT: King, Chadwick
; APPLICANT: Bell, Gregory
; TITLE OF INVENTION: ANTIBODIES AGAINST PARATHYROID HORMONE
; FILE REFERENCE: ABGENIX.092CPI
; CURRENT APPLICATION NUMBER: US/10/956,008
; CURRENT FILING DATE: 2004-09-30
; PRIOR APPLICATION NUMBER: 10/638,265
; PRIOR FILING DATE: 2003-08-08
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 50
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-956-008-50

Query Match      64.8%; Score 35; DB 6; Length 123;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 TYTFDS 10
Db      100 TYTFDS 105

RESULT 17
US-10-956-008-54
; Sequence 54, Application US/10956008
; Publication No. US20060062783A1
; GENERAL INFORMATION:
; APPLICANT: Roskos, Lorin
; APPLICANT: Poltz, Ian
; APPLICANT: King, Chadwick
; APPLICANT: Bell, Gregory
; TITLE OF INVENTION: ANTIBODIES AGAINST PARATHYROID HORMONE
; FILE REFERENCE: ABGENIX.092CPI
; CURRENT APPLICATION NUMBER: US/10/956,008
; CURRENT FILING DATE: 2004-09-30
; PRIOR APPLICATION NUMBER: 10/638,265
; PRIOR FILING DATE: 2003-08-08
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 54
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-956-008-54

Query Match      64.8%; Score 35; DB 6; Length 123;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 TYTFDS 10
Db      100 TYTFDS 105

RESULT 18
US-11-102-512-61
; Sequence 61, Application US/11102512
; Publication No. US20060062784A1
; GENERAL INFORMATION:
; APPLICANT: Grant et al., S.
; TITLE OF INVENTION: Compositions monovalent for CD40L binding and methods of use
; FILE REFERENCE: 8039/2132B
; CURRENT APPLICATION NUMBER: US/11/102,512
; CURRENT FILING DATE: 2005-04-08
; PRIOR APPLICATION NUMBER: 60/610,819
; PRIOR FILING DATE: 2004-09-17
; NUMBER OF SEQ ID NOS: 247
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 61
; LENGTH: 124
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-102-512-61

Query Match      64.8%; Score 35; DB 7; Length 124;
Best Local Similarity 75.0%; Pred. No. 20;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      3 LGTYFDS 10
Db      56 MGTYVADS 63

RESULT 19
US-10-793-626-1932
; Sequence 1932, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMBERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PUS3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1932
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-1932

Query Match      64.8%; Score 35; DB 6; Length 226;
Best Local Similarity 75.0%; Pred. No. 35;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      2 KLGYTYFDD 9
Db      211 KLGYTCFDD 218

RESULT 20
US-11-054-515-4
; Sequence 4, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
```



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; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 4
; LENGTH: 255
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-4

Query Match      64.8%; Score 35; DB 7; Length 255;
Best Local Similarity 55.6%; Pred. No. 40;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      1 VKLGTYYFD 9
Db      112 INVGPYFD 120

RESULT 21
US-11-054-515-1054
; Sequence 1054, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1054
; LENGTH: 255
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-5
```

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; LENGTH: 255
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1054

Query Match      64.8%; Score 35; DB 7; Length 255;
Best Local Similarity 55.6%; Pred. No. 40;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      1 VKLGTYYFD 9
Db      112 INVGPYFD 120

RESULT 22
US-11-054-515-1056
; Sequence 1056, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1056
; LENGTH: 255
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1056

Query Match      64.8%; Score 35; DB 7; Length 255;
Best Local Similarity 55.6%; Pred. No. 40;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      1 VKLGTYYFD 9
Db      112 INVGPYFD 120

RESULT 23
US-11-054-515-1065
; Sequence 1065, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1054
```

; PRIOR APPLICATION NUMBER: 60/580,347  
; PRIOR FILING DATE: 2004-06-18  
; PRIOR APPLICATION NUMBER: 10/293,418  
; PRIOR FILING DATE: 2002-11-14  
; PRIOR APPLICATION NUMBER: 60/331,469  
; PRIOR FILING DATE: 2001-11-16  
; PRIOR APPLICATION NUMBER: 60/340,817  
; PRIOR FILING DATE: 2001-12-19  
; PRIOR APPLICATION NUMBER: 09/880,748  
; PRIOR FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/293,499  
; PRIOR FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: 60/277,379  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/276,248  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/240,816  
; PRIOR FILING DATE: 2000-10-17  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 3247  
; SEQ ID NO 1065  
; LENGTH: 255  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-054-515-1065

Query Match 64.8%; Score 35; DB 7; Length 255;  
Best Local Similarity 55.6%; Pred. No. 40;  
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 VKLGTYYFD 9  
: : |||||  
Db 112 INVGPYYFD 120

RESULT 24  
US-11-054-515-1786  
; Sequence 1786, Application US/11054515  
; Publication No. US2005025532A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
; FILE REFERENCE: PF523P3  
; CURRENT APPLICATION NUMBER: US/11/054,515  
; CURRENT FILING DATE: 2005-02-10  
; PRIOR APPLICATION NUMBER: 60/543,296  
; PRIOR FILING DATE: 2004-02-11  
; PRIOR APPLICATION NUMBER: 60/580,347  
; PRIOR FILING DATE: 2004-06-18  
; PRIOR APPLICATION NUMBER: 10/293,418  
; PRIOR FILING DATE: 2002-11-14  
; PRIOR APPLICATION NUMBER: 60/331,469  
; PRIOR FILING DATE: 2001-11-16  
; PRIOR APPLICATION NUMBER: 60/340,817  
; PRIOR FILING DATE: 2001-12-19  
; PRIOR APPLICATION NUMBER: 09/880,748  
; PRIOR FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/293,499  
; PRIOR FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: 60/277,379  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/276,248  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/240,816  
; PRIOR FILING DATE: 2000-10-17  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 3247  
; SEQ ID NO 1786  
; LENGTH: 255  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-054-515-1786

Query Match 64.8%; Score 35; DB 7; Length 255;  
Best Local Similarity 55.6%; Pred. No. 40;  
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 VKLGTYYFD 9  
: : |||||  
Db 112 INVGPYYFD 120

RESULT 25  
US-11-266-444-4  
; Sequence 4, Application US/11266444  
; Publication No. US20060062789A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to B Lymphocyte Stimulators  
; FILE REFERENCE: PFS23P1D1  
; CURRENT APPLICATION NUMBER: US/11/266,444  
; CURRENT FILING DATE: 2005-11-04  
; PRIOR APPLICATION NUMBER: 09/880,746  
; PRIOR FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/212,210  
; PRIOR FILING DATE: 2000-06-16  
; PRIOR APPLICATION NUMBER: 60/240,816  
; PRIOR FILING DATE: 2000-10-17  
; PRIOR APPLICATION NUMBER: 60/276,248  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/277,379  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/293,499  
; PRIOR FILING DATE: 2001-05-25  
; NUMBER OF SEQ ID NOS: 3239  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 4  
; LENGTH: 255  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-266-444-4

Query Match 64.8%; Score 35; DB 7; Length 255;  
Best Local Similarity 55.6%; Pred. No. 40;  
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 VKLGTYYFD 9  
: : |||||  
Db 112 INVGPYYFD 120

RESULT 26  
US-11-266-444-1054  
; Sequence 1054, Application US/11266444  
; Publication No. US20060062789A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to B Lymphocyte Stimulators  
; FILE REFERENCE: PFS23P1D1  
; CURRENT APPLICATION NUMBER: US/11/266,444  
; CURRENT FILING DATE: 2005-11-04  
; PRIOR APPLICATION NUMBER: 09/880,746  
; PRIOR FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/212,210  
; PRIOR FILING DATE: 2000-06-16  
; PRIOR APPLICATION NUMBER: 60/240,816  
; PRIOR FILING DATE: 2000-10-17  
; PRIOR APPLICATION NUMBER: 60/276,248  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/277,379  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/293,499  
; PRIOR FILING DATE: 2001-05-25  
; NUMBER OF SEQ ID NOS: 3239  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1054

; LENGTH: 255  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-266-444-1054

Query Match 64.8%; Score 35; DB 7; Length 255;  
Best Local Similarity 55.6%; Pred. No. 40;  
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 VKLGTYYFD 9  
Db 112 INVGPYYFD 120

## RESULT 27

US-11-266-444-1056  
; Sequence 1056, Application US/11266444  
; Publication No. US20060062789A1  
; GENERAL INFORMATION:

; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to B Lymphocyte Stimulator  
; FILE REFERENCE: PF523PDI1  
; CURRENT APPLICATION NUMBER: US/11/266,444  
; CURRENT FILING DATE: 2005-11-04  
; PRIOR APPLICATION NUMBER: 09/880,746  
; PRIOR FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/212,210  
; PRIOR FILING DATE: 2000-06-16  
; PRIOR APPLICATION NUMBER: 60/240,816  
; PRIOR FILING DATE: 2000-10-17  
; PRIOR APPLICATION NUMBER: 60/276,248  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/277,379  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/293,499  
; PRIOR FILING DATE: 2001-05-25  
; NUMBER OF SEQ ID NOS: 3239  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1056  
; LENGTH: 255  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-266-444-1056

Query Match 64.8%; Score 35; DB 7; Length 255;  
Best Local Similarity 55.6%; Pred. No. 40;  
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 VKLGTYYFD 9  
Db 112 INVGPYYFD 120

## RESULT 28

US-11-266-444-1065  
; Sequence 1065, Application US/11266444  
; Publication No. US20060062789A1  
; GENERAL INFORMATION:

; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to B Lymphocyte Stimulator  
; FILE REFERENCE: PF523PDI1  
; CURRENT APPLICATION NUMBER: US/11/266,444  
; CURRENT FILING DATE: 2005-11-04  
; PRIOR APPLICATION NUMBER: 09/880,746  
; PRIOR FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/212,210  
; PRIOR FILING DATE: 2000-06-16  
; PRIOR APPLICATION NUMBER: 60/240,816  
; PRIOR FILING DATE: 2000-10-17  
; PRIOR APPLICATION NUMBER: 60/276,248  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/277,379  
; PRIOR FILING DATE: 2001-03-21

; PRIOR APPLICATION NUMBER: 60/293,499  
; PRIOR FILING DATE: 2001-05-25  
; NUMBER OF SEQ ID NOS: 3239  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1065  
; LENGTH: 255  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-266-444-1065

Query Match 64.8%; Score 35; DB 7; Length 255;  
Best Local Similarity 55.6%; Pred. No. 40;  
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 VKLGTYYFD 9  
Db 112 INVGPYYFD 120

## RESULT 29

US-11-266-444-1786  
; Sequence 1786, Application US/11266444  
; Publication No. US20060062789A1  
; GENERAL INFORMATION:

; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to B Lymphocyte Stimulator  
; FILE REFERENCE: PF523PDI1  
; CURRENT APPLICATION NUMBER: US/11/266,444  
; CURRENT FILING DATE: 2005-11-04  
; PRIOR APPLICATION NUMBER: 09/880,746  
; PRIOR FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/212,210  
; PRIOR FILING DATE: 2000-06-16  
; PRIOR APPLICATION NUMBER: 60/240,816  
; PRIOR FILING DATE: 2000-10-17  
; PRIOR APPLICATION NUMBER: 60/276,248  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/277,379  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/293,499  
; PRIOR FILING DATE: 2001-05-25  
; NUMBER OF SEQ ID NOS: 3239  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1786  
; LENGTH: 255  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-266-444-1786

Query Match 64.8%; Score 35; DB 7; Length 255;  
Best Local Similarity 55.6%; Pred. No. 40;  
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 VKLGTYYFD 9  
Db 112 INVGPYYFD 120

## RESULT 30

US-11-054-515-1773  
; Sequence 1773, Application US/11054515  
; Publication No. US2005025532A1  
; GENERAL INFORMATION:

; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
; FILE REFERENCE: PF523P3  
; CURRENT APPLICATION NUMBER: US/11/054,515  
; CURRENT FILING DATE: 2005-02-10  
; PRIOR APPLICATION NUMBER: 60/543,296  
; PRIOR FILING DATE: 2004-02-11  
; PRIOR APPLICATION NUMBER: 60/580,347  
; PRIOR FILING DATE: 2004-06-18  
; PRIOR APPLICATION NUMBER: 10/293,418

; PRIOR FILING DATE: 2002-11-14  
; PRIOR APPLICATION NUMBER: 60/331,469  
; PRIOR FILING DATE: 2001-11-16  
; PRIOR APPLICATION NUMBER: 60/340,817  
; PRIOR FILING DATE: 2001-12-19  
; PRIOR APPLICATION NUMBER: 09/880,748  
; PRIOR FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/293,499  
; PRIOR FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: 60/277,379  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/276,248  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/240,816  
; PRIOR FILING DATE: 2000-10-17  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 3247  
; SEQ ID NO 1773  
; LENGTH: 258  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-054-515-1773

Query Match 64.8%; Score 35; DB 7; Length 258;  
Best Local Similarity 55.6%; Pred. No. 40;  
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 VKLGYTFD 9  
: : |||||  
DB 112 INVGPYFD 120

## RESULT 31

US-11-266-444-1773  
; Sequence 1773, Application US/11266444  
; Publication No. US2006062789A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to B Lymphocyte Stimulat  
; FILE REFERENCE: PF523PDI  
; CURRENT APPLICATION NUMBER: US/11/266,444  
; CURRENT FILING DATE: 2005-11-04  
; PRIOR APPLICATION NUMBER: 09/880,746  
; PRIOR FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/212,210  
; PRIOR FILING DATE: 2000-06-16  
; PRIOR APPLICATION NUMBER: 60/240,816  
; PRIOR FILING DATE: 2000-10-17  
; PRIOR APPLICATION NUMBER: 60/276,248  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/277,379  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/293,499  
; PRIOR FILING DATE: 2001-05-25  
; NUMBER OF SEQ ID NOS: 3239  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1773  
; LENGTH: 258  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-266-444-1773

Query Match 64.8%; Score 35; DB 7; Length 258;  
Best Local Similarity 55.6%; Pred. No. 40;  
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 VKLGYTFD 9  
: : |||||  
DB 112 INVGPYFD 120

## RESULT 32

US-11-087-099-10597

; Sequence 10597, Application US/11087099  
; Publication No. US20060041961A1  
; GENERAL INFORMATION:  
; APPLICANT: Abad, Mark S. et al.  
; TITLE OF INVENTION: Genes and Uses for Plant Improvement  
; FILE REFERENCE: 38-21(53450)B EP  
; CURRENT APPLICATION NUMBER: US/11/087,099  
; CURRENT FILING DATE: 2005-03-22  
; NUMBER OF SEQ ID NOS: 12464  
; SEQ ID NO 10597  
; LENGTH: 287  
; TYPE: PRT  
; ORGANISM: Staphylococcus epidermidis ATCC 12228  
US-11-087-099-10597

Query Match 64.8%; Score 35; DB 7; Length 287;  
Best Local Similarity 75.0%; Pred. No. 45;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 KLGTYTFD 9  
: : |||||  
DB 272 KLGTYCFD 279

## RESULT 33

US-11-221-281-44  
; Sequence 44, Application US/11221281  
; Publication No. US20060062786A1  
; GENERAL INFORMATION:  
; APPLICANT: Salcedo et al.  
; TITLE OF INVENTION: Antibodies That Immunospecifically Bind To TRAIL Receptors  
; FILE REFERENCE: PF532P3  
; CURRENT APPLICATION NUMBER: US/11/221,281  
; CURRENT FILING DATE: 2005-09-08  
; PRIOR APPLICATION NUMBER: 60/608,449  
; PRIOR FILING DATE: 2004-09-10  
; PRIOR APPLICATION NUMBER: 10/838,977  
; PRIOR FILING DATE: 2004-05-05  
; PRIOR APPLICATION NUMBER: 60/495,139  
; PRIOR FILING DATE: 2003-08-15  
; PRIOR APPLICATION NUMBER: 60/468,105  
; PRIOR FILING DATE: 2003-05-06  
; PRIOR APPLICATION NUMBER: 10/292,486  
; PRIOR FILING DATE: 2002-11-13  
; PRIOR APPLICATION NUMBER: 60/403,376  
; PRIOR FILING DATE: 2002-08-15  
; PRIOR APPLICATION NUMBER: 60/377,973  
; PRIOR FILING DATE: 2002-05-07  
; PRIOR APPLICATION NUMBER: 60/331,309  
; PRIOR FILING DATE: 2001-11-14  
; PRIOR APPLICATION NUMBER: 09/986,149  
; PRIOR FILING DATE: 2001-11-07  
; PRIOR APPLICATION NUMBER: 60/327,359  
; PRIOR FILING DATE: 2001-10-09  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 51  
; SEQ ID NO 44  
; LENGTH: 128  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-221-281-44

Query Match 63.0%; Score 34; DB 7; Length 128;  
Best Local Similarity 71.4%; Pred. No. 31;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 GTTYFDS 10  
: : |||||  
DB 100 GSYTYDS 106

## RESULT 34

US-11-096-568A-18183

```
; Sequence 18183, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 18183
; LENGTH: 161
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(161)
; OTHER INFORMATION: Ceres Seq. ID no. 12363378
US-11-096-568A-18183

Query Match          63.0%; Score 34; DB 7; Length 161;
Best Local Similarity 71.4%; Pred. No. 39;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 VKLGTY 7
Db 133 IRLGTY 139

RESULT 35
US-11-096-568A-18181
; Sequence 18181, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 18181
; LENGTH: 208
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(208)
; OTHER INFORMATION: Ceres Seq. ID no. 12363376
US-11-096-568A-18181

Query Match          63.0%; Score 34; DB 7; Length 208;
Best Local Similarity 71.4%; Pred. No. 49;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 VKLGTY 7
Db 180 IRLGTY 186

RESULT 36
US-11-074-176-98
; Sequence 98, Application US/11074176
; Publication No. US20050250135A1
; GENERAL INFORMATION:
; APPLICANT: Klaenhammer, Todd R.
; APPLICANT: Russell, William M.
; APPLICANT: Altermann, Eric
; APPLICANT: McAuliffe, Olivia
; APPLICANT: Peril, Andrea Azcarate
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding
; TITLE OF INVENTION: Stress-Related Proteins and Uses Therefore
; FILE REFERENCE: 5051-694
```

```
; CURRENT APPLICATION NUMBER: US/11/074,176
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: 60/551,161
; PRIOR FILING DATE: 2004-03-08
; NUMBER OF SEQ ID NOS: 381
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 98
; LENGTH: 565
; TYPE: PRT
; ORGANISM: Lactobacillus acidophilus
US-11-074-176-98

Query Match          63.0%; Score 34; DB 7; Length 565;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KLGTYY 7
Db 413 KLGTYY 418

RESULT 37
US-11-201-825-41
; Sequence 41, Application US/11201825
; Publication No. US2006003481A1
; GENERAL INFORMATION:
; APPLICANT: TOBIN, JAMES F.
; TITLE OF INVENTION: COMBINATION THERAPY FOR DIABETES, OBESITY, AND
; TITLE OF INVENTION: CARDIOVASCULAR DISEASES USING GDF-8 INHIBITORS
; FILE REFERENCE: 08702.0106-00000
; CURRENT APPLICATION NUMBER: US/11/201,825
; CURRENT FILING DATE: 2005-08-11
; PRIOR APPLICATION NUMBER: 60/600,784
; PRIOR FILING DATE: 2004-08-12
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 41
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-201-825-41

Query Match          61.1%; Score 33; DB 7; Length 12;
Best Local Similarity 83.3%; Pred. No. 4.7;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 GTYYFD 9
Db 6 GSYTFD 11

RESULT 38
US-10-473-037-4
; Sequence 4, Application US/10473037
; Publication No. US20050260206A1
; GENERAL INFORMATION:
; APPLICANT: KYOWA HAKKO KOGYO CO., LTD.
; TITLE OF INVENTION: Agents for treatment of cancer using recombinant anti-GD3 antibo
; TITLE OF INVENTION: the antibody fragments
; FILE REFERENCE: 11374W01
; CURRENT APPLICATION NUMBER: US/10/473,037
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: JP2001-097483
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-473-037-4

Query Match          61.1%; Score 33; DB 6; Length 17;
```

```
Best Local Similarity 85.7%; Pred. No. 6.6;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GTTYFDS 10
Db 8 GTTYSDS 14

RESULT 39
US-11-054-669-48
; Sequence 48, Application US/11054669
; Publication No. US20050261480A1
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: SUPER HUMANIZED ANTIBODIES
; FILE REFERENCE: 30219/US/3
; CURRENT APPLICATION NUMBER: US/11/054,669
; CURRENT FILING DATE: 2005-02-08
; PRIOR APPLICATION NUMBER: US 10/194,975
; PRIOR FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 48
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-669-48

Query Match 61.1%; Score 33; DB 7; Length 97;
Best Local Similarity 85.7%; Pred. No. 36;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GTTYFDS 10
Db 56 GTTYADS 62

RESULT 40
US-11-093-274-32
; Sequence 32, Application US/11093274
; Publication No. US20050266008A1
; GENERAL INFORMATION:
; APPLICANT: Cardarelli, Robert
; APPLICANT: Kempe, Thomas
; APPLICANT: Cutter, Beth
; APPLICANT: Srinivasan, Mohan
; TITLE OF INVENTION: IRTA-5 ANTIBODIES AND THEIR USES
; FILE REFERENCE: 04280/1201101-US1
; CURRENT APPLICATION NUMBER: US/11/093,274
; CURRENT FILING DATE: 2005-03-28
; PRIOR APPLICATION NUMBER: 60/557,741
; PRIOR FILING DATE: 2004-03-29
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 32
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-093-274-32

Query Match 61.1%; Score 33; DB 7; Length 97;
Best Local Similarity 85.7%; Pred. No. 36;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GTTYFDS 10
Db 56 GTTYADS 62

RESULT 41
US-11-093-274-32
; Sequence 32, Application US/11093274
; Publication No. US20050266008A1
; GENERAL INFORMATION:
; APPLICANT: Cardarelli, Robert
; APPLICANT: Kempe, Thomas
; APPLICANT: Cutter, Beth
; APPLICANT: Srinivasan, Mohan
; TITLE OF INVENTION: IRTA-5 ANTIBODIES AND THEIR USES
; FILE REFERENCE: 04280/1201101-US1
; CURRENT APPLICATION NUMBER: US/11/093,274
; CURRENT FILING DATE: 2005-03-28
; PRIOR APPLICATION NUMBER: 60/557,741
; PRIOR FILING DATE: 2004-03-29
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 32
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-093-274-32

Query Match 61.1%; Score 33; DB 7; Length 97;
Best Local Similarity 85.7%; Pred. No. 36;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GTTYFDS 10
Db 56 GTTYADS 62

RESULT 42
US-11-102-512-31
; Sequence 31, Application US/11102512
; Publication No. US20060062784A1
; GENERAL INFORMATION:
; APPLICANT: Grant et al., S.
; TITLE OF INVENTION: Compositions monovalent for CD40L binding and methods of use
; FILE REFERENCE: 8039/2132B
; CURRENT APPLICATION NUMBER: US/11/102,512
; CURRENT FILING DATE: 2005-04-08
; PRIOR APPLICATION NUMBER: 60/610,819
; PRIOR FILING DATE: 2004-09-17
; NUMBER OF SEQ ID NOS: 247
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 31
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-102-512-31

Query Match 61.1%; Score 33; DB 7; Length 116;
Best Local Similarity 85.7%; Pred. No. 42;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GTTYFDS 10
Db 57 GTTYADS 63

RESULT 43
US-11-102-512-64
; Sequence 64, Application US/11102512
; Publication No. US20060062784A1
; GENERAL INFORMATION:
; APPLICANT: Grant et al., S.
; TITLE OF INVENTION: Compositions monovalent for CD40L binding and methods of use
; FILE REFERENCE: 8039/2132B
; CURRENT APPLICATION NUMBER: US/11/102,512
; CURRENT FILING DATE: 2005-04-08
; PRIOR APPLICATION NUMBER: 60/610,819
; PRIOR FILING DATE: 2004-09-17
; NUMBER OF SEQ ID NOS: 247
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 64
; LENGTH: 116
```

```
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-102-512-64

Query Match      61.1%; Score 33; DB 7; Length 116;
Best Local Similarity 85.7%; Pred. No. 42;
Matches 6; Conservative 0; Mismatches 0; Gaps 0;

QY      4 GTTYFDS 10
Db      57 GTTYADS 63

RESULT 44
US-11-102-512-76
; Sequence 76, Application US/11102512
; Publication No. US20060062784A1
; GENERAL INFORMATION:
; APPLICANT: Grant et al., S.
; TITLE OF INVENTION: Compositions monovalent for CD40L binding and methods of use
; FILE REFERENCE: 8039/2132B
; CURRENT APPLICATION NUMBER: US/11/102,512
; PRIOR FILING DATE: 2005-04-08
; PRIOR APPLICATION NUMBER: 60/610,819
; PRIOR FILING DATE: 2004-09-17
; NUMBER OF SEQ ID NOS: 247
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 76
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-102-512-76

Query Match      61.1%; Score 33; DB 7; Length 116;
Best Local Similarity 85.7%; Pred. No. 42;
Matches 6; Conservative 0; Mismatches 0; Gaps 0;

QY      4 GTTYFDS 10
Db      57 GTTYADS 63

RESULT 45
US-11-102-512-77
; Sequence 77, Application US/11102512
; Publication No. US20060062784A1
; GENERAL INFORMATION:
; APPLICANT: Grant et al., S.
; TITLE OF INVENTION: Compositions monovalent for CD40L binding and methods of use
; FILE REFERENCE: 8039/2132B
; CURRENT APPLICATION NUMBER: US/11/102,512
; PRIOR FILING DATE: 2005-04-08
; PRIOR APPLICATION NUMBER: 60/610,819
; PRIOR FILING DATE: 2004-09-17
; NUMBER OF SEQ ID NOS: 247
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 77
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-102-512-77

Query Match      61.1%; Score 33; DB 7; Length 116;
Best Local Similarity 85.7%; Pred. No. 42;
Matches 6; Conservative 0; Mismatches 0; Gaps 0;

QY      4 GTTYFDS 10
Db      57 GTTYADS 63

RESULT 46
US-10-925-366A-208
; Sequence 208, Application US/10925366A
; Publication No. US20050271663A1
; GENERAL INFORMATION:
; APPLICANT: Ignatovich, Olga
; APPLICANT: Benjamins, Steven
; APPLICANT: Grant, Steven
; APPLICANT: Jones, Philip
; APPLICANT: Basran, Neil
; APPLICANT: Brewis, Neil
; TITLE OF INVENTION: Compositions and Methods for Treating Inflammatory Disorders
; FILE REFERENCE: 8039/2105
; CURRENT APPLICATION NUMBER: US/10/925,366A
; CURRENT FILING DATE: 2004-08-24
; PRIOR APPLICATION NUMBER: US 10/744,774
; PRIOR FILING DATE: 2003-12-23
; PRIOR APPLICATION NUMBER: PCT/GB2003/002804
; PRIOR FILING DATE: 2003-06-30
; PRIOR APPLICATION NUMBER: PCT/GB2002/03014
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: GB 0230202.4
; PRIOR FILING DATE: 2002-12-27
; PRIOR APPLICATION NUMBER: GB 115841.9
; PRIOR FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: PCT/GB2004/002829
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: US 60/535,076
; PRIOR FILING DATE: 2004-01-08
; PRIOR APPLICATION NUMBER: PCT/GB2003/005646
; PRIOR FILING DATE: 2003-12-24
; PRIOR APPLICATION NUMBER: GB 0327706.8
; PRIOR FILING DATE: 2003-11-28
; PRIOR APPLICATION NUMBER: US 60/509,613
; PRIOR FILING DATE: 2003-10-08
; NUMBER OF SEQ ID NOS: 368
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 208
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Antibody Domain
US-10-925-366A-208

Query Match      61.1%; Score 33; DB 6; Length 118;
Best Local Similarity 85.7%; Pred. No. 43;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      4 GTTYFDS 10
Db      57 GTTYADS 63

RESULT 47
US-11-049-536-524
; Sequence 524, Application US/11049536
; Publication No. US20060024297A1
; GENERAL INFORMATION:
; APPLICANT: Wood, Clive R.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Pieters, Henk
; APPLICANT: Hoet, Rene
; APPLICANT: Hufton, Simon E.
; TITLE OF INVENTION: TIE COMPLEX BINDING PROTEINS
; FILE REFERENCE: 10280-128001
; CURRENT APPLICATION NUMBER: US/11/049,536
; CURRENT FILING DATE: 2005-02-02
; PRIOR APPLICATION NUMBER: US 10/916,840
; PRIOR FILING DATE: 2004-08-12
; PRIOR APPLICATION NUMBER: US 60/494,713
; PRIOR FILING DATE: 2003-08-12
; NUMBER OF SEQ ID NOS: 721
; SOFTWARE: FastSeq for Windows Version 4.0
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; SEQ ID NO 524
; LENGTH: 119
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: Antibody
US-11-049-536-524

Query Match          61.1%; Score 33; DB 7; Length 119;
Best Local Similarity 85.7%; Pred. No. 43;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      4 GTTYFDS 10
      |||||
Db      57 GTTYADS 63

RESULT 48
US-11-199-739-524
; Sequence 524, Application US/11199739
; Publication No. US20060057138A1
; GENERAL INFORMATION:
; APPLICANT: Wood, Clive R.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Pieters, Henk
; APPLICANT: Hoet, Rene
; APPLICANT: Hufton, Simon E.
; TITLE OF INVENTION: TIE COMPLEX BINDING PROTEINS
; FILE REFERENCE: 10280-135001
; CURRENT APPLICATION NUMBER: US/11/199,739
; PRIOR FILING DATE: 2005-08-09
; PRIOR APPLICATION NUMBER: US 11/049,536
; PRIOR FILING DATE: 2005-02-02
; PRIOR APPLICATION NUMBER: US 10/916,840
; PRIOR FILING DATE: 2004-08-12
; PRIOR APPLICATION NUMBER: US 60/494,713
; PRIOR FILING DATE: 2003-08-12
; NUMBER OF SEQ ID NOS: 726
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 524
; LENGTH: 119
; TYPE: PRT
; ORGANISM: ARTIFICIAL
; FEATURE:
; OTHER INFORMATION: Antibody
US-11-199-739-524

Query Match          61.1%; Score 33; DB 7; Length 119;
Best Local Similarity 85.7%; Pred. No. 43;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      4 GTTYFDS 10
      |||||
Db      57 GTTYADS 63

RESULT 49
US-11-201-825-14
; Sequence 14, Application US/11201825
; Publication No. US20060034831A1
; GENERAL INFORMATION:
; APPLICANT: TOBIN, JAMES F.
; TITLE OF INVENTION: COMBINATION THERAPY FOR DIABETES, OBESITY, AND
; FILE REFERENCE: 08702.0106-00000
; CURRENT APPLICATION NUMBER: US/11/201,825
; CURRENT FILING DATE: 2005-08-11
; PRIOR APPLICATION NUMBER: 60/600,784
; PRIOR FILING DATE: 2004-08-12
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 14
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-201-825-14

Query Match          61.1%; Score 33; DB 7; Length 121;
Best Local Similarity 83.3%; Pred. No. 44;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      4 GTTYFD 9
      |:|||
Db      104 GSYFD 109

RESULT 50
US-11-201-825-29
; Sequence 29, Application US/11201825
; Publication No. US20060034831A1
; GENERAL INFORMATION:
; APPLICANT: TOBIN, JAMES F.
; TITLE OF INVENTION: COMBINATION THERAPY FOR DIABETES, OBESITY, AND
; FILE REFERENCE: 08702.0106-00000
; CURRENT APPLICATION NUMBER: US/11/201,825
; CURRENT FILING DATE: 2005-08-11
; PRIOR APPLICATION NUMBER: 60/600,784
; PRIOR FILING DATE: 2004-08-12
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 29
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-201-825-29

Query Match          61.1%; Score 33; DB 7; Length 121;
Best Local Similarity 83.3%; Pred. No. 44;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      4 GTTYFD 9
      |:|||
Db      104 GSYFD 109

Search completed: April 6, 2006, 09:22:58
Job time :12.1695 secs
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OM protein - protein search, using sw model

Run on: April 6, 2006, 08:54:46 ; Search time 81.661 Seconds  
(without alignments)  
59.186 Million cell updates/sec

Title: US-10-089-500-6

Perfect score: 54

Sequence: 1 SASQDISNYLN 11

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

- A\_Geneseq\_21.\*  
1: Genesepi1980s.\*  
2: Genesepi1990s.\*  
3: Genesepi2000s.\*  
4: Genesepi2001s.\*  
5: Genesepi2002s.\*  
6: Genesepi2003as.\*  
7: Genesepi2003bs.\*  
8: Genesepi2004s.\*  
9: Genesepi2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	54	100.0	11	2	Aaw70614 Anti-VEGF
2	54	100.0	11	4	Aab811982 Ganglioside
3	54	100.0	11	5	Abp61183 Humanised
4	54	100.0	11	6	Abu11007 Modified
5	54	100.0	11	9	Adz57813 Ganglioside
6	54	100.0	103	7	Adf09995 Antibody
7	54	100.0	103	7	Adf10099 VEGF anti
8	54	100.0	107	2	Aaw86804 Variable
9	54	100.0	107	2	Aaw86805 Variable
10	54	100.0	107	2	Aaw70623 Humanised
11	54	100.0	107	2	Aaw70625 Humanised
12	54	100.0	107	5	Abp61192 Humanised
13	54	100.0	107	5	Abp61194 Humanised
14	54	100.0	107	9	Aea40449 Anti-VEGF
15	54	100.0	107	9	Aea40445 Anti-VEGF
16	54	100.0	107	9	Aea40440 Anti-VEGF
17	54	100.0	107	9	Aea40443 Anti-VEGF
18	54	100.0	107	9	Aea40450 Anti-VEGF
19	54	100.0	107	9	Aea40452 Anti-VEGF
20	54	100.0	107	9	Aea40447 Anti-VEGF
21	54	100.0	107	9	Aea40446 Anti-VEGF
22	54	100.0	107	9	Aea40439 Anti-VEGF
23	54	100.0	107	9	Aea40444 Anti-VEGF
24	54	100.0	107	9	Aea40442 Anti-VEGF

25	54	100.0	107	9	AEA40451	Aea40451 Anti-VEGF
26	54	100.0	107	9	AEA40448	Aea40448 Anti-VEGF
27	54	100.0	107	9	AEA40722	Aea40722 Anti-VEGF
28	54	100.0	107	9	AEA40441	Aea40441 Anti-VEGF
29	54	100.0	108	2	AAW70620	Aaw70620 Anti-VEGF
30	54	100.0	108	2	AAW70618	Aaw70618 Anti-VEGF
31	54	100.0	108	2	AAW70696	Aaw70696 Anti-VEGF
32	54	100.0	108	4	AAB81988	Aab81988 Ganglioside
33	54	100.0	108	4	AAB81986	Aab81986 Ganglioside
34	54	100.0	108	4	AAB81990	Aab81990 Ganglioside
35	54	100.0	108	5	ABP61189	Abp61189 Murine an
36	54	100.0	108	5	ABP61265	Abp61265 Humanised
37	54	100.0	108	5	ABP61187	Abp61187 Humanised
38	54	100.0	108	6	ABU11011	Abu11011 Modified
39	54	100.0	108	6	ABU11013	Abu11013 Modified
40	54	100.0	108	8	ADG31770	Adg31770 V(L) doma
41	54	100.0	108	8	ADG31782	Adg31782 V(L) doma
42	54	100.0	108	8	ADG31768	Adg31768 V(L) doma
43	54	100.0	108	8	ADG31893	Adg31893 V(L) prot
44	54	100.0	108	9	ADX80647	Adx80647 Humanised
45	54	100.0	108	9	ADZ57819	Adz57819 Ganglioside
46	54	100.0	108	9	ADZ57822	Adz57822 Ganglioside
47	54	100.0	108	9	ADZ57823	Adz57823 Ganglioside
48	54	100.0	108	9	ADZ57817	Adz57817 Ganglioside
49	54	100.0	108	9	ADZ57820	Adz57820 Ganglioside
50	54	100.0	110	2	AAW70673	Aaw70673 Anti-VEGF
51	54	100.0	110	2	AAW70677	Aaw70677 Anti-VEGF
52	54	100.0	110	2	AAW70687	Aaw70687 Anti-VEGF
53	54	100.0	110	2	AAW70675	Aaw70675 Anti-VEGF
54	54	100.0	110	3	AAB05897	Aab05897 Humanised
55	54	100.0	110	3	AAB13380	Aab13380 Anti-VEGF
56	54	100.0	110	3	AAB13376	Aab13376 F(ab)-12
57	54	100.0	110	5	ABP61242	Abp61242 Humanised
58	54	100.0	110	5	ABP61256	Abp61256 Humanised
59	54	100.0	110	5	ABP61244	Abp61244 Humanised
60	54	100.0	110	5	ABP61246	Abp61246 Humanised
61	54	100.0	128	2	AAR33257	Aar33257 Rat immun
62	54	100.0	128	2	AAR53340	Aar53340 KM641 H C
63	54	100.0	128	2	AAZ28368	Aay28368 PKM641 LA
64	54	100.0	128	3	AAAB01628	Aab01628 Murine im
65	54	100.0	128	4	AAAB1994	Aab81994 Ganglioside
66	54	100.0	128	4	AAAB1995	Aab81995 Ganglioside
67	54	100.0	128	4	AAAB1997	Aab81997 Ganglioside
68	54	100.0	128	4	AAAB1978	Aab81978 Ganglioside
69	54	100.0	128	4	AAAB1996	Aab81996 Ganglioside
70	54	100.0	128	4	AAAB1999	Aab81999 Ganglioside
71	54	100.0	128	4	AAAB1993	Aab81993 Ganglioside
72	54	100.0	128	4	AAAB1992	Aab81992 Ganglioside
73	54	100.0	128	4	AAAB1998	Aab81998 Ganglioside
74	54	100.0	128	6	ABU11003	Abu11003 Modified
75	54	100.0	214	7	ADC26154	Adc26154 Parent an
76	54	100.0	237	2	AAW70703	Aaw70703 Protein e
77	54	100.0	237	5	ABB81107	Abb81107 Anti-VEGF
78	54	100.0	237	5	ABP51952	Abp51952 Plasmid p
79	54	100.0	237	8	ADO14128	Ado14128 Plasmid p
80	54	100.0	237	8	ADO14131	Ado14131 Plasmid p
81	54	100.0	237	8	ADQ90703	Adq90703 Anti-VEGF
82	54	100.0	237	8	ADQ90701	Adq90701 Anti-VEGF
83	54	100.0	237	8	ADQ90705	Adq90705 Anti-VEGF
84	54	100.0	237	8	ADQ90709	Adq90709 Anti-VEGF
85	54	100.0	237	8	ADQ90723	Adq90723 Anti-VEGF
86	54	100.0	237	8	ADQ90721	Adq90721 Anti-VEGF
87	54	100.0	237	8	ADQ90707	Adq90707 Anti-VEGF
88	54	100.0	650	5	ABP61241	Abp61241 Phage-d1a
89	51	94.4	108	9	ABE21884	Aeb21884 Human DC-
90	51	94.4	109	4	ABE62050	Aeb62050 Mouse mon
91	51	94.4	109	6	ABP72768	Abp72768 Anti-full
92	50	92.6	11	3	AAAY94220	Aay94220 Murine 16
93	50	92.6	11	6	AAG63614	Aag63614 Complemen
94	50	92.6	11	6	ABJ18553	Abj18553 Ganglioside
95	50	92.6	11	7	ADJ74691	Adj74691 Human ant
96	50	92.6	11	8	ADP47264	Adp47264 Human pho
97	50	92.6	11	8	ADU38479	Adu38479 Mouse ant

98	50	92.6	11	9	ADX98291	Adx98291 Human ant	171	50	92.6	108	8	ADQ75247	Adq75247 Immunoglo
99	50	92.6	11	9	AEA45021	Aea45021 Apolipop	172	50	92.6	108	9	AEA45097	Aea45097 ApoE-CTD
100	50	92.6	75	2	AAW62802	AAw62802 Amino aci	173	50	92.6	108	9	AEb21885	AEb21885 Human DC-
101	50	92.6	75	2	AAW62818	AAw62818 Amino aci	174	50	92.6	108	9	AEb21887	AEb21887 Human DC-
102	50	92.6	76	2	AAW80980	AAw80980 Variable	175	50	92.6	109	8	AAW52039	AAw52039 Light cha
103	50	92.6	76	2	ABO04825	ABo04825 Human epi	176	50	92.6	109	8	ADG25821	ADg25821 Anti-CD30
104	50	92.6	76	9	AEA17737	Aea17737 Hybridoma	177	50	92.6	109	9	AEb21858	AEb21858 Human DC-
105	50	92.6	90	4	ABB19441	ABb19441 Protein #	178	50	92.6	111	4	AAg63627	AAg63627 Amino aci
106	50	92.6	90	4	AAW67153	AAw67153 Human bon	179	50	92.6	113	7	ADD28271	ADD28271 Human het
107	50	92.6	90	4	AAW54766	AAw54766 Human bra	180	50	92.6	120	4	ABG11908	ABg11908 Novel hum
108	50	92.6	90	4	ABG48819	ABg48819 Human liv	181	50	92.6	121	9	AEA88810	AEA88810 Murine SA
109	50	92.6	90	4	AAW02744	AAw02744 Peptide #	182	50	92.6	127	2	AAW29010	AAw29010 p146-k3 p
110	50	92.6	90	4	ABG36817	ABg36817 Human pep	183	50	92.6	127	2	AAW11817	AAw11817 Humanised
111	50	92.6	95	6	ABO27123	ABo27123 Human ger	184	50	92.6	127	2	AAW11815	AAw11815 Mouse ant
112	50	92.6	95	6	ABO27124	ABo27124 Human ger	185	50	92.6	127	2	AAW60033	AAw60033 Mouse ant
113	50	92.6	95	6	ADC99830	ADc99830 Germline	186	50	92.6	127	2	AAW60035	AAw60035 Human ant
114	50	92.6	95	7	ADD05434	ADD05434 Anti-MUC1	187	50	92.6	127	9	AEA88780	AEA88780 Murine SA
115	50	92.6	95	7	ADP10073	ADp10073 VEGF anti	188	50	92.6	129	9	ADX98258	ADx98258 Human ant
116	50	92.6	95	7	ADF09968	ADF09968 Antibody	189	50	92.6	131	2	AAW84553	AAw84553 MAB SCH94
117	50	92.6	95	7	ADF10074	ADF10074 Antibody	190	50	92.6	131	8	ADI26634	ADI26634 Human ant
118	50	92.6	95	7	ADF09969	ADF09969 Antibody	191	50	92.6	164	7	ADD28243	ADD28243 Human het
119	50	92.6	95	7	ADF10175	ADF10175 Antibody	192	50	92.6	164	9	ADV86830	ADv86830 Bacillus
120	50	92.6	95	7	ADP09872	ADp09872 Anti-MUC1	193	50	92.6	214	8	ADK52358	ADk52358 Human ant
121	50	92.6	95	7	ADJ80244	ADj80244 Kappa ge	194	50	92.6	215	8	ADO19050	ADO19050 Murine an
122	50	92.6	95	7	ADJ80244	ADj80244 Kappa ge	195	50	92.6	233	4	ABA49242	ABa49242 Chimeric
123	50	92.6	95	7	ADJ80244	ADj80244 Kappa ge	196	50	92.6	238	2	AAW21880	AAw21880 Amino aci
124	50	92.6	95	8	ADO07313	ADO07313 Human ant	197	50	92.6	238	9	AEb45883	AEb45883 Human mon
125	50	92.6	95	8	ADO07312	ADO07312 Human ant	198	50	92.6	240	4	AAW63665	AAw63665 Amino aci
126	50	92.6	95	8	ADU86533	ADu86533 Immunoglo	199	50	92.6	241	2	AAW21882	AAw21882 Amino aci
127	50	92.6	95	8	ADU86534	ADu86534 Immunoglo	200	50	92.6	246	8	ADH50844	ADh50844 SGIII RFB
128	50	92.6	95	9	ADY75418	ADy75418 Human ger	201	50	92.6	246	8	ADH50847	ADh50847 SGV RFB4
129	50	92.6	95	9	ADY75417	ADy75417 Human ger	202	50	92.6	246	8	ADH50843	ADh50843 RFB4 spec
130	50	92.6	95	9	ADY75417	ADy75417 Human ger	203	50	92.6	246	8	ADH50845	ADh50845 SGIII var
131	50	92.6	95	9	ABE13628	ABe13628 Human var	204	50	92.6	246	8	ADH50846	ADh50846 SGIV RFB4
132	50	92.6	95	9	ABE13576	ABe13576 Human var	205	50	92.6	262	8	ADT02523	ADt02523 Anti-CD22
133	50	92.6	95	9	ABE13575	ABe13575 Human var	206	50	92.6	262	8	AAW44226	AAw44226 Chimeric
134	50	92.6	98	9	ADY31694	ADy31694 Anti-huma	207	50	92.6	272	8	ADO19054	ADO19054 Human ant
135	50	92.6	104	2	AAW62822	AAw62822 Amino aci	208	50	92.6	273	2	AAW52865	AAw52865 Anti-infl
136	50	92.6	104	2	AAW62821	AAw62821 Amino aci	209	50	92.6	286	8	ADN06991	ADn06991 Human EFG
137	50	92.6	104	2	AAW62804	AAw62804 Amino aci	210	50	92.6	289	4	AAW63631	AAw63631 Amino aci
138	50	92.6	105	2	AAW80978	AAw80978 Kappa lig	211	50	92.6	299	4	AAW63636	AAw63636 Amino aci
139	50	92.6	105	2	AAW80968	AAw80968 Kappa lig	212	50	92.6	299	6	ABU09530	ABu09530 Hamster a
140	50	92.6	105	2	AAW80974	AAw80974 Kappa lig	213	50	92.6	502	8	ADN97515	ADn97515 Artificial
141	50	92.6	105	6	ABO04838	ABo04838 Human epi	214	50	92.6	551	6	ABU09531	ABu09531 Hangter a
142	50	92.6	105	6	ABO04842	ABo04842 Human epi	215	50	92.6	555	4	AAU19871	AAu19871 Activation
143	50	92.6	105	6	ABO04831	ABo04831 Human epi	216	50	92.6	565	4	AAU19873	AAu19873 Activation
144	50	92.6	105	9	AEA17755	Aea17755 Hybridoma	217	50	92.6	577	4	AAU19872	AAu19872 Activation
145	50	92.6	105	9	AEA17751	Aea17751 Hybridoma	218	50	92.6	704	4	AAU19888	AAu19888 MLV envel
146	50	92.6	105	9	AEA17745	Aea17745 Hybridoma	219	50	92.6	731	9	AEC08431	Aec08431 SCFV-2-1G
147	50	92.6	106	8	ADP22224	ADp22224 Human ant	220	49	90.7	112	4	AAE00697	AAe00697 Human imm
148	50	92.6	106	8	ADP22224	ADp22224 Human ant	221	47	87.0	11	7	ADJ74697	ADj74697 Human ant
149	50	92.6	107	6	AAW60998	AAw60998 anti-CD22	222	47	87.0	11	8	ADM78087	ADM78087 Human SJB
150	50	92.6	107	6	ABJ18571	ABj18571 Ganglios	223	47	87.0	11	9	AEb70913	AEb70913 Toll-like
151	50	92.6	107	6	ABJ18574	ABj18574 Ganglios	224	47	87.0	11	9	AEb72797	AEb72797 Anti-ITa1
152	50	92.6	107	6	AAO27199	AAo27199 Murine an	225	47	87.0	11	9	AEC20789	Aec20789 M-CSF spe
153	50	92.6	107	6	AAO27194	AAo27194 Chimeric	226	47	87.0	104	2	AAW62819	AAw62819 Amino aci
154	50	92.6	107	7	ADC84579	ADc84579 CDR3 heav	227	47	87.0	105	2	AAW80964	AAw80964 Kappa lig
155	50	92.6	107	8	ADH50840	ADh50840 Mouse ant	228	47	87.0	105	9	AEA17741	AEA17741 Hybridoma
156	50	92.6	107	8	ADP22412	ADp22412 Human ant	229	47	87.0	107	2	AAW77302	AAw77302 Variable
157	50	92.6	107	8	ADQ09630	ADq09630 Variable	230	47	87.0	107	2	AAW49812	AAw49812 Amino aci
158	50	92.6	107	8	ADT02531	ADt02531 Anti-CD22	231	47	87.0	107	2	AAW49811	AAw49811 Amino aci
159	50	92.6	107	8	ADW75670	ADw75670 Novel mod	232	47	87.0	107	2	AAW22428	AAw22428 TM27 anti
160	50	92.6	107	8	ADW75668	ADw75668 Novel mod	233	47	87.0	107	6	ABR55867	ABr55867 Anti-glyc
161	50	92.6	107	9	ADY85028	ADy85028 Monoclon	234	47	87.0	107	6	ABR55866	ABr55866 Human imm
162	50	92.6	107	9	AEA50145	AEA50145 Anti-CD22	235	47	87.0	107	7	ADC99797	ADc99797 Anti-huma
163	50	92.6	107	9	AEb45976	AEb45976 Human mon	236	47	87.0	107	7	ADD05401	ADD05401 Anti-MUC1
164	50	92.6	108	2	AAW04177	AAw04177 Variant v	237	47	87.0	107	7	ADF09839	ADf09839 Human ant
165	50	92.6	108	2	AAW00834	AAw00834 Variable	238	47	87.0	107	8	ADN49723	ADn49723 Variable
166	50	92.6	108	2	AAW16620	AAw16620 Anti-huma	239	47	87.0	107	8	ADN49724	ADn49724 Variable
167	50	92.6	108	3	AAW94216	AAw94216 Murine co	240	47	87.0	107	8	ADU74399	ADu74399 Human imm
168	50	92.6	108	4	AAU02534	AAu02534 Anti-adip	241	47	87.0	107	8	ADU74400	ADu74400 Mouse ant
169	50	92.6	108	7	ADL91347	ADl91347 VL chain	242	47	87.0	107	9	AEb72785	AEb72785 Anti-ITa1
170	50	92.6	108	8	ADH50842	ADh50842 Human VL#	243	47	87.0	108	8	ADN41877	ADn41877 Humanised

244	47	87.0	108	9	AEb70912	Toll-like	317	45	83.3	107	3	AAy95138	AAy95138	Anti-gp12
245	47	87.0	109	9	ADY96965	Human imm	318	45	83.3	107	3	AAy95139	AAy95139	Anti-gp12
246	47	87.0	109	9	ADY96965	Human imm	319	45	83.3	107	6	ABO10814	ABO10814	Mouse mon
247	47	87.0	109	9	AEb21853	Human DC-	320	45	83.3	107	9	ADZ47655	ADZ47655	Mouse ant
248	47	87.0	109	9	AEb21856	Human DC-	321	45	83.3	108	6	ABO10817	ABO10817	Human ger
249	47	87.0	109	9	AEb21859	Human DC-	322	45	83.3	108	6	ABO10815	ABO10815	Mouse mon
250	47	87.0	112	7	ADZ28273	Human bet	323	45	83.3	108	6	ABO10816	ABO10816	Human ger
251	47	87.0	115	7	ADD28272	Human bet	324	45	83.3	108	9	ADZ47742	ADZ47742	Mouse ant
252	47	87.0	119	8	ADM78045	Human SKB	325	45	83.3	109	9	ABO10818	ABO10818	Mouse/hum
253	47	87.0	126	2	AR12237	Mouse MAB	326	45	83.3	110	9	ADZ47745	ADZ47745	CDR-graft
254	47	87.0	127	2	AR12359	Light (ka	327	45	83.3	113	7	ADZ28280	ADZ28280	Human het
255	47	87.0	127	2	AR39265	Mouse C4G	328	45	83.3	126	2	AAZ29015	AAZ29015	pUC-RVh-P
256	47	87.0	127	2	AR95946	HNK-20 va	329	45	83.3	126	2	AAZ29013	AAZ29013	pUC-RVh-P
257	47	87.0	127	2	AAW49809	Variable	330	45	83.3	127	2	AAZ28670	AAZ28670	ppm-k3 pr
258	47	87.0	166	7	ADD28244	Human het	331	45	83.3	127	2	AAZ99003	AAZ99003	MAB VLI7E
259	47	87.0	166	9	ADY66831	Bacillus	332	45	83.3	247	6	AAO27255	AAO27255	Antibody
260	47	87.0	212	5	ABP51955	Humanised	333	45	83.3	247	6	AAO27252	AAO27252	Antibody
261	47	87.0	214	2	AAZ30776	AAZ30776 H52L6-158	334	45	83.3	247	6	AAO27256	AAO27256	Antibody
262	47	87.0	214	2	AAZ43338	Complel	335	45	83.3	247	6	AAO27254	AAO27254	Antibody
263	47	87.0	214	2	AAW00373	Anti-CD18	336	45	83.3	247	6	AAO27253	AAO27253	Antibody
264	47	87.0	214	2	AAW34504	Light cha	337	45	83.3	247	8	ADK42705	ADK42705	Mutant M1
265	47	87.0	214	2	AAW34506	Light cha	338	45	83.3	247	8	ADK42703	ADK42703	M18 scFv
266	47	87.0	214	2	AAW49815	Amino aci	339	45	83.3	247	8	ADK42701	ADK42701	14B7 scFv
267	47	87.0	214	2	AAW95615	Humanized	340	45	83.3	247	9	ADZ79632	ADZ79632	Anti-Baci
268	47	87.0	214	2	AAW30632	Recombina	341	45	83.3	247	9	ADZ79630	ADZ79630	Anti-Baci
269	47	87.0	214	2	AAW08754	Human ant	342	45	83.3	247	9	ADZ79628	ADZ79628	Anti-Baci
270	47	87.0	214	2	AAW66777	rhuWAb CD	343	45	83.3	256	3	AAZ55072	AAZ55072	Interleuk
271	47	87.0	214	5	ABG31889	Humanised	344	45	83.3	260	3	AAZ55075	AAZ55075	Single ch
272	47	87.0	214	6	ABR55870	Human imm	345	45	83.3	277	2	AAW96342	AAW96342	sfvMHC-1
273	47	87.0	214	8	ADK18342	Amino aci	346	45	83.3	302	2	AAZ60206	AAZ60206	Bispecifi
274	47	87.0	214	8	ADN41870	Human aci	347	45	83.3	367	3	AAZ55078	AAZ55078	Single ch
275	47	87.0	214	8	ADN49727	Human imm	348	45	83.3	381	3	AAZ55079	AAZ55079	Single ch
276	47	87.0	214	8	ADU74403	Human imm	349	45	83.3	504	7	ADD25787	ADD25787	Binding d
277	47	87.0	214	9	AEb27968	Humanized	350	45	83.3	504	9	ADY21738	ADY21738	Anti-CD3
278	47	87.0	233	2	AEC20774	M-CSF spe	351	45	83.3	519	3	AAZ55080	AAZ55080	Single ch
279	47	87.0	233	2	AAZ30777	pH52-9.0	352	45	83.3	546	3	AAZ55074	AAZ55074	Single ch
280	47	87.0	234	4	AAZ90612	Human sec	353	45	83.3	555	7	ADZ66039	ADZ66039	Anti-CD3
281	47	87.0	234	5	ABG65461	Human alb	354	45	83.3	555	8	ADK00036	ADK00036	Chimaeric
282	47	87.0	234	8	ADL78728	Albumin f	355	45	83.3	555	9	ADY22069	ADY22069	Antibody
283	47	87.0	237	2	AAW95622	pS1130 ex	356	45	83.3	555	9	ADY22137	ADY22137	Antibody
284	47	87.0	237	2	AAW30634	Recombina	357	45	83.3	601	3	AAZ07461	AAZ07461	An immuno
285	47	87.0	237	6	ABZ66784	Protein e	358	45	83.3	601	6	ABG72265	ABG72265	Recombina
286	47	87.0	237	6	ABZ72745	Anti-CD18	359	45	83.3	626	3	AAZ55081	AAZ55081	Single ch
287	47	87.0	237	9	ABZ72796	E. coli S	360	45	83.3	637	5	AAZ55365	AAZ55365	Diphtheri
288	47	87.0	537	3	AAZ03664	Anti-CD7	361	45	83.3	638	5	AAZ55370	AAZ55370	Diphtheri
289	47	87.0	650	6	ABR62591	Anti-CD7	362	45	83.3	640	3	AAZ55082	AAZ55082	Single ch
290	47	87.0	651	6	ABR62590	Anti-CD7	363	45	83.3	642	5	AAZ55382	AAZ55382	Diphtheri
291	47	87.0	667	6	ABP97414	Anti-huma	364	45	83.3	642	6	AAZ29675	AAZ29675	Anti-T ce
292	46	85.2	106	5	ABG76532	HCV E1 an	365	45	83.3	643	5	AAZ55390	AAZ55390	Diphtheri
293	46	85.2	107	6	ABP59985	Antibody	366	45	83.3	643	6	AAZ29670	AAZ29670	Anti-T ce
294	46	85.2	107	7	ADZ69648	Humanised	367	45	83.3	652	5	AAZ55448	AAZ55448	Immunotox
295	46	85.2	107	8	ADN49402	Murine an	368	45	83.3	656	5	AAZ55383	AAZ55383	Diphtheri
296	46	85.2	107	9	AEb03867	B-Cell pha	369	45	83.3	657	5	AAZ55389	AAZ55389	Diphtheri
297	46	85.2	108	9	ADZ86671	Anti-FLJ3	370	45	83.3	895	5	AAZ55369	AAZ55369	Diphtheri
298	46	85.2	209	2	AAZ64204	Monoclon	371	45	83.3	895	5	AAZ55368	AAZ55368	Diphtheri
299	45	83.3	11	8	ADQ17118	Murine an	372	45	83.3	895	5	AAZ55374	AAZ55374	Diphtheri
300	45	83.3	72	8	ADU04141	Murine im	373	45	83.3	896	6	AAZ29673	AAZ29673	Anti-T ce
301	45	83.3	72	8	ADU04139	Murine im	374	45	83.3	896	5	AAZ55366	AAZ55366	Diphtheri
302	45	83.3	95	9	ADZ47744	Human ger	375	45	83.3	896	5	AAZ55373	AAZ55373	Diphtheri
303	45	83.3	95	9	ADZ47743	Human ger	376	45	83.3	896	5	AAZ55373	AAZ55373	Diphtheri
304	45	83.3	104	2	AAW01291	VL region	377	45	83.3	896	6	AAZ29672	AAZ29672	Anti-T ce
305	45	83.3	104	3	AAW01291	VL region	378	45	83.3	896	6	AAZ29671	AAZ29671	Anti-T ce
306	45	83.3	104	3	AAZ98252	Anti-gp12	379	45	83.3	896	6	AAZ29676	AAZ29676	Anti-T ce
307	45	83.3	104	3	AAZ95143	Anti-gp12	380	45	83.3	899	5	ADZ01023	ADZ01023	Amino aci
308	45	83.3	105	6	ABO04827	Human epi	381	45	83.3	899	5	AAZ55375	AAZ55375	Diphtheri
309	45	83.3	107	2	AAZ30768	Murine an	382	45	83.3	899	6	AAZ29674	AAZ29674	Anti-T ce
310	45	83.3	107	2	AAZ30769	huxCD3v9,	383	44	81.5	11	2	AAW24543	AAW24543	CDR #1 of
311	45	83.3	107	2	AAZ54319	Anti-HIV	384	44	81.5	11	7	ADZ93795	ADZ93795	Antibody
312	45	83.3	107	2	AAW01286	VL region	385	44	81.5	11	7	ADZ47405	ADZ47405	Human ant
313	45	83.3	107	2	AAW01287	VL region	386	44	81.5	11	8	ADP47046	ADP47046	Murine li
314	45	83.3	107	3	AAW01287	VL region	387	44	81.5	11	9	ADW04827	ADW04827	PAPP-A im
315	45	83.3	107	3	AAZ98247	Anti-gp12	388	44	81.5	11	9	AEZ53696	AEZ53696	Novel hum
316	45	83.3	107	3	AAZ98248	Anti-gp12	389	44	81.5	11	9	AEZ46217	AEZ46217	Apollipop

390	44	81.5	86	2	AAW62806	Aaw62806	Amino aci	463	42	77.8	11	9	AEA45353	Apolipop
391	44	81.5	101	2	AAW22577	Aar22577	Light cha	464	42	77.8	11	9	AEA4925	Human ant
392	44	81.5	106	5	AAW76516	Abg76516	HCV E1 an	465	42	77.8	11	9	ABE17166	EphA2-spe
393	44	81.5	107	4	AAW93661	Ag93661	Human ant	466	42	77.8	11	9	AEA42966	EphA2 ant
394	44	81.5	107	6	ABR54919	Abt54919	Light cha	467	42	77.8	106	8	ADT89014	Murine p1
395	44	81.5	107	6	ABO27468	Abt27468	Anti-Rh(D	468	42	77.8	106	9	AEA48163	Rat anti-
396	44	81.5	107	7	ADO51596	Ado51596	Human TAG	469	42	77.8	106	9	AEA48152	Rat anti-
397	44	81.5	107	8	ADG34381	Adg34381	Humanised	470	42	77.8	106	9	ABE13715	Human L3
398	44	81.5	107	9	ABE19295	Abt19295	IGG kappa	471	42	77.8	106	9	ABE13711	Human ant
399	44	81.5	108	1	AAW81246	Asp81246	Anti-precu	472	42	77.8	107	2	AAW54259	Anti-HIV
400	44	81.5	108	2	AAW54062	Aar54062	Anti-canc	473	42	77.8	107	2	AAW01282	VL region
401	44	81.5	108	2	AAW54258	Aar54258	Anti-HIV	474	42	77.8	107	3	AAW98243	Anti-gp12
402	44	81.5	108	2	AAW01281	Aaw01281	VL region	475	42	77.8	107	3	AAW95134	Anti-gp12
403	44	81.5	108	3	AAW98242	Aay98242	Anti-gp12	476	42	77.8	107	5	AAE28876	Human KDR
404	44	81.5	108	3	AAW95133	Aay95133	Human pho	477	42	77.8	107	6	ABU26769	VEGF bind
405	44	81.5	108	8	ADP47107	Adp47107	Human pho	478	42	77.8	107	7	ADD24430	Human lig
406	44	81.5	109	7	ADC99781	Adc99781	Anti-huma	479	42	77.8	107	8	ADT80807	Human KDR
407	44	81.5	109	7	ADD05385	Ado05385	Anti-MUC1	480	42	77.8	107	8	ADE85729	Human Eph
408	44	81.5	109	9	ADP09823	Adp09823	Human ant	481	42	77.8	107	8	ADK18283	KDR bindi
409	44	81.5	109	9	ADY96968	Ady96968	Human imm	482	42	77.8	107	8	ADL23067	Human Eph
410	44	81.5	111	1	AAW81870	Asp81870	Anti-precu	483	42	77.8	107	8	ADY32226	Human Eph
411	44	81.5	113	7	ADD28277	Adt28277	Human het	484	42	77.8	107	9	AEA34924	Human ant
412	44	81.5	115	8	ADU86518	Adu86518	Immunoglo	485	42	77.8	107	9	ABE17165	EphA2-spe
413	44	81.5	116	9	ADW04825	Adw04825	PAPP-A im	486	42	77.8	107	9	AEA42965	EphA2 ant
414	44	81.5	120	9	AEA53330	Aes53330	Novel hum	487	42	77.8	108	7	ADL91349	VL chain
415	44	81.5	120	9	AEA53960	Aes53960	Novel hum	488	42	77.8	108	8	ADO36376	Intracell
416	44	81.5	122	2	AAW24538	Aaw24538	Immunoglo	489	42	77.8	108	8	ADQ75249	Immunoglo
417	44	81.5	122	2	AAW29579	Aar29579	CLN-IGG k	490	42	77.8	109	9	ABE21855	Human DC-
418	44	81.5	126	2	AAW54064	Aar54064	Anti-canc	491	42	77.8	111	4	AAW63656	Amino aci
419	44	81.5	236	3	AAW96297	Aay96297	Human IGF	492	42	77.8	111	6	ABJ38615	Hepatitis
420	44	81.5	236	7	ADD93785	Adt93785	Monoclonal	493	42	77.8	113	7	ADD28274	Human het
421	44	81.5	243	8	ADN36307	Adn36307	Hamster a	494	42	77.8	127	2	AAW32121	Anti-CD4
422	44	81.5	260	5	ABP41164	Abp41164	Human ova	495	42	77.8	142	2	AAW81311	Rat monoc
423	44	81.5	634	6	ABW82300	Abw82300	CD19:zeta	496	42	77.8	238	9	ABE45863	Human mon
424	43	79.6	11	2	AAW52525	Aar52525	36-71 lig	497	42	77.8	240	6	ABJ38559	Hepatitis
425	43	79.6	11	7	ADJ74696	Adj74696	Human ant	498	42	77.8	299	4	AAW63660	Amino aci
426	43	79.6	11	9	ADV21303	Adv21303	Human ant	499	41	75.9	11	4	AAW63644	Complemen
427	43	79.6	11	9	ADV21351	Adv21351	Human ant	500	41	75.9	11	6	ABJ38602	Hepatitis
428	43	79.6	11	9	AEA45343	Aea45343	Apolipop	501	41	75.9	11	9	ADP44913	Apolipop
429	43	79.6	11	9	AEA45515	Aea45515	Apolipop	502	41	75.9	17	8	ADP71369	CDR sequ
430	43	79.6	78	4	AAW33247	Aaw33247	Novel hum	503	41	75.9	105	6	ABO04833	Kappa lig
431	43	79.6	102	3	AAW71446	Aay71446	Humanised	504	41	75.9	105	6	ABO04833	Human epi
432	43	79.6	102	3	AAW71454	Aay71454	Humanised	505	41	75.9	105	9	AEAI7747	Hybridoma
433	43	79.6	105	3	AAW71455	Aay71455	Humanised	506	41	75.9	107	2	AAW92082	Murine l3
434	43	79.6	107	9	ADV21349	Adv21349	Human ant	507	41	75.9	107	2	AAW92083	Murine l3
435	43	79.6	107	9	ADV21301	Adv21301	Human ant	508	41	75.9	107	5	ABG31429	Humanised
436	43	79.6	108	3	AAW71450	Aay71450	Humanised	509	41	75.9	107	5	ABG31430	Amino aci
437	43	79.6	108	3	AAW71445	Aay71445	Murine mo	510	41	75.9	107	6	AAO23067	Murine K8
438	43	79.6	108	3	AAW56678	Aay56678	Anti-inte	511	41	75.9	107	6	ADP03929	Murine-ex
439	43	79.6	108	3	AAW56704	Aay56704	Murine an	512	41	75.9	107	7	ADP03926	Murine-ex
440	43	79.6	109	2	AAW52040	Aar52040	Light cha	513	41	75.9	108	4	AAW62785	Human HIV
441	43	79.6	109	9	ADY96957	Ady96957	Human imm	514	41	75.9	108	9	AEA44959	Apolipop
442	43	79.6	109	9	ADY96992	Ady96992	Human imm	515	41	75.9	109	9	ADY96959	Human imm
443	43	79.6	113	7	ADY28279	Adt28279	Human het	516	41	75.9	112	4	AAW63654	Amino aci
444	43	79.6	139	7	ADY90904	Adf90904	Human hep	517	41	75.9	112	6	ABJ38613	Hepatitis
445	43	79.6	247	9	ADV21472	Adv21472	Mature fo	518	41	75.9	127	6	AAO23065	Murine K8
446	43	79.6	248	9	ADV21478	Adv21478	Mature fo	519	41	75.9	127	7	ABR62342	Anti-HLA-
447	43	79.6	496	9	ADV21537	Adv21537	Mature fo	520	41	75.9	128	2	AAW09426	ME4 Light
448	43	79.6	497	9	ADV21541	Adv21541	Mature fo	521	41	75.9	128	2	AAW06215	MAB ME4
449	43	79.6	501	9	ADV21519	Adv21519	Mature fo	522	41	75.9	128	2	AAW85062	Mouse ME4
450	43	79.6	501	9	ADV21529	Adv21529	Mature fo	523	41	75.9	128	6	ABU58896	Mouse ant
451	43	79.6	503	9	ADV21509	Adv21509	Mature fo	524	41	75.9	129	2	AAW57482	Humanized
452	43	79.6	503	9	ADV21499	Adv21499	Mature fo	525	41	75.9	129	2	AAW52085	Humanised
453	43	79.6	11	4	AAW63650	Aag63650	Complemen	526	41	75.9	129	5	ABG31444	Amino aci
454	42	77.8	11	5	AAE28888	Aae28888	Human KDR	527	41	75.9	131	2	AAW26240	Monoclonal
455	42	77.8	11	6	ABJ26781	Abj26781	VEGF bind	528	41	75.9	142	2	AAW98410	3H1 Light
456	42	77.8	11	6	ABJ38608	Abj38608	Hepatitis	529	41	75.9	142	2	AAW99686	Monoclonal
457	42	77.8	11	7	ADD24450	Add24450	Human lig	530	41	75.9	142	2	AAE04727	Mouse ant
458	42	77.8	11	7	ADD80827	Add80827	Human var	531	41	75.9	142	2	AAW26728	Anti-idio
459	42	77.8	11	8	ADE85730	Ade85730	Human Eph	532	41	75.9	142	3	AAW49961	Murine MA
460	42	77.8	11	8	ADK18303	Adk18303	KDR bindi	533	41	75.9	142	5	AAO14016	Mouse 3H1
461	42	77.8	11	8	ADL23068	Adl23068	Human Eph	534	41	75.9	142	5	ABW08119	Antibody
462	42	77.8	11	9	ADY32303	Ady32303	Human Eph	535	41	75.9	142	6	AAO16294	Mouse 3H1

536	41	75.9	142	7	ADC16715	Adcl6715 Light cha	609	39	72.2	56	2	AAy02523	Clone sel
537	41	75.9	152	8	ADK52350	Adk52350 Human ant	610	39	72.2	56	2	AAy02500	Clone sel
538	41	75.9	234	2	ARI3050	ARI3050 CD4 -speci	611	39	72.2	56	2	AAy02513	Clone sel
539	41	75.9	231	3	AEA1023	AEA1023 Human ant	612	39	72.2	56	2	AAy02510	Clone sel
540	41	75.9	241	6	ABJ38593	ABj38593 Hepatitis	613	39	72.2	56	2	AAy02480	Clone sel
541	41	75.9	300	4	AG63658	AG63658 Amino aci	614	39	72.2	56	2	AAy02507	Clone sel
542	41	75.9	355	2	AAW35125	AAw35125 R. pipien	615	39	72.2	56	2	AAy02476	Clone sel
543	41	75.9	355	2	AAW35129	AAw35129 R. pipien	616	39	72.2	56	2	AAy02493	Clone sel
544	41	75.9	358	2	AAW35127	AAw35127 R. pipien	617	39	72.2	56	2	AAy02501	Clone sel
545	41	75.9	358	2	AAW35130	AAw35130 R. pipien	618	39	72.2	56	2	AAy02519	Clone sel
546	41	75.9	360	2	AAW35128	AAw35128 R. pipien	619	39	72.2	56	2	AAy02489	Clone sel
547	41	75.9	379	2	AAW35126	AAw35126 R. pipien	620	39	72.2	56	2	AAy02499	Clone sel
548	40	74.1	11	2	AAW23433	AAw23433 CDR-1 of	621	39	72.2	56	2	AAy02521	Clone sel
549	40	74.1	11	9	AEA45034	AEA45034 Apolipop	622	39	72.2	56	2	AAy02490	Clone sel
550	40	74.1	11	9	AEA46057	AEA46057 Apolipop	623	39	72.2	56	2	AAy02473	Clone sel
551	40	74.1	88	3	AAy56671	AAy56671 Partial p	624	39	72.2	56	2	AAy02491	Clone sel
552	40	74.1	107	9	ADY85024	ADy85024 Monoclon	625	39	72.2	56	2	AAy02495	Clone sel
553	40	74.1	108	2	AAW54320	AAw54320 Anti-HIV	626	39	72.2	56	2	AAy02514	Clone sel
554	40	74.1	108	2	AAW01288	AAw01288 VL region	627	39	72.2	56	2	AAy02474	Clone sel
555	40	74.1	108	2	AAW23439	AAw23439 Modified	628	39	72.2	56	2	AAy02475	Clone sel
556	40	74.1	108	2	AAW23440	AAw23440 Modified	629	39	72.2	56	2	AAy02477	Clone sel
557	40	74.1	108	2	AAW23442	AAw23442 hW12 lig	630	39	72.2	56	2	AAy02506	Clone sel
558	40	74.1	108	2	AAW23436	AAw23436 rW12 lig	631	39	72.2	74	2	AAW62805	Amino aci
559	40	74.1	108	3	AAy98249	AAy98249 Anti-gp12	632	39	72.2	76	2	AAW80981	Variable
560	40	74.1	108	3	AAy95140	AAy95140 Anti-gp12	633	39	72.2	76	6	ABO04843	Human epi
561	40	74.1	108	4	AAW93598	AAW93598 Human ant	634	39	72.2	76	9	AEA17738	Hybridoma
562	40	74.1	108	6	ABO27405	ABO27405 Anti-Rh(D	635	39	72.2	88	2	AAW59619	Anti-RSV
563	40	74.1	108	8	ADP47111	ADp47111 Human pho	636	39	72.2	88	3	AAy56654	Partial p
564	40	74.1	108	9	AEA45110	AEA45110 Apolipop	637	39	72.2	88	3	AAy56659	Partial p
565	40	74.1	111	4	AAW63629	AAW63629 Amino aci	638	39	72.2	88	8	ADU04217	Human imm
566	40	74.1	128	3	AAy56736	AAy56736 Amino aci	639	39	72.2	91	8	ADL70194	Gonadotro
567	40	74.1	236	9	ABE45855	ABE45855 Human mon	640	39	72.2	95	2	AAW72065	
568	40	74.1	299	4	AAW63633	AAW63633 Amino aci	641	39	72.2	95	2	AAW72058	
569	40	74.1	299	4	AAW63638	AAW63638 Amino aci	642	39	72.2	95	6	AAE35900	Human 012
570	40	74.1	7201	4	ABB71136	ABb71136 Drosophil	643	39	72.2	95	6	ABJ18693	Antibody
571	39.5	73.1	12	5	AAU70358	AAu70358 Mouse kap	644	39	72.2	95	6	ABO27122	Human ger
572	39.5	73.1	109	8	ADR40433	ADR40433 Mouse kap	645	39	72.2	95	6	ABO27121	Human ger
573	39.5	73.1	109	8	ADR40351	ADR40351 Mouse kap	646	39	72.2	95	7	ADB75645	Human pro
574	39	72.2	11	2	AAW13920	AAw13920 Fragment	647	39	72.2	95	7	ADC99814	Germline
575	39	72.2	11	2	AAW10225	AAw10225 CDR-graft	648	39	72.2	95	7	ADD05418	Anti-MUC1
576	39	72.2	11	4	AAW99149	AAW99149 Human scf	649	39	72.2	95	7	ADP10077	VEGF anti
577	39	72.2	11	4	AAW63647	AAW63647 Complemen	650	39	72.2	95	7	ADF09973	Antibody
578	39	72.2	11	5	AAO17647	AAO17647 Human FAP	651	39	72.2	95	7	ADF10179	Antibody
579	39	72.2	11	5	AAO17639	AAO17639 Human FAP	652	39	72.2	95	7	ADF10078	VEGF anti
580	39	72.2	11	6	ABJ38605	ABj38605 Hepatitis	653	39	72.2	95	7	ADF09972	Antibody
581	39	72.2	11	7	ADJ74695	ADj74695 Human ant	654	39	72.2	95	7	ADF10180	Antibody
582	39	72.2	11	7	ADJ74690	ADj74690 Human ant	655	39	72.2	95	7	ADF09856	Anti-MUC1
583	39	72.2	11	8	ADO84598	ADO84598 H23 anti-g	656	39	72.2	95	7	ADJ80242	Vkappa ge
584	39	72.2	11	8	ADR38843	ADR38843 Mouse lig	657	39	72.2	95	7	ADJ80241	Vkappa ge
585	39	72.2	11	8	ADS52438	ADs52438 Fab targe	658	39	72.2	95	7	ADP03925	Murine-ex
586	39	72.2	11	9	ADV21399	ADv21399 Human ant	659	39	72.2	95	8	ADO07310	Human ant
587	39	72.2	11	9	ADV21367	ADv21367 Human ant	660	39	72.2	95	8	ADO07311	Human ant
588	39	72.2	11	9	ADM04875	ADM04875 PAP-A im	661	39	72.2	95	9	ADY54709	Human V k
589	39	72.2	11	9	ADM04851	ADM04851 PAP-A im	662	39	72.2	95	9	ADY75416	Human ger
590	39	72.2	11	9	ADM77468	ADM77468 Human pla	663	39	72.2	95	9	ADY75415	Human ger
591	39	72.2	11	9	AEA53531	AEA53531 Novel hum	664	39	72.2	95	9	AEA53913	Novel hum
592	39	72.2	11	9	AEA53686	AEA53686 Novel hum	665	39	72.2	95	9	AEA53904	Novel hum
593	39	72.2	11	9	AEA54023	AEA54023 Apolipop	666	39	72.2	95	9	AEA53979	Novel hum
594	39	72.2	11	9	AEA45191	AEA45191 Apolipop	667	39	72.2	95	9	AEA53988	Novel hum
595	39	72.2	11	9	AEA46107	AEA46107 Apolipop	668	39	72.2	95	9	AEA53961	Novel hum
596	39	72.2	11	9	AEA44928	AEA44928 Apolipop	669	39	72.2	95	9	ABE13579	Human var
597	39	72.2	11	9	AEA45190	AEA45190 Apolipop	670	39	72.2	95	9	ABE13580	Human var
598	39	72.2	11	9	ABE28763	ABE28763 Human CDR	671	39	72.2	95	9	ABE13632	Human var
599	39	72.2	13	7	ADB78565	ADB78565 Rat F997-	672	39	72.2	95	9	ABE13633	Human var
600	39	72.2	52	9	AEC20827	AEC20827 Human var	673	39	72.2	95	9	AEC20816	Human var
601	39	72.2	55	2	AAy02515	AAy02515 Clone sel	674	39	72.2	96	5	ABG77155	Germline
602	39	72.2	56	2	AAy02498	AAy02498 Clone sel	675	39	72.2	96	8	ADR28576	Human ant
603	39	72.2	56	2	AAy02502	AAy02502 Clone sel	676	39	72.2	96	9	AEA53877	Novel hum
604	39	72.2	56	2	AAy02478	AAy02478 Clone sel	677	39	72.2	96	9	AEA53985	Novel hum
605	39	72.2	56	2	AAy02483	AAy02483 Clone sel	678	39	72.2	96	9	AEA53964	Novel hum
606	39	72.2	56	2	AAy02492	AAy02492 Clone sel	679	39	72.2	96	9	AEA53996	Novel hum
607	39	72.2	56	2	AAy02511	AAy02511 Clone sel	680	39	72.2	102	9	ADY33965	Anti-Tie
608	39	72.2	56	2	AAy02479	AAy02479 Clone sel	681	39	72.2	103	4	ANG93599	Human ant

682	39	72.2	103	6	ABO27406	Abc27406 Anti-Rh(D	755	39	72.2	108	6	ABP96010	Abp96010 HSA antiB
683	39	72.2	104	8	ADU86527	Adu86527 Immunoglo	756	39	72.2	108	6	AAO16704	Aao16704 Human ant
684	39	72.2	105	2	AAW52237	Aaw52237 Antibody	757	39	72.2	108	6	AAO16706	Aao16706 Human ant
685	39	72.2	105	5	ABG76554	Abg76554 HCV E1 an	758	39	72.2	108	6	AAE35210	Aae35210 Human Ige
686	39	72.2	105	7	ADP033985	Adp033985 Murine-ex	759	39	72.2	108	6	ABO27462	Abc27462 Anti-Rh(D
687	39	72.2	106	7	ABR61522	Abt61522 Human SA-	760	39	72.2	108	6	ABO27407	Abc27407 Anti-Rh(D
688	39	72.2	106	8	ADR47411	Adt47411 Human ger	761	39	72.2	108	6	ABO27396	Abc27396 Anti-Rh(D
689	39	72.2	106	8	ADY72816	Ady72816 Anti-hepa	762	39	72.2	108	6	ABO27458	Abc27458 Anti-Rh(D
690	39	72.2	106	8	ADY72815	Ady72815 Anti-hepa	763	39	72.2	108	7	ADB78583	Adb78583 Rat F997-
691	39	72.2	106	9	ADX011785	Adx011785 SARS coro	764	39	72.2	108	7	ADL91345	Adl91345 VL chain
692	39	72.2	106	9	ABE45972	Aeb45972 Human mon	765	39	72.2	108	7	ADL91337	Adl91337 VL chain
693	39	72.2	107	2	AAR54261	Aar54261 Anti-HIV	766	39	72.2	108	8	ABG75343	Abg75343 Antibody
694	39	72.2	107	2	AAR54260	Aar54260 Anti-HIV	767	39	72.2	108	8	ADL92461	Adl92461 Single do
695	39	72.2	107	2	AAW01283	Aaw01283 VL region	768	39	72.2	108	8	ADL92386	Adl92386 Anti-RSA
696	39	72.2	107	2	AAW01284	Aaw01284 VL region	769	39	72.2	108	8	ADL92463	Adl92463 Single do
697	39	72.2	107	2	AAW080817	Aaw080817 Amino aci	770	39	72.2	108	8	ADO36372	Ado36372 Intracell
698	39	72.2	107	2	AAW80972	Aaw80972 Kappa lig	771	39	72.2	108	8	ADO36364	Ado36364 Intracell
699	39	72.2	107	3	AAW98245	Aay98245 Anti-gp12	772	39	72.2	108	8	ADO36397	Ado36397 Intracell
700	39	72.2	107	3	AAW98244	Aay98244 Anti-gp12	773	39	72.2	108	8	ADP66622	Adp66622 Anti-RAS
701	39	72.2	107	3	AAW95136	Aay95136 Anti-gp12	774	39	72.2	108	8	ADP66654	Adp66654 Anti-RAS
702	39	72.2	107	3	AAW95135	Aay95135 Anti-gp12	775	39	72.2	108	8	ADP75245	Adp75245 Immunoglo
703	39	72.2	107	4	AAG65567	Agg65567 Amino aci	776	39	72.2	108	8	ADQ75237	Adq75237 Immunoglo
704	39	72.2	107	4	AAG93646	Agg93646 Human ant	777	39	72.2	108	8	ADP47299	Adp47299 Human pho
705	39	72.2	107	4	AAG93596	Agg93596 Human ant	778	39	72.2	108	8	ADP47294	Adp47294 Human pho
706	39	72.2	107	4	AAG93597	Agg93597 Human ant	779	39	72.2	108	8	ADP47113	Adp47113 Human pho
707	39	72.2	107	4	AAG93656	Agg93656 Human ant	780	39	72.2	108	8	ADQ14601	Adq14601 Single-do
708	39	72.2	107	4	AAG93663	Agg93663 Human ant	781	39	72.2	108	8	ADQ77184	Adq77184 VK C3 seq
709	39	72.2	107	4	AAG93664	Agg93664 Human ant	782	39	72.2	108	8	ADQ77191	Adq77191 Dummy vk
710	39	72.2	107	4	AAG93664	Agg93664 Human ant	783	39	72.2	108	8	ADQ77182	Adq77182 VK K8 seq
711	39	72.2	107	4	AAG93594	Agg93594 Human ant	784	39	72.2	108	8	ADQ77182	Adq77182 VK K8 seq
712	39	72.2	107	4	AAG93595	Agg93595 Human ant	785	39	72.2	108	8	ADQ90912	Adq90912 Vb/Ck pro
713	39	72.2	107	4	AAG93590	Agg93590 Human ant	786	39	72.2	108	8	ADQ79346	Adq79346 Anti-RAS
714	39	72.2	107	5	AAO17151	Aao17151 Human end	787	39	72.2	108	8	ADS78333	Ads78333 Kappa du
715	39	72.2	107	6	ABP96012	Abp96012 HSA antiB	788	39	72.2	108	8	ADS78331	Ads78331 DPkappa9-
716	39	72.2	107	6	ABO04835	Abc04835 Human epi	789	39	72.2	108	8	ADS16567	Adsl16567 Human ant
717	39	72.2	107	6	ABO27451	Abc27451 Anti-Rh(D	790	39	72.2	108	8	ADT88240	Adt88240 Human ant
718	39	72.2	107	6	ABO27401	Abc27401 Anti-Rh(D	791	39	72.2	108	8	ADU86526	Adu86526 Immunoglo
719	39	72.2	107	6	ABO27453	Abc27453 Anti-Rh(D	792	39	72.2	108	8	ADU86517	Adu86517 Immunoglo
720	39	72.2	107	6	ABO27471	Abc27471 Anti-Rh(D	793	39	72.2	108	8	ADU86525	Adu86525 Immunoglo
721	39	72.2	107	6	ABO27403	Abc27403 Anti-Rh(D	794	39	72.2	108	8	ADU86524	Adu86524 Immunoglo
722	39	72.2	107	6	ABO27463	Abc27463 Anti-Rh(D	795	39	72.2	108	9	ADZ42046	Adz42046 Ig L chai
723	39	72.2	107	6	ABO27402	Abc27402 Anti-Rh(D	796	39	72.2	108	9	ADZ42049	Adz42049 Ig L chai
724	39	72.2	107	6	ABO27397	Abc27397 Anti-Rh(D	797	39	72.2	108	9	ADZ42053	Adz42053 Ig L chai
725	39	72.2	107	6	ABO27470	Abc27470 Anti-Rh(D	798	39	72.2	108	9	ADZ42054	Adz42054 Ig L chai
726	39	72.2	107	6	ABO27404	Abc27404 Anti-Rh(D	799	39	72.2	108	9	ADZ42050	Adz42050 Ig L chai
727	39	72.2	107	7	ADP03948	Adp03948 Murine-ex	800	39	72.2	108	9	ADZ42056	Adz42056 Ig L chai
728	39	72.2	107	7	ADP03949	Adp03949 Murine-ex	801	39	72.2	108	9	ADZ42052	Adz42052 Ig L chai
729	39	72.2	107	7	ADP03928	Adp03928 Murine-ex	802	39	72.2	108	9	ADZ42055	Adz42055 Ig L chai
730	39	72.2	107	7	ADP03927	Adp03927 Murine-ex	803	39	72.2	108	9	ADZ42048	Adz42048 Ig L chai
731	39	72.2	107	8	ADN49404	Adn49404 Human ant	804	39	72.2	108	9	ADZ42057	Adz42057 Ig L chai
732	39	72.2	107	8	ADO06815	Ado06815 Virucidal	805	39	72.2	108	9	ADZ41145	Adz41145 Dummy Vka
733	39	72.2	107	8	ADO06843	Ado06843 Virucidal	806	39	72.2	108	9	ADZ70452	Adz70452 Human pro
734	39	72.2	107	8	ADO06814	Ado06814 Virucidal	807	39	72.2	108	9	AEA41088	Aea41088 Germline
735	39	72.2	107	8	ADP22402	Adp22402 Human ant	808	39	72.2	108	9	AEA44964	Aea44964 Apolipoppr
736	39	72.2	107	8	ADQ90913	Adq90913 Vb/Ck pro	809	39	72.2	108	9	AEA45211	Aea45211 Apolipoppr
737	39	72.2	107	8	ADT55242	Adt55242 Amino aci	810	39	72.2	108	9	AEA45215	Aea45215 Apolipoppr
738	39	72.2	107	9	ADV21397	Adv21397 Human ant	811	39	72.2	108	9	AEA45202	Aea45202 Apolipoppr
739	39	72.2	107	9	ADV21365	Adv21365 Human ant	812	39	72.2	108	9	AEA45217	Aea45217 Apolipoppr
740	39	72.2	107	9	ADX98407	Adx98407 Human ant	813	39	72.2	108	9	AEA45216	Aea45216 Apolipoppr
741	39	72.2	107	9	AEA17749	Aea17749 Hybridoma	814	39	72.2	108	9	AEA45212	Aea45212 Apolipoppr
742	39	72.2	107	9	AEA1073	Aea1073 Germline	815	39	72.2	108	9	AEA45213	Aea45213 Apolipoppr
743	39	72.2	107	9	AEA50163	Aea50163 Anti-CD22	816	39	72.2	108	9	AEA45218	Aea45218 Apolipoppr
744	39	72.2	107	9	ABE45968	Aeb45968 Human mon	817	39	72.2	108	9	AEA45203	Aea45203 Apolipoppr
745	39	72.2	108	2	AAW13530	Aaw13530 Anti-mela	818	39	72.2	108	9	AEA45205	Aea45205 Apolipoppr
746	39	72.2	108	2	AAW13521	Aaw13521 Anti-mela	819	39	72.2	108	9	AEA45206	Aea45206 Apolipoppr
747	39	72.2	108	2	AAW10229	Aaw10229 CDR-graft	820	39	72.2	108	9	AEA45209	Aea45209 Apolipoppr
748	39	72.2	108	2	AAW10231	Aaw10231 CDR-graft	821	39	72.2	108	9	AEA45214	Aea45214 Apolipoppr
749	39	72.2	108	4	AAE62772	Aae62772 Human HIV	822	39	72.2	108	9	AEA45099	Aea45099 Apolipoppr
750	39	72.2	108	4	AAG93589	Agg93589 Human ant	823	39	72.2	108	9	AEA45207	Aea45207 Apolipoppr
751	39	72.2	108	4	AAG93600	Agg93600 Human ant	824	39	72.2	108	9	AEA45221	Aea45221 Apolipoppr
752	39	72.2	108	4	AAG93655	Agg93655 Human ant	825	39	72.2	108	9	AEA45970	Aea45970 Human mon
753	39	72.2	108	4	AAW93651	Aaw93651 Human ant	826	39	72.2	109	2	AAR13658	Aar13658 Murine OK
754	39	72.2	108	6	ABP96009	Abp96009 HSA antiB	827	39	72.2	109	2	AAW26797	Aaw26797 Anti-gp54

828	39	72.2	109	7	ADL91355	Adl91355	VL chain	901	39	72.2	240	4	AAB46004	Aab46004	Human MUC
829	39	72.2	109	8	ADP66617	Adp66617	Anti-RAS	902	39	72.2	240	4	AAB46018	Aab46018	Human MUC
830	39	72.2	109	8	ADP66621	Adp66621	Anti-RAS	903	39	72.2	240	4	AAB46038	Aab46038	Human TF
831	39	72.2	109	8	ADP96649	Adp96649	Anti-RAS	904	39	72.2	240	4	AAB46042	Aab46042	Human TF
832	39	72.2	109	8	ADP96653	Adp96653	Anti-RAS	905	39	72.2	240	4	AAB46051	Aab46051	Human TF
833	39	72.2	109	8	ADO79341	Ado79341	Anti-RAS	906	39	72.2	240	4	AAB46008	Aab46008	Human MUC
834	39	72.2	109	8	ADO79345	Ado79345	Anti-RAS	907	39	72.2	240	4	AAB46017	Aab46017	Human MUC
835	39	72.2	109	9	ADZ42047	Adz42047	Ig L chain	908	39	72.2	240	4	AAB46021	Aab46021	Human MUC
836	39	72.2	110	9	ABE46923	Aeb46923	Variable	909	39	72.2	240	4	AAB46041	Aab46041	Human TF
837	39	72.2	111	4	AG63655	Aeg63655	Amino aci	910	39	72.2	240	4	AAB46003	Aab46003	Human MUC
838	39	72.2	111	6	ABJ38614	Abj38614	Hepatitis	911	39	72.2	240	4	AAB46014	Aab46014	Human MUC
839	39	72.2	111	8	ADP47305	Adp47305	Human pho	912	39	72.2	240	4	AAB46050	Aab46050	Human TF
840	39	72.2	111	8	ADP47306	Adp47306	Human pho	913	39	72.2	240	4	AAB46006	Aab46006	Human MUC
841	39	72.2	111	8	ADP47301	Adp47301	Human pho	914	39	72.2	240	4	AAB46020	Aab46020	Human MUC
842	39	72.2	113	2	AAW13924	Aaw13924	Light cha	915	39	72.2	240	4	AAB46039	Aab46039	Human TF
843	39	72.2	113	7	ADD28275	Add28275	Human het	916	39	72.2	240	4	AAB46044	Aab46044	Human TF
844	39	72.2	113	9	ADY50130	Ady50130	Endotheli	917	39	72.2	240	4	AAB45999	Aab45999	Human MUC
845	39	72.2	114	2	AAW13922	Aaw13922	Light cha	918	39	72.2	240	4	AAB46047	Aab46047	Human TF
846	39	72.2	114	4	AG65563	Aeg65563	Amino aci	919	39	72.2	240	4	AAB46048	Aab46048	Human TF
847	39	72.2	114	7	ADD28276	Add28276	Human het	920	39	72.2	240	4	AAB45996	Aab45996	Human MUC
848	39	72.2	116	9	ADW04849	Adw04849	PAPP-A im	921	39	72.2	240	4	AAB46019	Aab46019	Human MUC
849	39	72.2	116	9	ADW04873	Adw04873	PAPP-A im	922	39	72.2	240	4	AAB45995	Aab45995	Human MUC
850	39	72.2	116	9	ADY50090	Ady50090	Endotheli	923	39	72.2	240	4	AAB46005	Aab46005	Human MUC
851	39	72.2	118	5	AAO14050	Aao14050	Human ant	924	39	72.2	240	4	AAB46046	Aab46046	Human TF
852	39	72.2	118	5	AAO14053	Aao14053	Humanised	925	39	72.2	240	4	AAB46012	Aab46012	Human MUC
853	39	72.2	119	9	AEA53382	Aea53382	Novel hum	926	39	72.2	240	4	AAB46015	Aab46015	Human MUC
854	39	72.2	119	9	AEA53995	Aea53995	Novel hum	927	39	72.2	240	4	AAB45991	Aab45991	Human MUC
855	39	72.2	121	9	AEA53234	Aea53234	Novel hum	928	39	72.2	240	4	AAB46045	Aab46045	Human TF
856	39	72.2	121	9	AEA53876	Aea53876	Novel hum	929	39	72.2	240	4	AAB45994	Aab45994	Human MUC
857	39	72.2	124	3	AAV56719	Aav56719	Amino aci	930	39	72.2	240	4	AAB46016	Aab46016	Human MUC
858	39	72.2	124	8	ADO84981	Ado84981	H23 antiq	931	39	72.2	240	6	ABP95997	Abp95997	Human eer
859	39	72.2	129	3	AAV56724	Aav56724	Amino aci	932	39	72.2	240	6	ABJ38594	Abj38594	Hepatitis
860	39	72.2	132	2	AAW22842	Aaw22842	Human ant	933	39	72.2	240	8	ADL92369	Adl92369	Human pha
861	39	72.2	134	3	AAV93720	Aav93720	The kappa	934	39	72.2	240	8	ADQ77165	Adq77165	HSA Heavy
862	39	72.2	134	6	AAE35903	Aae35903	Human 11.	935	39	72.2	240	9	ADW11302	Adw11302	Human C-t
863	39	72.2	137	2	AAV24378	Aay24378	Human mon	936	39	72.2	240	9	AEBA6929	Aeb46929	Human CD1
864	39	72.2	150	3	AAV93722	Aay93722	The kappa	937	39	72.2	240	9	AEBA6937	Aeb46937	Human CD1
865	39	72.2	150	6	AAE35904	Aae35904	Human 11.	938	39	72.2	240	9	AEBA6939	Aeb46939	Human CD1
866	39	72.2	164	7	ADD28246	Adadd28246	Human het	939	39	72.2	241	9	ADV21480	Adv21480	Mature fo
867	39	72.2	164	9	ADV86833	Adv86833	Bacillus	940	39	72.2	241	9	AEBA6935	Aeb46935	Human CD1
868	39	72.2	165	7	ADD28245	Adadd28245	Human het	941	39	72.2	241	9	AEBA6931	Aeb46931	Human CD1
869	39	72.2	165	9	ADV86832	Adv86832	Bacillus	942	39	72.2	243	9	ADV21484	Adv21484	Mature fo
870	39	72.2	214	8	ADR23360	Adr23360	Human CD7	943	39	72.2	243	9	ADW90303	Adw90303	Phage scf
871	39	72.2	214	8	ADR23358	Adr23358	Human CD7	944	39	72.2	243	9	ADX01791	Adx01791	SARS coro
872	39	72.2	214	8	ADR23366	Adr23366	Human CD7	945	39	72.2	244	8	ADH34565	Adh34565	scFv SC02
873	39	72.2	214	8	ADR23364	Adr23364	Human CD7	946	39	72.2	244	8	ADR23318	Adr23318	Human CD7
874	39	72.2	214	9	ADW11300	Adw11300	Human C-t	947	39	72.2	244	8	ADR23330	Adr23330	Human CD7
875	39	72.2	214	9	ADW90321	Adw90321	Phage scf	948	39	72.2	244	8	ADR23332	Adr23332	Human CD7
876	39	72.2	214	9	ADX01873	Adx01873	SARS coro	949	39	72.2	244	9	ADW11304	Adw11304	Human C-t
877	39	72.2	214	9	ADY50072	Ady50072	Endotheli	950	39	72.2	244	9	ADW11306	Adw11306	Human C-t
878	39	72.2	214	9	AEBA6966	Aeb46966	CD1a spec	951	39	72.2	245	2	AAW26800	Aaw26800	Anti-gp54
879	39	72.2	236	9	AEBA5893	Aeb45893	Human mon	952	39	72.2	245	8	ADR23320	Adr23320	Human CD7
880	39	72.2	237	3	AAV96298	Aay96298	Human IGF	953	39	72.2	245	9	ADW90309	Adw90309	Phage scf
881	39	72.2	224	4	AAV99373	Aab99373	Human int	954	39	72.2	245	9	ADW90311	Adw90311	Phage scf
882	39	72.2	224	4	ABW75006	Abw75006	Anti-IL8	955	39	72.2	245	9	ADW90306	Adw90306	Phage scf
883	39	72.2	230	4	ABW46049	Aab46049	Human TF	956	39	72.2	245	9	ADW90305	Adw90305	Phage scf
884	39	72.2	234	2	AAW10233	Aaw10233	TF8-SG9 C	957	39	72.2	245	9	ADX01807	Adx01807	SARS coro
885	39	72.2	237	3	AAV96298	Aay96298	Human IGF	958	39	72.2	245	9	ADX01803	Adx01803	SARS coro
886	39	72.2	240	2	AAV02472	Aay02472	A single	959	39	72.2	245	9	ADX01797	Adx01797	SARS coro
887	39	72.2	240	4	ABW45993	Aab45993	Human MUC	960	39	72.2	245	9	ADX01795	Adx01795	SARS coro
888	39	72.2	240	4	ABW46000	Aab46000	Human MUC	961	39	72.2	247	9	ADW90316	Adw90316	Phage scf
889	39	72.2	240	4	ABW46002	Aab46002	Human MUC	962	39	72.2	247	9	ADW90308	Adw90308	Phage scf
890	39	72.2	240	4	ABW46010	Aab46010	Human MUC	963	39	72.2	247	9	ADX01840	Adx01840	SARS coro
891	39	72.2	240	4	ABW46040	Aab46040	Human TF	964	39	72.2	247	9	ADX01801	Adx01801	SARS coro
892	39	72.2	240	4	ABW45997	Aab45997	Human MUC	965	39	72.2	248	9	ADW90310	Adw90310	Phage scf
893	39	72.2	240	4	ABW46013	Aab46013	Human MUC	966	39	72.2	248	9	ADX01805	Adx01805	SARS coro
894	39	72.2	240	4	ABW45992	Aab45992	Human MUC	967	39	72.2	248	8	ADR23322	Adr23322	Human CD7
895	39	72.2	240	4	ABW46001	Aab46001	Human MUC	968	39	72.2	249	8	ADR23326	Adr23326	Human CD7
896	39	72.2	240	4	ABW46043	Aab46043	Human TF	969	39	72.2	249	9	ADW90313	Adw90313	Phage scf
897	39	72.2	240	4	ABW46007	Aab46007	Human MUC	970	39	72.2	249	9	ADW90314	Adw90314	Phage scf
898	39	72.2	240	4	ABW46009	Aab46009	Human MUC	971	39	72.2	249	9	ADW90304	Adw90304	Phage scf
899	39	72.2	240	4	ABW46011	Aab46011	Human MUC	972	39	72.2	249	9	ADX01836	Adx01836	SARS coro
900	39	72.2	240	4	ABW46018	Aab46018	Human MUC	973	39	72.2	249	9	ADX01793	Adx01793	SARS coro



974 39 72.2 249 9 ADX01834 SARS coro  
 975 39 72.2 249 9 ADX01811 SARS coro  
 976 39 72.2 249 9 ADX01813 SARS coro  
 977 39 72.2 250 5 ADP45163 Human Bly  
 978 39 72.2 250 7 ADG95990 Single ch  
 979 39 72.2 253 5 AAO14057 Anti-FAPA  
 980 39 72.2 255 5 AAO14054 Anti-FAPA  
 981 39 72.2 260 5 AAO14056 Anti-FAPA  
 982 39 72.2 260 5 AAO14055 Anti-FAPA  
 983 39 72.2 262 5 AAO14058 Anti-FAPA  
 984 39 72.2 288 5 AAO17154 Human end  
 985 39 72.2 291 8 ADN06993 Human EFG  
 986 39 72.2 291 8 ADN06992 Human EFG  
 987 39 72.2 299 4 AAG63659 Amino aci  
 988 39 72.2 389 6 ADA33046 Acinetoba  
 989 39 72.2 459 7 ADC96561 E. faeciu  
 990 39 72.2 466 7 ADH88782 Enterococ  
 991 39 72.2 494 9 ADV21531 Mature fo  
 992 39 72.2 494 9 ADV21521 Mature fo  
 993 39 72.2 496 9 ADV21501 Mature fo  
 994 39 72.2 496 9 ADV21511 Mature fo  
 995 39 72.2 496 9 ADV21523 Mature fo  
 996 39 72.2 496 9 ADV21533 Mature fo  
 997 39 72.2 498 9 ADV21503 Mature fo  
 998 39 72.2 498 9 ADV21513 Mature fo  
 999 39 72.2 523 3 AAY44994 HD708CFV-  
 1000 39 72.2 524 3 AAY44995 HD708CFV-

## ALIGNMENTS

RESULT 1  
 AAW70614  
 ID AAW70614 standard; peptide; 11 AA.

XX AC AAW70614;

XX DT 27-JAN-1999 (first entry)

XX DE Anti-VEGF antibody light chain hypervariable region CDRL1.

XX KW Light chain hypervariable region; murine; humanised antibody;

XX KW anti-vascular endothelial growth factor antibody; anti-VEGF antibody;

XX KW VEGF-induced angiogenesis; tumour; retinal disorder;

XX KW age-related macular degeneration; diabetic retinopathy;

XX KW rheumatoid arthritis; psoriasis; atherosclerosis; Grave's disease.

XX OS Synthetic.

XX OS Mus sp.

XX FN WO9845331-A2.

XX PD 15-OCT-1998.

XX PF 03-APR-1998; 98WO-US006604.

XX PR 07-APR-1997; 97US-00833504.

XX PR 06-AUG-1997; 97US-00908469.

XX PA (GETH ) GENENTECH INC.

XX PI Baca M, Wells JA, Presta LG, Lowman HB, Chen YM;

XX DR WPI; 1998-568337/48.

XX PT New humanised antibody with affinity for vascular endothelial growth factor - for treatment of tumours, retinal disease and other angiogenic PT states, also related nucleic acid, vectors and transformed cells.

XX PS Claim 9; Page 80; 100pp; English.

XX CC The present sequence represents a light chain hypervariable region of the

CC murine anti-vascular endothelial growth factor (anti-VEGF) antibody. The sequence is used to construct the humanised anti-VEGF antibody of the invention. The humanised antibodies are used to inhibit VEGF-induced CC angiogenesis, particularly for treating or preventing tumours (of any CC type) and retinal disorders (e.g. age-related macular degeneration or CC diabetic retinopathy). They can also be used to treat other conditions CC that involve angiogenesis, e.g. rheumatoid arthritis, psoriasis, CC atherosclerosis, Grave's disease, etc

XX SQ Sequence 11 AA;

Query Match 100.0%; Score 54; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 0.0052;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SASQDISNYLN 11  
 |||||  
 Db 1 SASQDISNYLN 11

RESULT 2

AAB81982

ID AAB81982 standard; peptide; 11 AA.

XX AC AAB81982;

XX DT 03-JUL-2001 (first entry)

XX DE Ganglioside GD3 specific antibody related peptide SEQ ID NO: 6.

XX KW Ganglioside; GD3; complementarity determining region; CDR; antibody;

XX KW cancer.

XX OS Mus musculus.

XX FN WO200123432-A1.

XX PD 05-APR-2001.

XX PF 29-SEP-2000; 2000WO-JP006774.

XX PR 30-SEP-1999; 99JP-00278291.

XX PR 06-APR-2000; 2000JP-00105088.

XX PA (KTOW ) KYOWA HAKKO KOGYO KK.

XX PI Hanai N, Shitara K, Nakamura K, Niwa R;

XX DR WPI; 2001-266143/27.

XX PT New human type complementation-determining region-transplanted antibody and derivatives against ganglioside GD3, useful in diagnosis and therapy of e.g. tumors, with low antigenicity, little side effects but potent activity in cancer.

XX PS Claim 4; Page 141; 183pp; Japanese.

XX CC The present invention describes a monoclonal antibody which can react specifically with ganglioside GD3. The antibody and its derivatives are useful in the diagnosis and therapy of tumours, particularly cancer CC diagnosis. The present sequence is a protein used in the exemplification CC of the invention

XX SQ Sequence 11 AA;

Query Match 100.0%; Score 54; DB 4; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 0.0052;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SASQDISNYLN 11  
 |||||  
 Db 1 SASQDISNYLN 11



```

RESULT 3
ABP61183
ID ABP61183 standard; peptide; 11 AA.
XX AC
XX ABP61183;
XX DT
XX 20-SEP-2002 (first entry)
XX DE
XX Humanised anti-VEGF antibody light chain hypervariable domain, CDRL1.
XX KW
XX Cytostatic; ophthalmological; humanised; antibody; anti-VEGF; VEGF;
XX KW vascular endothelial growth factor; angiogenesis inhibitor; tumour;
XX KW retinal disorder; intraocular neovascular disorder; light chain;
XX KW hypervariable domain; CDRL1.
XX OS
XX Homo sapiens.
XX OS
XX Mus sp.
XX OS
XX Synthetic.
XX XX
XX US2002032315-A1.
XX PN
XX 14-MAR-2002.
XX PD
XX 06-APR-1998; 98US-00056160.
XX PF
XX 06-AUG-1997; 97US-0054856P.
XX PR
XX (BACA/) BACA M.
XX PA (WELL/) WELLS J A.
XX PA (PRES/) PRESTA L G.
XX PA (LOWM/) LOWMAN H B.
XX PA (CHEN/) CHEN Y M.
XX XX
XX Baca M, Wells JA, Presta LG, Lowman HB, Chen YM;
XX PI
XX WPI; 2002-517920/55.
XX DR
XX New humanized anti-VEGF (vascular endothelial growth factor) antibodies
XX PT or their variants, useful for inhibiting VEGF-induced angiogenesis in a
XX PT mammal, particularly for treating tumor or retinal disorders.
XX PT
XX Claim 9; Page 31; 47pp; English.
XX PS
XX The present invention relates to humanised anti-VEGF (vascular
XX CC endothelial growth factor) antibodies or a variant of a parent anti-VEGF
XX CC antibody, which binds human VEGF. The anti-VEGF antibodies are useful for
XX CC inhibiting VEGF-induced angiogenesis in a mammal (particularly a human),
XX CC particularly those having a tumour or a retinal disorder e.g. intraocular
XX CC neovascular disorders. The present sequence is an exemplary light chain
XX CC hypervariable domain of the humanised anti-VEGF antibody of the invention
XX CC
XX Sequence 11 AA;
XX Query Match 100.0%; Score 54; DB 5; Length 11;
XX Best Local Similarity 100.0%; Pred. No. 0.0052;
XX Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 1 SASQDISNYLN 11
XX DB 1 SASQDISNYLN 11
XX RESULT 4
XX ABU11007
XX ID ABU11007 standard; peptide; 11 AA.
XX AC
XX ABU11007;
XX XX
XX 04-FEB-2003 (first entry)
XX DT
XX Modified ganglioside GD3 antibody associated peptide #4.
XX DE
XX

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KW Ganglioside GD3; anti-ganglioside GD3 antibody; tumour; melanoma.
XX OS
XX Mus musculus.
XX XX
XX WO200278739-A1.
XX PN
XX 10-OCT-2002.
XX PD
XX 29-MAR-2002; 2002WO-JP003170.
XX PF
XX 29-MAR-2001; 2001JP-00097483.
XX PR
XX (KYOW ) KYOWA HAKKO KOGYO KK.
XX PA
XX Shitara K, Niwa R, Kanazawa J, Asada M;
XX PI
XX WPI; 2003-067410/06.
XX DR
XX Drugs containing genetically-modified antibody against ganglioside GD3,
XX PT its fragment, immunocompetent cell activators or/and antitumor agents in
XX PT combination, applicable in treating malignant tumor like melanoma.
XX PT
XX Claim 6; Page 99; 121pp; Japanese.
XX PS
XX The invention describes drugs contain a genetically-modified antibody
XX CC against ganglioside GD3 or its fragment and at least 1 of a substance
XX CC capable of activating immunocompetent cells and a substance having an
XX CC antitumor activity in combination. The drugs can be used to treat tumour
XX CC like melanoma and can provide a treatment with enhanced therapeutic
XX CC effect and little side-reactions, particularly to relieve problems of
XX CC side-effects during the conventional single administration. This sequence
XX CC represents a peptide associated with the anti- ganglioside GD3 antibody
XX CC
XX Sequence 11 AA;
XX Query Match 100.0%; Score 54; DB 6; Length 11;
XX Best Local Similarity 100.0%; Pred. No. 0.0052;
XX Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 1 SASQDISNYLN 11
XX DB 1 SASQDISNYLN 11
XX RESULT 5
XX ADZ57813
XX ID ADZ57813 standard; peptide; 11 AA.
XX XX
XX AC ADZ57813;
XX XX
XX 30-JUN-2005 (first entry)
XX DT
XX Ganglioside GD3 binding antibody associated CDRI SEQ ID NO 17.
XX DE
XX Cytostatic; antibody engineering; cancer; neoplasm; ganglioside; GD3;
XX KW pharmaceutical.
XX KW
XX OS
XX Mus musculus.
XX XX
XX WO2005035577-A1.
XX PN
XX 21-APR-2005.
XX PD
XX 08-OCT-2004; 2004WO-JP015314.
XX PF
XX 08-OCT-2003; 2003JP-00350161.
XX PR
XX (KYOW ) KYOWA HAKKO KOGYO KK.
XX PA
XX Iida S, Satoh M, Urakubo M, Wakitani M, Uchida K, Niwa R;
XX PI Shitara K;
XX PI
XX WPI; 2005-346195/35.
XX DR

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XX Antibody composition for treating ganglioside GD3 associated disease e.g.  
 PT cancer, comprises genetically modified antibody molecule, which  
 PT specifically binds to ganglioside GD3 and has N-glycoside-binding sugar  
 PT chain in its Fc domain.  
 XX  
 XX Claim 9; SEQ ID NO 17; 124pp; Japanese.  
 PS  
 XX The invention describes an antibody composition (I), comprising a  
 CC genetically modified antibody molecule which specifically binds to  
 CC ganglioside GD3 and has an N-glycoside-binding complex sugar chain in its  
 CC Fc domain, where the N-glycoside-binding complex sugar chain is a sugar  
 CC chain having no fucose attached to N-acetylglucosamine at the reducing  
 CC end of the sugar chain. Also described are: a transformant (II) capable  
 CC of producing (II), obtained by introducing DNA that encodes the antibody  
 CC molecule which specifically binds with ganglioside GD3, to a host cell;  
 CC producing (II), involving cultivating (I) in a culture medium, such that  
 CC C1 (sic) is produced and accumulated in the culture, extracting and  
 CC purifying C1 from the culture medium; a pharmaceutical (III) containing  
 CC C1 as an active ingredient; and a therapeutic agent (A1) for ganglioside  
 CC GD3 associated disease, comprising C1 as an active ingredient. (I) is  
 CC useful for treating GD3 associated disease, which involves administering  
 CC (I), where the GD3 associated disease is cancer. (A1) is also useful for  
 CC treating GD3 associated disease. (II) is useful for producing (I). (I) is  
 CC useful for manufacturing a therapeutic agent for GD3 associated disease.  
 CC This sequence represents a ganglioside GD3 binding antibody associated  
 CC peptide.  
 XX

Sequence 11 AA;

Query Match 100.0%; Score 54; DB 9; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 0.0052;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SASQDISNYLN 11  
 |||||  
 Db 1 SASQDISNYLN 11

RESULT 6  
 ADF09995  
 ID ADF09995 standard; protein; 103 AA.

AC ADF09995;

XX 12-FEB-2004 (first entry)

XX Antibody light chain variable region 1C28(1D-33).

XX Antibody; stability; solubility; antigen binding affinity;  
 KW variable region; human.

XX Homo sapiens.

XX WO2003074679-A2.

XX 12-SEP-2003.

XX 03-MAR-2003; 2003WO-US006598.

XX 01-MAR-2002; 2002US-0360843P.

XX 29-MAY-2002; 2002US-0384197P.

XX (XENC-) XENCOR.

XX Lazar GA, Desjarlais JR, Marshall SA, Dahiyat B;

XX WPI; 2003-722066/68.

XX Computer optimization of physicochemical properties of antibodies  
 PT comprises analyzing the interactions of amino acids at variable  
 PT positions.

PS Disclosure; Fig 2b; 135pp; English.

XX The present invention relates to a method for optimizing at least one  
 CC physico-chemical property of an antibody by a computational screening  
 CC method. The method comprises: receiving a template antibody structure;  
 CC selecting at least one variable position belonging to the antibody  
 CC structure; selecting at least one amino acid to be considered at the  
 CC variable position(s); analyzing the interaction of each selected amino  
 CC acid at each variable position with at least part of the remainder of the  
 CC antibody, including the selected amino acids at other variable positions;  
 CC and identifying a set of at least one antibody sequence with at least one  
 CC optimized physico-chemical property. The method is useful for optimizing  
 CC the physico-chemical properties of an antibody, especially the stability,  
 CC solubility, or antigen binding affinity. The optimized antibody may be  
 CC useful for treating a patient. The present sequence is an antibody  
 CC variable region sequence used to illustrate the invention.

Sequence 103 AA;

Query Match 100.0%; Score 54; DB 7; Length 103;  
 Best Local Similarity 100.0%; Pred. No. 0.067;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SASQDISNYLN 11  
 |||||  
 Db 24 SASQDISNYLN 34

RESULT 7

ADFI0099

ID ADF10099 standard; protein; 103 AA.

XX ADF10099;

XX 12-FEB-2004 (first entry)

XX VEGF antibody light chain variable region 1C28.

XX Antibody; stability; solubility; antigen binding affinity;  
 KW variable region; human; VEGF.

XX Homo sapiens.

XX WO2003074679-A2.

XX 12-SEP-2003.

XX 03-MAR-2003; 2003WO-US006598.

XX 01-MAR-2002; 2002US-0360843P.

XX 29-MAY-2002; 2002US-0384197P.

XX (XENC-) XENCOR.

XX Lazar GA, Desjarlais JR, Marshall SA, Dahiyat B;

XX WPI; 2003-722066/68.

XX Computer optimization of physicochemical properties of antibodies  
 PT comprises analyzing the interactions of amino acids at variable  
 PT positions.

XX Example 6; Fig 16b; 135pp; English.

XX The present invention relates to a method for optimizing at least one  
 CC physico-chemical property of an antibody by a computational screening  
 CC method. The method comprises: receiving a template antibody structure;  
 CC selecting at least one variable position belonging to the antibody  
 CC structure; selecting at least one amino acid to be considered at the  
 CC variable position(s); analyzing the interaction of each selected amino  
 CC acid at each variable position with at least part of the remainder of the  
 CC antibody, including the selected amino acids at other variable positions;  
 CC and identifying a set of at least one antibody sequence with at least one

CC optimized physico-chemical property. The method is useful for optimizing  
 CC the physico-chemical properties of an antibody, especially the stability,  
 CC solubility, or antigen binding affinity. The optimized antibody may be  
 CC useful for treating a patient. The present sequence is an antibody  
 CC variable region sequence used to illustrate the invention.

XX Sequence 103 AA;

Query Match 100.0%; Score 54; DB 7; Length 103;  
 Best Local Similarity 100.0%; Pred. No. 0.067;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SASQDISNYLN 11  
 |||||  
 Db 24 SASQDISNYLN 34

RESULT 8

AAW86804  
 ID AAW86804 standard; protein; 107 AA.

XX AC AAW86804;

XX DT 26-FEB-1999 (first entry)

XX DE Variable Light domain 1.

XX KW Complementarily-determining regions; CDRs; murine; antibody; VEGF;  
 KW vascular endothelial growth factor; humanised antibody; tumour;  
 KW mitogenic.

XX OS Homo sapiens.

XX PN WO9845332-A2.

XX PD 15-OCT-1998.

XX PF 03-APR-1998; 98WO-US006724.

XX PR 07-APR-1997; 97US-00833504.

XX PA (GETH ) GENENTECH INC.

XX PI Wells JA, Baca M, Presta LG;

XX DR WPI; 1998-594479/50.

XX PT New humanised antibody with specific alterations in human framework -  
 PT specifically reactive with vascular endothelial growth factor, useful for  
 PT inhibiting tumour growth.

XX PS Claim 6; Page 30-31; 45pp; English.

XX CC AAW86804 is the variable light region of the humanised A4.6.1 variant  
 CC hu2.0. This variant contains only the complementarily-determining regions  
 CC (CDRs) from the murine antibody grafted on to a human light chain K  
 CC subgroup I and heavy chain subgroup III framework. Antibodies are  
 CC especially reactive with vascular endothelial growth factor (VEGF) and  
 CC are used to inhibit growth of tumours by inhibiting mitogenic signalling

XX SQ Sequence 107 AA;

Query Match 100.0%; Score 54; DB 2; Length 107;  
 Best Local Similarity 100.0%; Pred. No. 0.07;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SASQDISNYLN 11  
 |||||  
 Db 24 SASQDISNYLN 34

RESULT 9

AAW86805

ID AAW86805 standard; protein; 107 AA.

XX AC AAW86805;

XX DT 26-FEB-1999 (first entry)

XX DE Variable Light domain 2.

XX KW Antibody; VEGF; vascular endothelial growth factor; humanised antibody;  
 KW tumour; mitogenic; phage sorting.

XX OS Homo sapiens.

XX PN WO9845332-A2.

XX PD 15-OCT-1998.

XX PF 03-APR-1998; 98WO-US006724.

XX PR 07-APR-1997; 97US-00833504.

XX PA (GETH ) GENENTECH INC.

XX PI Wells JA, Baca M, Presta LG;

XX DR WPI; 1998-594479/50.

XX PT New humanised antibody with specific alterations in human framework -  
 PT specifically reactive with vascular endothelial growth factor, useful for  
 PT inhibiting tumour growth.

XX PS Claim 3; Page 31; 45pp; English.

XX CC AAW86805 is the variable light region of the humanised A4.6.1 variant  
 CC hu2.10. This variant is the consensus humanised clone obtained from phage  
 CC sorting experiments. These antibodies are especially reactive with  
 CC vascular endothelial growth factor (VEGF) and are used to inhibit growth  
 CC of tumours by inhibiting mitogenic signalling

XX SQ Sequence 107 AA;

Query Match 100.0%; Score 54; DB 2; Length 107;  
 Best Local Similarity 100.0%; Pred. No. 0.07;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SASQDISNYLN 11  
 |||||  
 Db 24 SASQDISNYLN 34

RESULT 10

AAW70623

ID AAW70623 standard; peptide; 107 AA.

XX AC AAW70623;

XX DT 27-JAN-1999 (first entry)

XX DE Humanised murine antibody A4.6.1 variant hu2.0 variable light domain.

XX KW Light variable domain; murine; humanised antibody;  
 KW anti-vascular endothelial growth factor antibody; anti-VEGF antibody;  
 KW VEGF-induced angiogenesis; tumour; retinal disorder;  
 KW age-related macular degeneration; diabetic retinopathy;  
 KW rheumatoid arthritis; psoriasis; atherosclerosis; Grave's disease.

XX OS Synthetic.

XX OS Mus sp.

XX OS Homo sapiens.

XX PN WO9845331-A2.

XX PD 15-OCT-1998.

XX 03-APR-1998; 98WO-US006604.  
 PF  
 XX 07-APR-1997; 97US-00833504.  
 PR  
 XX 06-AUG-1997; 97US-00908469.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Baca M, Wells JA, Presta LG, Lowman HB, Chen YM;  
 XX  
 DR WPI; 1998-568337/48.  
 XX  
 XX New humanised antibody with affinity for vascular endothelial growth  
 PT factor - for treatment of tumours, retinal disease and other angiogenic  
 PT states, also related nucleic acid, vectors and transformed cells.  
 XX  
 XX Example 2; Fig 5A; 100pp; English.  
 XX  
 CC The present sequence represents a variable light domain of the humanised  
 CC murine anti-vascular endothelial growth factor (anti-VEGF) antibody to  
 CC variant hu2.0. The sequence is used in the course of the invention to  
 CC construct the humanised anti-VEGF antibody of the invention. The  
 CC humanised antibodies are used to inhibit VEGF-induced angiogenesis,  
 CC particularly for treating or preventing tumours (of any type) and retinal  
 CC disorders (e.g. age-related macular degeneration or diabetic  
 CC retinopathy). They can also be used to treat other conditions that  
 CC involve angiogenesis, e.g. rheumatoid arthritis, psoriasis,  
 CC atherosclerosis, Grave's disease, etc  
 XX  
 XX Sequence 107 AA;  
 SQ  
 Query Match 100.0%; Score 54; DB 2; Length 107;  
 Best Local Similarity 100.0%; Pred. NO. 0.07;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 SASQDISNYLN 11  
 |||||  
 Db 24 SASQDISNYLN 34  
 |||||  
 RESULT 11  
 AAW70625  
 ID AAW70625 standard; peptide; 107 AA.  
 XX  
 AC AAW70625;  
 XX  
 DT 27-JAN-1999 (first entry)  
 XX  
 DE Humanised murine antibody A4.6.1 variant hu2.10 variable light domain.  
 XX  
 KW Light variable domain; murine; humanised antibody;  
 KW anti-vascular endothelial growth factor antibody; anti-VEGF antibody;  
 KW VEGF-induced angiogenesis; tumour; retinal disorder;  
 KW age-related macular degeneration; diabetic retinopathy;  
 KW rheumatoid arthritis; psoriasis; atherosclerosis; Grave's disease.  
 XX  
 OS Synthetic.  
 OS Mus sp.  
 OS Homo sapiens.  
 XX  
 PN W09845331-A2.  
 XX  
 PD 15-OCT-1998.  
 XX  
 XX 03-APR-1998; 98WO-US006604.  
 PF  
 XX 07-APR-1997; 97US-00833504.  
 PR  
 XX 06-AUG-1997; 97US-00908469.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Baca M, Wells JA, Presta LG, Lowman HB, Chen YM;  
 XX

DR WPI; 1998-568337/48.  
 XX  
 PT New humanised antibody with affinity for vascular endothelial growth  
 PT factor - for treatment of tumours, retinal disease and other angiogenic  
 PT states, also related nucleic acid, vectors and transformed cells.  
 XX  
 XX Example 2; Fig 5A; 100pp; English.  
 XX  
 CC The present sequence represents a variable light domain of the humanised  
 CC murine anti-vascular endothelial growth factor (anti-VEGF) antibody to  
 CC variant hu2.10. The sequence is used in the course of the invention to  
 CC construct the humanised anti-VEGF antibody of the invention. The  
 CC humanised antibodies are used to inhibit VEGF-induced angiogenesis,  
 CC particularly for treating or preventing tumours (of any type) and retinal  
 CC disorders (e.g. age-related macular degeneration or diabetic  
 CC retinopathy). They can also be used to treat other conditions that  
 CC involve angiogenesis, e.g. rheumatoid arthritis, psoriasis,  
 CC atherosclerosis, Grave's disease, etc  
 XX  
 XX Sequence 107 AA;  
 SQ  
 Query Match 100.0%; Score 54; DB 2; Length 107;  
 Best Local Similarity 100.0%; Pred. NO. 0.07;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 SASQDISNYLN 11  
 |||||  
 Db 24 SASQDISNYLN 34  
 |||||  
 RESULT 12  
 ABP61192  
 ID ABP61192 standard; protein; 107 AA.  
 XX  
 AC ABP61192;  
 XX  
 DT 20-SEP-2002 (first entry)  
 XX  
 DE Humanised anti-VEGF antibody A4.6.1 variant variable light domain hu2.0.  
 XX  
 KW Cytostatic; ophthalmological; humanised; antibody; anti-VEGF; VEGF;  
 KW vascular endothelial growth factor; angiogenesis inhibitor; tumour;  
 KW retinal disorder; intraocular neovascular disorder; light chain;  
 KW variable domain.  
 XX  
 OS Homo sapiens.  
 OS Mus sp.  
 OS Synthetic.  
 XX  
 PN US2002032315-A1.  
 XX  
 PD 14-MAR-2002.  
 XX  
 XX 06-APR-1998; 98US-00056160.  
 PF  
 XX 06-AUG-1997; 97US-0054856P.  
 PR  
 XX (BACA/) BACA M.  
 XX (WELL/) WELLS J A.  
 XX (PRES/) PRESTA L G.  
 XX (LOWM/) LOWMAN H B.  
 XX (CHEN/) CHEN Y M.  
 XX  
 XX Baca M, Wells JA, Presta LG, Lowman HB, Chen YM;  
 PI  
 XX WPI; 2002-517920/55.  
 DR  
 XX New humanized anti-VEGF (vascular endothelial growth factor) antibodies  
 PT or their variants, useful for inhibiting VEGF-induced angiogenesis in a  
 PT mammal, particularly for treating tumor or retinal disorders.  
 XX  
 XX Example 2; Fig 5; 47pp; English.  
 XX

CC The present invention relates to humanised anti-VEGF (vascular  
CC endothelial growth factor) antibodies or a variant of a parent anti-VEGF  
CC antibody, which binds human VEGF. The anti-VEGF antibodies are useful for  
CC inhibiting VEGF-induced angiogenesis in a mammal (particularly a human),  
CC particularly those having a tumour or a retinal disorder e.g. intraocular  
CC neovascular disorders. The present sequence is an exemplary light chain  
CC variable domain of the humanised anti-VEGF antibody of the invention  
XX  
XX Sequence 107 AA;  
SQ

Query Match 100.0%; Score 54; DB 5; Length 107;  
Best Local Similarity 100.0%; Pred. No. 0.07;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SASQDISNYLN 11  
Db 24 SASQDISNYLN 34  
|||||

RESULT 13  
ABP61194  
ID ABP61194 standard; protein; 107 AA.  
XX  
XX AC ABP61194;  
XX  
XX DT 20-SEP-2002 (first entry)  
XX  
XX DE Humanised anti-VEGF antibody A4.6.1 variant variable light domain hu2.10.  
XX  
XX KW Cytostatic; ophthalmological; humanised; antibody; anti-VEGF; VEGF;  
KW vascular endothelial growth factor; angiogenesis inhibitor; tumour;  
KW retinal disorder; intraocular neovascular disorder; light chain;  
KW variable domain.  
XX  
XX OS Homo sapiens.  
XX Mus sp.  
XX Synthetic.  
XX  
XX FN US2002032315-A1.  
XX  
XX PD 14-MAR-2002.  
XX  
XX PF 06-APR-1998; 98US-00056160.  
XX  
XX PR 06-AUG-1997; 97US-0054856P.  
XX  
XX PA (BACA/) BACA M.  
XX (WELL/) WELLS J A.  
XX (PRES/) PRESTA L G.  
XX (LOWM/) LOWMAN H B.  
XX (CHEN/) CHEN Y M.  
XX  
XX PI Baca M, Wells JA, Presta LG, Lowman HB, Chen YM;  
XX  
XX DR WPI; 2002-517920/55.  
XX  
XX PT New humanized anti-VEGF (vascular endothelial growth factor) antibodies  
XX or their variants, useful for inhibiting VEGF-induced angiogenesis in a  
XX mammal, particularly for treating tumor or retinal disorders.  
XX  
XX PS Example 2; Fig 5; 47pp; English.  
XX  
XX CC The present invention relates to humanised anti-VEGF (vascular  
XX endothelial growth factor) antibodies or a variant of a parent anti-VEGF  
XX antibody, which binds human VEGF. The anti-VEGF antibodies are useful for  
XX inhibiting VEGF-induced angiogenesis in a mammal (particularly a human),  
XX particularly those having a tumour or a retinal disorder e.g. intraocular  
XX neovascular disorders. The present sequence is an exemplary light chain  
XX variable domain of the humanised anti-VEGF antibody of the invention  
XX  
XX SQ Sequence 107 AA;  
SQ

Query Match 100.0%; Score 54; DB 5; Length 107;  
Best Local Similarity 100.0%; Pred. No. 0.07;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SASQDISNYLN 11  
Db 24 SASQDISNYLN 34  
|||||

RESULT 14  
AEA40449  
ID AEA40449 standard; protein; 107 AA.  
XX  
XX AC AEA40449;  
XX  
XX DT 25-AUG-2005 (first entry)  
XX  
XX DE Anti-VEGF antibody light chain variable region SEQ ID NO 11.  
XX  
XX KW vascular endothelial growth factor; VEGF; diagnosis; cancer;  
KW rheumatoid arthritis; hypervascularity; endometriosis; psoriasis;  
KW diabetic retinopathy; angiogenic; immune disorder; inflammation;  
KW musculoskeletal disease; neoplasm; genitourinary disease;  
KW gynecology and obstetrics; dermatological disease;  
KW cardiovascular disease; ocular disease; Cystostatic; Antirheumatic;  
KW Antiarthritic; Vasotropic; Antiinflammatory; Vulnery; Gynaecological;  
KW Antipsoriatic; Antidiabetic; Ophthalmological; Immunotherapy;  
KW light chain variable region; antibody.  
XX  
XX OS Synthetic.  
XX  
XX FN WO2005054273-A2.  
XX  
XX PD 16-JUN-2005.  
XX  
XX PF 22-NOV-2004; 2004WO-US039501.  
XX  
XX PR 26-NOV-2003; 2003US-00723434.  
XX  
XX PA (ABMA-) ABMAXIS INC.  
XX  
XX PI Zhong P, Luo P, Wang KC, Hsieh M, Li Y;  
XX  
XX DR WPI; 2005-435361/44.  
XX  
XX PT New monoclonal antibody that specifically binds to human vascular  
XX endothelial growth factor, useful for treating diseases associated with  
XX abnormal angiogenesis such as cancer, rheumatoid arthritis, psoriasis,  
XX diabetic retinopathy.  
XX  
XX PS Claim 18; SEQ ID NO 11; 111pp; English.  
XX  
XX CC The invention relates to a monoclonal antibody that specifically binds to  
XX a human vascular endothelial growth factor (VEGF) with dissociation  
XX constant Kd equal to or lower than 0.2 nM. The monoclonal antibody is  
XX useful for diagnosing and treating diseases associated with abnormal  
XX angiogenesis such as cancer, rheumatoid arthritis, ischemic-reperfusion  
XX related brain edema and injury, cortical ischemia, ovarian hyperplasia  
XX and hypervascularity, endometriosis, psoriasis, diabetic retinopathy, and  
XX other ocular angiogenic diseases. The present sequence represents the  
XX amino acid sequence of the light chain variable region of an anti-VEGF  
XX antibody.  
XX  
XX SQ Sequence 107 AA;  
SQ

Query Match 100.0%; Score 54; DB 9; Length 107;  
Best Local Similarity 100.0%; Pred. No. 0.07;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SASQDISNYLN 11  
Db 24 SASQDISNYLN 34  
|||||

```

RESULT 15
AEA40445
ID AEA40445 standard; protein; 107 AA.
XX AC AEA40445;
XX DT 25-AUG-2005 (first entry)
XX DE Anti-VEGF antibody light chain variable region SEQ ID NO 7.
XX KW vascular endothelial growth factor; VEGF; diagnosis; cancer;
XX KW rheumatoid arthritis; hypervascularity; endometriosis; psoriasis;
XX KW diabetic retinopathy; antiangiogenic; immune disorder; inflammation;
XX KW musculoskeletal disease; neoplasm; genitourinary disease;
XX KW gynecology and obstetrics; dermatological disease;
XX KW cardiovascular disease; ocular disease; cytostatic; antirheumatic;
XX KW antiarthritic; vasotropic; antiinflammatory; vulnery; gynaecological;
XX KW antipsoriatic; antidiabetic; ophthalmological; immunotherapy;
XX KW light chain variable region; antibody.
XX OS Synthetic.
XX FN WO2005054273-A2.
XX PD 16-JUN-2005.
XX PF 22-NOV-2004; 2004WO-US039501.
XX PR 26-NOV-2003; 2003US-00723434.
XX PA (ABMA-) ABMAXIS INC.
XX PI Zhong P, Luo P, Wang KC, Haieh M, Li Y;
XX WPI; 2005-435361/44.
XX DR New monoclonal antibody that specifically binds to human vascular
XX PT endothelial growth factor, useful for treating diseases associated with
XX PT abnormal angiogenesis such as cancer, rheumatoid arthritis, psoriasis,
XX PT diabetic retinopathy.
XX PS Claim 18; SEQ ID NO 7; 111pp; English.
XX CC The invention relates to a monoclonal antibody that specifically binds to
XX CC a human vascular endothelial growth factor (VEGF) with dissociation
XX CC constant Kd equal to or lower than 0.2 nM. The monoclonal antibody is
XX CC useful for diagnosing and treating diseases associated with abnormal
XX CC angiogenesis such as cancer, rheumatoid arthritis, ischemic-reperfusion
XX CC related brain edema and injury, cortical ischemia, ovarian hyperplasia
XX CC and hypervascularity, endometriosis, psoriasis, diabetic retinopathy, and
XX CC other ocular angiogenic diseases. The present sequence represents the
XX CC amino acid sequence of the light chain variable region of an anti-VEGF
XX CC antibody.
XX SQ Sequence 107 AA;
Query Match 100.0%; Score 54; DB 9; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.07;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SASQDISNYLN 11
DB 24 SASQDISNYLN 34
RESULT 16
AEA40440
ID AEA40440 standard; protein; 107 AA.
XX AC AEA40440;
XX DT 25-AUG-2005 (first entry)
XX DE Anti-VEGF antibody light chain variable region SEQ ID NO 5.
XX KW vascular endothelial growth factor; VEGF; diagnosis; cancer;
XX KW rheumatoid arthritis; hypervascularity; endometriosis; psoriasis;
XX KW diabetic retinopathy; antiangiogenic; immune disorder; inflammation;
XX KW musculoskeletal disease; neoplasm; genitourinary disease;
XX KW gynecology and obstetrics; dermatological disease;
XX KW cardiovascular disease; ocular disease; cytostatic; antirheumatic;
XX KW antiarthritic; vasotropic; antiinflammatory; vulnery; gynaecological;
XX KW antipsoriatic; antidiabetic; ophthalmological; immunotherapy;
XX KW light chain variable region; antibody.
XX OS Synthetic.
XX FN WO2005054273-A2.
XX PD 16-JUN-2005.
XX PF 22-NOV-2004; 2004WO-US039501.
XX PR 26-NOV-2003; 2003US-00723434.
XX PA (ABMA-) ABMAXIS INC.
XX PI Zhong P, Luo P, Wang KC, Haieh M, Li Y;
XX WPI; 2005-435361/44.
XX DR New monoclonal antibody that specifically binds to human vascular
XX PT endothelial growth factor, useful for treating diseases associated with
XX PT abnormal angiogenesis such as cancer, rheumatoid arthritis, psoriasis,
XX PT diabetic retinopathy.
XX PS Claim 18; SEQ ID NO 7; 111pp; English.
XX CC The invention relates to a monoclonal antibody that specifically binds to
XX CC a human vascular endothelial growth factor (VEGF) with dissociation
XX CC constant Kd equal to or lower than 0.2 nM. The monoclonal antibody is
XX CC useful for diagnosing and treating diseases associated with abnormal
XX CC angiogenesis such as cancer, rheumatoid arthritis, ischemic-reperfusion
XX CC related brain edema and injury, cortical ischemia, ovarian hyperplasia
XX CC and hypervascularity, endometriosis, psoriasis, diabetic retinopathy, and
XX CC other ocular angiogenic diseases. The present sequence represents the
XX CC amino acid sequence of the light chain variable region of an anti-VEGF
XX CC antibody.
XX SQ Sequence 107 AA;
Query Match 100.0%; Score 54; DB 9; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.07;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SASQDISNYLN 11
DB 24 SASQDISNYLN 34
RESULT 17
AEA40443
ID AEA40443 standard; protein; 107 AA.
XX AC AEA40443;
XX DT 25-AUG-2005 (first entry)
XX DE Anti-VEGF antibody light chain variable region SEQ ID NO 5.
XX KW vascular endothelial growth factor; VEGF; diagnosis; cancer;
XX KW rheumatoid arthritis; hypervascularity; endometriosis; psoriasis;
XX KW diabetic retinopathy; antiangiogenic; immune disorder; inflammation;
XX KW musculoskeletal disease; neoplasm; genitourinary disease;
XX KW gynecology and obstetrics; dermatological disease;
XX KW cardiovascular disease; ocular disease; cytostatic; antirheumatic;
XX KW antiarthritic; vasotropic; antiinflammatory; vulnery; gynaecological;
XX KW antipsoriatic; antidiabetic; ophthalmological; immunotherapy;
XX KW light chain variable region; antibody.
XX OS Synthetic.
XX FN WO2005054273-A2.
XX PD 16-JUN-2005.
XX PF 22-NOV-2004; 2004WO-US039501.
XX PR 26-NOV-2003; 2003US-00723434.
XX PA (ABMA-) ABMAXIS INC.
XX PI Zhong P, Luo P, Wang KC, Haieh M, Li Y;
XX WPI; 2005-435361/44.
XX DR New monoclonal antibody that specifically binds to human vascular
XX PT endothelial growth factor, useful for treating diseases associated with
XX PT abnormal angiogenesis such as cancer, rheumatoid arthritis, psoriasis,
XX PT diabetic retinopathy.
XX PS Claim 18; SEQ ID NO 2; 111pp; English.
XX CC The invention relates to a monoclonal antibody that specifically binds to
XX CC a human vascular endothelial growth factor (VEGF) with dissociation
XX CC constant Kd equal to or lower than 0.2 nM. The monoclonal antibody is
XX CC useful for diagnosing and treating diseases associated with abnormal
XX CC angiogenesis such as cancer, rheumatoid arthritis, ischemic-reperfusion
XX CC related brain edema and injury, cortical ischemia, ovarian hyperplasia
XX CC and hypervascularity, endometriosis, psoriasis, diabetic retinopathy, and
XX CC other ocular angiogenic diseases. The present sequence represents the
XX CC amino acid sequence of the light chain variable region of an anti-VEGF
XX CC antibody.
XX SQ Sequence 107 AA;
Query Match 100.0%; Score 54; DB 9; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.07;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SASQDISNYLN 11
DB 24 SASQDISNYLN 34

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KW Antiarthritic; Vasotropic; Antiinflammatory; Vulnerary; Gynaecological;  
 KW Antipsoriatic; Antidiabetic; Ophthalmological; Immunotherapy;  
 KW light chain variable region; antibody.  
 OS Synthetic.  
 XX WO2005054273-A2.  
 XX 16-JUN-2005.  
 PD 22-NOV-2004; 2004WO-US039501.  
 XX 26-NOV-2003; 2003US-00723434.  
 XX (ABMA-) AEMAXIS INC.  
 XX Zhong P, Luo P, Wang KC, Hsieh M, Li Y;  
 PI WPI; 2005-435361/44.  
 DR  
 XX New monoclonal antibody that specifically binds to human vascular  
 PT endothelial growth factor, useful for treating diseases associated with  
 PT abnormal angiogenesis such as cancer, rheumatoid arthritis, psoriasis,  
 PT diabetic retinopathy.  
 XX Claim 18; SEQ ID NO 5; 111pp; English.  
 PS The invention relates to a monoclonal antibody that specifically binds to  
 CC a human vascular endothelial growth factor (VEGF) with dissociation  
 CC constant Kd equal to or lower than 0.2 nM. The monoclonal antibody is  
 CC useful for diagnosing and treating diseases associated with abnormal  
 CC angiogenesis such as cancer, rheumatoid arthritis, ischemic-reperfusion  
 CC related brain edema and injury, cortical ischemia, ovarian hyperplasia  
 CC and hypervascularity, endometriosis, psoriasis, diabetic retinopathy, and  
 CC other ocular angiogenic diseases. The present sequence represents the  
 CC amino acid sequence of the light chain variable region of an anti-VEGF  
 CC antibody.  
 XX Sequence 107 AA;  
 SQ Query Match 100.0%; Score 54; DB 9; Length 107;  
 Best Local Similarity 100.0%; Pred. No. 0.07;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SASQDISNYLN 11  
 |||||  
 DB 24 SASQDISNYLN 34  
 RESULT 18  
 AEA40450  
 ID AEA40450 standard; protein; 107 AA.  
 XX AEA40450;  
 AC  
 XX 25-AUG-2005 (first entry)  
 DT  
 DE Anti-VEGF antibody light chain variable region SEQ ID NO 12.  
 XX  
 KW vascular endothelial growth factor; VEGF; diagnosis; cancer;  
 KW rheumatoid arthritis; hypervascularity; endometriosis; psoriasis;  
 KW diabetic retinopathy; antiangiogenic; immune disorder; inflammation;  
 KW musculoskeletal disease; neoplasm; genitourinary disease;  
 KW gynecology and obstetrics; dermatological disease;  
 KW cardiovascular disease; ocular disease; cytostatic; Antirheumatic;  
 KW Antiarthritic; Vasotropic; Antiinflammatory; Vulnerary; Gynaecological;  
 KW Antipsoriatic; Antidiabetic; Ophthalmological; Immunotherapy;  
 KW light chain variable region; antibody.  
 OS Synthetic.  
 XX WO2005054273-A2.  
 XX

KW Antiarthritic; Vasotropic; Antiinflammatory; Vulnerary; Gynaecological;  
 KW Antipsoriatic; Antidiabetic; Ophthalmological; Immunotherapy;  
 KW light chain variable region; antibody.  
 OS Synthetic.  
 XX WO2005054273-A2.  
 XX 16-JUN-2005.  
 PD 22-NOV-2004; 2004WO-US039501.  
 XX 26-NOV-2003; 2003US-00723434.  
 XX (ABMA-) AEMAXIS INC.  
 XX Zhong P, Luo P, Wang KC, Hsieh M, Li Y;  
 PI WPI; 2005-435361/44.  
 DR  
 XX New monoclonal antibody that specifically binds to human vascular  
 PT endothelial growth factor, useful for treating diseases associated with  
 PT abnormal angiogenesis such as cancer, rheumatoid arthritis, psoriasis,  
 PT diabetic retinopathy.  
 XX Claim 18; SEQ ID NO 12; 111pp; English.  
 PS The invention relates to a monoclonal antibody that specifically binds to  
 CC a human vascular endothelial growth factor (VEGF) with dissociation  
 CC constant Kd equal to or lower than 0.2 nM. The monoclonal antibody is  
 CC useful for diagnosing and treating diseases associated with abnormal  
 CC angiogenesis such as cancer, rheumatoid arthritis, ischemic-reperfusion  
 CC related brain edema and injury, cortical ischemia, ovarian hyperplasia  
 CC and hypervascularity, endometriosis, psoriasis, diabetic retinopathy, and  
 CC other ocular angiogenic diseases. The present sequence represents the  
 CC amino acid sequence of the light chain variable region of an anti-VEGF  
 CC antibody.  
 XX Sequence 107 AA;  
 SQ Query Match 100.0%; Score 54; DB 9; Length 107;  
 Best Local Similarity 100.0%; Pred. No. 0.07;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SASQDISNYLN 11  
 |||||  
 DB 24 SASQDISNYLN 34  
 RESULT 19  
 AEA40452  
 ID AEA40452 standard; protein; 107 AA.  
 XX AEA40452;  
 AC  
 XX 25-AUG-2005 (first entry)  
 DT  
 DE Anti-VEGF antibody light chain variable region SEQ ID NO 14.  
 XX  
 KW vascular endothelial growth factor; VEGF; diagnosis; cancer;  
 KW rheumatoid arthritis; hypervascularity; endometriosis; psoriasis;  
 KW diabetic retinopathy; antiangiogenic; immune disorder; inflammation;  
 KW musculoskeletal disease; neoplasm; genitourinary disease;  
 KW gynecology and obstetrics; dermatological disease;  
 KW cardiovascular disease; ocular disease; cytostatic; Antirheumatic;  
 KW Antiarthritic; Vasotropic; Antiinflammatory; Vulnerary; Gynaecological;  
 KW Antipsoriatic; Antidiabetic; Ophthalmological; Immunotherapy;  
 KW light chain variable region; antibody.  
 OS Synthetic.  
 XX WO2005054273-A2.  
 XX 16-JUN-2005.  
 PD 22-NOV-2004; 2004WO-US039501.  
 XX 26-NOV-2003; 2003US-00723434.  
 XX (ABMA-) AEMAXIS INC.  
 XX

PD 16-JUN-2005.  
 XX 22-NOV-2004; 2004WO-US039501.  
 XX 26-NOV-2003; 2003US-00723434.  
 XX (ABMA-) AEMAXIS INC.  
 XX Zhong P, Luo P, Wang KC, Hsieh M, Li Y;  
 PI WPI; 2005-435361/44.  
 DR  
 XX New monoclonal antibody that specifically binds to human vascular  
 PT endothelial growth factor, useful for treating diseases associated with  
 PT abnormal angiogenesis such as cancer, rheumatoid arthritis, psoriasis,  
 PT diabetic retinopathy.  
 XX Claim 18; SEQ ID NO 12; 111pp; English.  
 PS The invention relates to a monoclonal antibody that specifically binds to  
 CC a human vascular endothelial growth factor (VEGF) with dissociation  
 CC constant Kd equal to or lower than 0.2 nM. The monoclonal antibody is  
 CC useful for diagnosing and treating diseases associated with abnormal  
 CC angiogenesis such as cancer, rheumatoid arthritis, ischemic-reperfusion  
 CC related brain edema and injury, cortical ischemia, ovarian hyperplasia  
 CC and hypervascularity, endometriosis, psoriasis, diabetic retinopathy, and  
 CC other ocular angiogenic diseases. The present sequence represents the  
 CC amino acid sequence of the light chain variable region of an anti-VEGF  
 CC antibody.  
 XX Sequence 107 AA;  
 SQ Query Match 100.0%; Score 54; DB 9; Length 107;  
 Best Local Similarity 100.0%; Pred. No. 0.07;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SASQDISNYLN 11  
 |||||  
 DB 24 SASQDISNYLN 34  
 RESULT 19  
 AEA40452  
 ID AEA40452 standard; protein; 107 AA.  
 XX AEA40452;  
 AC  
 XX 25-AUG-2005 (first entry)  
 DT  
 DE Anti-VEGF antibody light chain variable region SEQ ID NO 14.  
 XX  
 KW vascular endothelial growth factor; VEGF; diagnosis; cancer;  
 KW rheumatoid arthritis; hypervascularity; endometriosis; psoriasis;  
 KW diabetic retinopathy; antiangiogenic; immune disorder; inflammation;  
 KW musculoskeletal disease; neoplasm; genitourinary disease;  
 KW gynecology and obstetrics; dermatological disease;  
 KW cardiovascular disease; ocular disease; cytostatic; Antirheumatic;  
 KW Antiarthritic; Vasotropic; Antiinflammatory; Vulnerary; Gynaecological;  
 KW Antipsoriatic; Antidiabetic; Ophthalmological; Immunotherapy;  
 KW light chain variable region; antibody.  
 OS Synthetic.  
 XX WO2005054273-A2.  
 XX 16-JUN-2005.  
 PD 22-NOV-2004; 2004WO-US039501.  
 XX 26-NOV-2003; 2003US-00723434.  
 XX (ABMA-) AEMAXIS INC.  
 XX

PI Zhong P, Luo P, Wang KC, Hsieh M, Li Y;  
 XX WPI; 2005-435361/44.  
 XX New monoclonal antibody that specifically binds to human vascular  
 PT endothelial growth factor, useful for treating diseases associated with  
 PT abnormal angiogenesis such as cancer, rheumatoid arthritis, psoriasis,  
 PT diabetic retinopathy.  
 XX  
 PS Claim 18; SEQ ID NO 14; 111pp; English.  
 XX The invention relates to a monoclonal antibody that specifically binds to  
 CC a human vascular endothelial growth factor (VEGF) with dissociation  
 CC constant Kd equal to or lower than 0.2 nM. The monoclonal antibody is  
 CC useful for diagnosing and treating diseases associated with abnormal  
 CC angiogenesis such as cancer, rheumatoid arthritis, ischemic-reperfusion  
 CC related brain edema and injury, cortical ischemia, ovarian hyperplasia  
 CC and hypervascularity, endometriosis, psoriasis, diabetic retinopathy, and  
 CC other ocular angiogenic diseases. The present sequence represents the  
 CC amino acid sequence of the light chain variable region of an anti-VEGF  
 CC antibody.  
 XX  
 SQ Sequence 107 AA;  
 Query Match 100.0%; Score 54; DB 9; Length 107;  
 Best Local Similarity 100.0%; Pred. NO. 0.07;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 SASQDISNYLN 11  
 |||||  
 Db 24 SASQDISNYLN 34  
 |||||  
 RESULT 20  
 AEA40447  
 ID AEA40447 standard; protein; 107 AA.  
 XX  
 AC AEA40447;  
 XX  
 DT 25-AUG-2005 (first entry)  
 XX  
 DE Anti-VEGF antibody light chain variable region SEQ ID NO 9.  
 XX  
 KW vascular endothelial growth factor; VEGF; diagnosis; cancer;  
 KW rheumatoid arthritis; hypervascularity; endometriosis; psoriasis;  
 KW diabetic retinopathy; angiogenic; immune disorder; inflammation;  
 KW musculoskeletal disease; neoplasm; genitourinary disease;  
 KW gynecology and obstetrics; dermatological disease;  
 KW cardiovascular disease; ocular disease; cytostatic; Antirheumatic;  
 KW Antiarthritic; Vasotropic; Antiinflammatory; Vulnery; Gynaecological;  
 KW Antipsoriatic; Antidiabetic; Ophthalmological; Immunotherapy;  
 KW light chain variable region; antibody.  
 XX  
 OS Synthetic.  
 XX  
 PN WO2005054273-A2.  
 XX  
 PD 16-JUN-2005.  
 XX  
 PF 22-NOV-2004; 2004WO-US039501.  
 XX  
 PR 26-NOV-2003; 2003US-00723434.  
 XX  
 PA (ABMA-) ABMAXIS INC.  
 XX  
 PI Zhong P, Luo P, Wang KC, Hsieh M, Li Y;  
 XX WPI; 2005-435361/44.  
 XX New monoclonal antibody that specifically binds to human vascular  
 PT endothelial growth factor, useful for treating diseases associated with  
 PT abnormal angiogenesis such as cancer, rheumatoid arthritis, psoriasis,  
 PT diabetic retinopathy.  
 XX

XX Claim 18; SEQ ID NO 9; 111pp; English.  
 XX The invention relates to a monoclonal antibody that specifically binds to  
 CC a human vascular endothelial growth factor (VEGF) with dissociation  
 CC constant Kd equal to or lower than 0.2 nM. The monoclonal antibody is  
 CC useful for diagnosing and treating diseases associated with abnormal  
 CC angiogenesis such as cancer, rheumatoid arthritis, ischemic-reperfusion  
 CC related brain edema and injury, cortical ischemia, ovarian hyperplasia  
 CC and hypervascularity, endometriosis, psoriasis, diabetic retinopathy, and  
 CC other ocular angiogenic diseases. The present sequence represents the  
 CC amino acid sequence of the light chain variable region of an anti-VEGF  
 CC antibody.  
 XX  
 SQ Sequence 107 AA;  
 Query Match 100.0%; Score 54; DB 9; Length 107;  
 Best Local Similarity 100.0%; Pred. NO. 0.07;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 SASQDISNYLN 11  
 |||||  
 Db 24 SASQDISNYLN 34  
 |||||  
 RESULT 21  
 AEA40446  
 ID AEA40446 standard; protein; 107 AA.  
 XX  
 AC AEA40446;  
 XX  
 DT 25-AUG-2005 (first entry)  
 XX  
 DE Anti-VEGF antibody light chain variable region SEQ ID NO 8.  
 XX  
 KW vascular endothelial growth factor; VEGF; diagnosis; cancer;  
 KW rheumatoid arthritis; hypervascularity; endometriosis; psoriasis;  
 KW diabetic retinopathy; angiogenic; immune disorder; inflammation;  
 KW musculoskeletal disease; neoplasm; genitourinary disease;  
 KW gynecology and obstetrics; dermatological disease;  
 KW cardiovascular disease; ocular disease; cytostatic; Antirheumatic;  
 KW Antiarthritic; Vasotropic; Antiinflammatory; Vulnery; Gynaecological;  
 KW Antipsoriatic; Antidiabetic; Ophthalmological; Immunotherapy;  
 KW light chain variable region; antibody.  
 XX  
 OS Synthetic.  
 XX  
 PN WO2005054273-A2.  
 XX  
 PD 16-JUN-2005.  
 XX  
 PF 22-NOV-2004; 2004WO-US039501.  
 XX  
 PR 26-NOV-2003; 2003US-00723434.  
 XX  
 PA (ABMA-) ABMAXIS INC.  
 XX  
 PI Zhong P, Luo P, Wang KC, Hsieh M, Li Y;  
 XX WPI; 2005-435361/44.  
 XX New monoclonal antibody that specifically binds to human vascular  
 PT endothelial growth factor, useful for treating diseases associated with  
 PT abnormal angiogenesis such as cancer, rheumatoid arthritis, psoriasis,  
 PT diabetic retinopathy.  
 XX



CC related brain edema and injury, cortical ischemia, ovarian hyperplasia  
 CC and hypervascularity, endometriosis, psoriasis, diabetic retinopathy, and  
 CC other ocular angiogenic diseases. The present sequence represents the  
 CC amino acid sequence of the light chain variable region of an anti-VEGF  
 CC antibody.

XX  
 SQ Sequence 107 AA;

Query Match 100.0%; Score 54; DB 9; Length 107;  
 Best Local Similarity 100.0%; Pred. No. 0.07;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASQDISNYLN 11  
 |||||  
 Db 24 SASQDISNYLN 34

RESULT 22

AEA40439  
 ID AEA40439 standard; protein; 107 AA.

XX  
 AC AEA40439;

DT 25-AUG-2005 (first entry)

XX Anti-VEGF antibody light chain variable region SEQ ID NO 1.

XX vascular endothelial growth factor; VEGF; diagnosis; cancer;  
 KW rheumatoid arthritis; hypervascularity; endometriosis; psoriasis;  
 KW diabetic retinopathy; angiogenic; immune disorder; inflammation;  
 KW musculoskeletal disease; neoplasm; genitourinary disease;  
 KW gynecology and obstetrics; dermatological disease;  
 KW cardiovascular disease; ocular disease; cytostatic; antirheumatic;  
 KW antiarthritic; vasotropic; antiinflammatory; vulnery; gynaecological;  
 KW antipsoriatic; antidiabetic; ophthalmological; immunotherapy;  
 KW light chain variable region; antibody.

XX Synthetic.

XX WO2005054273-A2.

XX 16-JUN-2005.

XX 22-NOV-2004; 2004WO-US039501.

XX 26-NOV-2003; 2003US-00723434.

XX (ABMA-) ABMAXIS INC.

XX Zhong P, Luo P, Wang KC, Hsieh M, Li Y;

XX WPI; 2005-435361/44.

XX New monoclonal antibody that specifically binds to human vascular  
 PT endothelial growth factor, useful for treating diseases associated with  
 PT abnormal angiogenesis such as cancer, rheumatoid arthritis, psoriasis,  
 PT diabetic retinopathy.

XX Claim 29; SEQ ID NO 1; 111pp; English.

XX The invention relates to a monoclonal antibody that specifically binds to  
 CC a human vascular endothelial growth factor (VEGF) with dissociation  
 CC constant Kd equal to or lower than 0.2 nM. The monoclonal antibody is  
 CC useful for diagnosing and treating diseases associated with abnormal  
 CC angiogenesis such as cancer, rheumatoid arthritis, ischemic-reperfusion  
 CC related brain edema and injury, cortical ischemia, ovarian hyperplasia  
 CC and hypervascularity, endometriosis, psoriasis, diabetic retinopathy, and  
 CC other ocular angiogenic diseases. The present sequence represents the  
 CC amino acid sequence of the light chain variable region of an anti-VEGF  
 CC antibody.

XX Sequence 107 AA;

Query Match 100.0%; Score 54; DB 9; Length 107;  
 Best Local Similarity 100.0%; Pred. No. 0.07;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASQDISNYLN 11  
 |||||  
 Db 24 SASQDISNYLN 34

RESULT 23

AEA40444  
 ID AEA40444 standard; protein; 107 AA.

XX  
 AC AEA40444;

DT 25-AUG-2005 (first entry)

XX Anti-VEGF antibody light chain variable region SEQ ID NO 6.

XX vascular endothelial growth factor; VEGF; diagnosis; cancer;  
 KW rheumatoid arthritis; hypervascularity; endometriosis; psoriasis;  
 KW diabetic retinopathy; angiogenic; immune disorder; inflammation;  
 KW musculoskeletal disease; neoplasm; genitourinary disease;  
 KW gynecology and obstetrics; dermatological disease;  
 KW cardiovascular disease; ocular disease; cytostatic; antirheumatic;  
 KW antiarthritic; vasotropic; antiinflammatory; vulnery; gynaecological;  
 KW antipsoriatic; antidiabetic; ophthalmological; immunotherapy;  
 KW light chain variable region; antibody.

XX Synthetic.

XX WO2005054273-A2.

XX 16-JUN-2005.

XX 22-NOV-2004; 2004WO-US039501.

XX 26-NOV-2003; 2003US-00723434.

XX (ABMA-) ABMAXIS INC.

XX Zhong P, Luo P, Wang KC, Hsieh M, Li Y;

XX WPI; 2005-435361/44.

XX New monoclonal antibody that specifically binds to human vascular  
 PT endothelial growth factor, useful for treating diseases associated with  
 PT abnormal angiogenesis such as cancer, rheumatoid arthritis, psoriasis,  
 PT diabetic retinopathy.

XX Claim 18; SEQ ID NO 6; 111pp; English.

XX The invention relates to a monoclonal antibody that specifically binds to  
 CC a human vascular endothelial growth factor (VEGF) with dissociation  
 CC constant Kd equal to or lower than 0.2 nM. The monoclonal antibody is  
 CC useful for diagnosing and treating diseases associated with abnormal  
 CC angiogenesis such as cancer, rheumatoid arthritis, ischemic-reperfusion  
 CC related brain edema and injury, cortical ischemia, ovarian hyperplasia  
 CC and hypervascularity, endometriosis, psoriasis, diabetic retinopathy, and  
 CC other ocular angiogenic diseases. The present sequence represents the  
 CC amino acid sequence of the light chain variable region of an anti-VEGF  
 CC antibody.

XX Sequence 107 AA;

Query Match 100.0%; Score 54; DB 9; Length 107;  
 Best Local Similarity 100.0%; Pred. No. 0.07;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASQDISNYLN 11  
 |||||  
 Db 24 SASQDISNYLN 34

```

RESULT 24
AEA40442
ID AEA40442 standard; protein; 107 AA.
XX AC AEA40442;
XX DT 25-AUG-2005 (first entry)
XX DE Anti-VEGF antibody light chain variable region SEQ ID NO 4.
XX KW vascular endothelial growth factor; VEGF; diagnosis; cancer;
XX KW rheumatoid arthritis; hypervascularity; endometriosis; psoriasis;
XX KW diabetic retinopathy; antiangiogenic; immune disorder; inflammation;
XX KW musculoskeletal disease; neoplasm; genitourinary disease;
XX KW gynecology and obstetrics; dermatological disease;
XX KW cardiovascular disease; ocular disease; cytostatic; antirheumatic;
XX KW antiarthritic; vasotropic; antiinflammatory; vulnery; gynaecological;
XX KW antiporiatic; antidiabetic; ophthalmological; immunotherapy;
XX KW light chain variable region; antibody.
XX OS Synthetic.
XX PN WO2005054273-A2.
XX PD 16-JUN-2005.
XX PF 22-NOV-2004; 2004WO-US039501.
XX PR 26-NOV-2003; 2003US-00723434.
XX PA (ABMA-) ABMAXIS INC.
XX PI Zhong P, Luo P, Wang KC, Hsieh M, Li Y;
XX DR WPI; 2005-435361/44.
XX PT New monoclonal antibody that specifically binds to human vascular
XX PT endothelial growth factor, useful for treating diseases associated with
XX PT abnormal angiogenesis such as cancer, rheumatoid arthritis, psoriasis,
XX PT diabetic retinopathy.
XX PS Claim 18; SEQ ID NO 4; 111pp; English.
XX CC The invention relates to a monoclonal antibody that specifically binds to
XX CC a human vascular endothelial growth factor (VEGF) with dissociation
XX CC constant Kd equal to or lower than 0.2 nM. The monoclonal antibody is
XX CC useful for diagnosing and treating diseases associated with abnormal
XX CC angiogenesis such as cancer, rheumatoid arthritis, ischemic-reperfusion
XX CC related brain edema and injury, cortical ischemia, ovarian hyperplasia
XX CC and hypervascularity, endometriosis, psoriasis, diabetic retinopathy, and
XX CC other ocular angiogenic diseases. The present sequence represents the
XX CC amino acid sequence of the light chain variable region of an anti-VEGF
XX CC antibody.
XX SQ Sequence 107 AA;
Query Match 100.0%; Score 54; DB 9; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.07;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 SASQDISNYLN 11
Db 24 SASQDISNYLN 34
RESULT 25
AEA40451
ID AEA40451 standard; protein; 107 AA.
XX AC AEA40451;
XX DT 25-AUG-2005 (first entry)
XX DE Anti-VEGF antibody light chain variable region SEQ ID NO 10.
XX KW vascular endothelial growth factor; VEGF; diagnosis; cancer;
XX KW rheumatoid arthritis; hypervascularity; endometriosis; psoriasis;
XX KW diabetic retinopathy; antiangiogenic; immune disorder; inflammation;
XX KW musculoskeletal disease; neoplasm; genitourinary disease;
XX KW gynecology and obstetrics; dermatological disease;
XX KW cardiovascular disease; ocular disease; cytostatic; antirheumatic;
XX KW antiarthritic; vasotropic; antiinflammatory; vulnery; gynaecological;
XX KW antiporiatic; antidiabetic; ophthalmological; immunotherapy;
XX KW light chain variable region; antibody.
XX OS Synthetic.
XX PN WO2005054273-A2.
XX PD 16-JUN-2005.
XX PF 22-NOV-2004; 2004WO-US039501.
XX PR 26-NOV-2003; 2003US-00723434.
XX PA (ABMA-) ABMAXIS INC.
XX PI Zhong P, Luo P, Wang KC, Hsieh M, Li Y;
XX DR WPI; 2005-435361/44.
XX PT New monoclonal antibody that specifically binds to human vascular
XX PT endothelial growth factor, useful for treating diseases associated with
XX PT abnormal angiogenesis such as cancer, rheumatoid arthritis, psoriasis,
XX PT diabetic retinopathy.
XX PS Claim 18; SEQ ID NO 4; 111pp; English.
XX CC The invention relates to a monoclonal antibody that specifically binds to
XX CC a human vascular endothelial growth factor (VEGF) with dissociation
XX CC constant Kd equal to or lower than 0.2 nM. The monoclonal antibody is
XX CC useful for diagnosing and treating diseases associated with abnormal
XX CC angiogenesis such as cancer, rheumatoid arthritis, ischemic-reperfusion
XX CC related brain edema and injury, cortical ischemia, ovarian hyperplasia
XX CC and hypervascularity, endometriosis, psoriasis, diabetic retinopathy, and
XX CC other ocular angiogenic diseases. The present sequence represents the
XX CC amino acid sequence of the light chain variable region of an anti-VEGF
XX CC antibody.
XX SQ Sequence 107 AA;
Query Match 100.0%; Score 54; DB 9; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.07;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 SASQDISNYLN 11
Db 24 SASQDISNYLN 34

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XX DE Anti-VEGF antibody light chain variable region SEQ ID NO 13.
XX KW vascular endothelial growth factor; VEGF; diagnosis; cancer;
XX KW rheumatoid arthritis; hypervascularity; endometriosis; psoriasis;
XX KW diabetic retinopathy; antiangiogenic; immune disorder; inflammation;
XX KW musculoskeletal disease; neoplasm; genitourinary disease;
XX KW gynecology and obstetrics; dermatological disease;
XX KW cardiovascular disease; ocular disease; cytostatic; antirheumatic;
XX KW antiarthritic; vasotropic; antiinflammatory; vulnery; gynaecological;
XX KW antiporiatic; antidiabetic; ophthalmological; immunotherapy;
XX KW light chain variable region; antibody.
XX OS Synthetic.
XX PN WO2005054273-A2.
XX PD 16-JUN-2005.
XX PF 22-NOV-2004; 2004WO-US039501.
XX PR 26-NOV-2003; 2003US-00723434.
XX PA (ABMA-) ABMAXIS INC.
XX PI Zhong P, Luo P, Wang KC, Hsieh M, Li Y;
XX DR WPI; 2005-435361/44.
XX PT New monoclonal antibody that specifically binds to human vascular
XX PT endothelial growth factor, useful for treating diseases associated with
XX PT abnormal angiogenesis such as cancer, rheumatoid arthritis, psoriasis,
XX PT diabetic retinopathy.
XX PS Claim 18; SEQ ID NO 13; 111pp; English.
XX CC The invention relates to a monoclonal antibody that specifically binds to
XX CC a human vascular endothelial growth factor (VEGF) with dissociation
XX CC constant Kd equal to or lower than 0.2 nM. The monoclonal antibody is
XX CC useful for diagnosing and treating diseases associated with abnormal
XX CC angiogenesis such as cancer, rheumatoid arthritis, ischemic-reperfusion
XX CC related brain edema and injury, cortical ischemia, ovarian hyperplasia
XX CC and hypervascularity, endometriosis, psoriasis, diabetic retinopathy, and
XX CC other ocular angiogenic diseases. The present sequence represents the
XX CC amino acid sequence of the light chain variable region of an anti-VEGF
XX CC antibody.
XX SQ Sequence 107 AA;
Query Match 100.0%; Score 54; DB 9; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.07;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 SASQDISNYLN 11
Db 24 SASQDISNYLN 34
RESULT 26
AEA40448
ID AEA40448 standard; protein; 107 AA.
XX AC AEA40448;
XX DT 25-AUG-2005 (first entry)
XX DE Anti-VEGF antibody light chain variable region SEQ ID NO 10.
XX KW vascular endothelial growth factor; VEGF; diagnosis; cancer;
XX KW rheumatoid arthritis; hypervascularity; endometriosis; psoriasis;
XX KW diabetic retinopathy; antiangiogenic; immune disorder; inflammation;
XX KW musculoskeletal disease; neoplasm; genitourinary disease;
XX KW gynecology and obstetrics; dermatological disease;

```

KW cardiovascular disease; ocular disease; Cytostatic; Antirheumatic;  
 KW Antiarthritic; Vasotropic; Antiinflammatory; Vulnerary; Gynaecological;  
 KW Antipsoriatic; Antidiabetic; Ophthalmological; Immunotherapy;  
 KW light chain variable region; antibody.  
 XX Synthetic.  
 XX WO2005054273-A2.  
 XX 16-JUN-2005.  
 XX PD 22-NOV-2004; 2004WO-US039501.  
 XX PF 26-NOV-2003; 2003US-00723434.  
 XX PR (ABMA-) ABMAXIS INC.  
 XX PI Zhong P, Luo P, Wang KC, Hsieh M, Li Y;  
 XX WPI; 2005-435361/44.  
 XX DR New monoclonal antibody that specifically binds to human vascular  
 XX endothelial growth factor, useful for treating diseases associated with  
 XX PT abnormal angiogenesis such as cancer, rheumatoid arthritis, psoriasis,  
 XX PA diabetic retinopathy.  
 XX PI Zhong P, Luo P, Wang KC, Hsieh M, Li Y;  
 XX WPI; 2005-435361/44.  
 XX DR New monoclonal antibody that specifically binds to human vascular  
 XX endothelial growth factor, useful for treating diseases associated with  
 XX PT abnormal angiogenesis such as cancer, rheumatoid arthritis, psoriasis,  
 XX PA diabetic retinopathy.  
 XX PI Claim 18; SEQ ID NO 10; 11pp; English.  
 XX CC The invention relates to a monoclonal antibody that specifically binds to  
 CC a human vascular endothelial growth factor (VEGF) with dissociation  
 CC constant Kd equal to or lower than 0.2 nM. The monoclonal antibody is  
 CC useful for diagnosing and treating diseases associated with abnormal  
 CC angiogenesis such as cancer, rheumatoid arthritis, ischemic-reperfusion  
 CC related brain edema and injury, cortical ischemia, ovarian hyperplasia  
 CC and hypervascularity, endometriosis, psoriasis, diabetic retinopathy, and  
 CC other ocular angiogenic diseases. The present sequence represents the  
 CC amino acid sequence of the light chain variable region of an anti-VEGF  
 CC antibody.  
 XX SQ Sequence 107 AA;  
 Query Match 100.0%; Score 54; DB 9; Length 107;  
 Best Local Similarity 100.0%; Pred. No. 0.07; Mismatches 0; Gaps 0;  
 Matches 11; Conservative 0; Indels 0; Indels 0; Gaps 0;  
 Qy 1 SASQDISNYLN 11  
 |||||  
 Db 24 SASQDISNYLN 34  
 RESULT 27  
 AEA40722  
 ID AEA40722 standard; protein; 107 AA.  
 AC AEA40722;  
 XX 25-AUG-2005 (first entry)  
 DT Anti-VEGF antibody light chain variable region SEQ ID NO 284.  
 DE vascular endothelial growth factor; VEGF; diagnosis; cancer;  
 KW rheumatoid arthritis; hypervascularity; endometriosis; psoriasis;  
 KW diabetic retinopathy; angiogenic; immune disorder; inflammation;  
 KW musculoskeletal disease; neoplasm; genitourinary disease;  
 KW gynecology and obstetrics; dermatological disease;  
 KW cardiovascular disease; ocular disease; Cytostatic; Antirheumatic;  
 KW Antiarthritic; Vasotropic; Antiinflammatory; Vulnerary; Gynaecological;  
 KW Antipsoriatic; Antidiabetic; Ophthalmological; Immunotherapy;  
 KW light chain variable region; antibody.  
 XX Synthetic.  
 XX WO2005054273-A2.  
 XX PD 22-NOV-2004; 2004WO-US039501.  
 XX PF 26-NOV-2003; 2003US-00723434.  
 XX PR (ABMA-) ABMAXIS INC.

XX 16-JUN-2005.  
 XX PD 22-NOV-2004; 2004WO-US039501.  
 XX PF 26-NOV-2003; 2003US-00723434.  
 XX PR (ABMA-) ABMAXIS INC.  
 XX PI Zhong P, Luo P, Wang KC, Hsieh M, Li Y;  
 XX WPI; 2005-435361/44.  
 XX DR New monoclonal antibody that specifically binds to human vascular  
 XX endothelial growth factor, useful for treating diseases associated with  
 XX PT abnormal angiogenesis such as cancer, rheumatoid arthritis, psoriasis,  
 XX PA diabetic retinopathy.  
 XX PI Disclosure; SEQ ID NO 284; 11pp; English.  
 XX CC The invention relates to a monoclonal antibody that specifically binds to  
 CC a human vascular endothelial growth factor (VEGF) with dissociation  
 CC constant Kd equal to or lower than 0.2 nM. The monoclonal antibody is  
 CC useful for diagnosing and treating diseases associated with abnormal  
 CC angiogenesis such as cancer, rheumatoid arthritis, ischemic-reperfusion  
 CC related brain edema and injury, cortical ischemia, ovarian hyperplasia  
 CC and hypervascularity, endometriosis, psoriasis, diabetic retinopathy, and  
 CC other ocular angiogenic diseases. The present sequence represents the  
 CC amino acid sequence of the light chain variable region of an anti-VEGF  
 CC antibody.  
 XX SQ Sequence 107 AA;  
 Query Match 100.0%; Score 54; DB 9; Length 107;  
 Best Local Similarity 100.0%; Pred. No. 0.07; Mismatches 0; Gaps 0;  
 Matches 11; Conservative 0; Indels 0; Indels 0; Gaps 0;  
 Qy 1 SASQDISNYLN 11  
 |||||  
 Db 24 SASQDISNYLN 34  
 RESULT 28  
 AEA40441  
 ID AEA40441 standard; protein; 107 AA.  
 AC AEA40441;  
 XX 25-AUG-2005 (first entry)  
 DT Anti-VEGF antibody light chain variable region SEQ ID NO 3.  
 DE vascular endothelial growth factor; VEGF; diagnosis; cancer;  
 KW rheumatoid arthritis; hypervascularity; endometriosis; psoriasis;  
 KW diabetic retinopathy; angiogenic; immune disorder; inflammation;  
 KW musculoskeletal disease; neoplasm; genitourinary disease;  
 KW gynecology and obstetrics; dermatological disease;  
 KW cardiovascular disease; ocular disease; Cytostatic; Antirheumatic;  
 KW Antiarthritic; Vasotropic; Antiinflammatory; Vulnerary; Gynaecological;  
 KW Antipsoriatic; Antidiabetic; Ophthalmological; Immunotherapy;  
 KW light chain variable region; antibody.  
 XX Synthetic.  
 XX WO2005054273-A2.  
 XX PD 16-JUN-2005.  
 XX PF 22-NOV-2004; 2004WO-US039501.  
 XX PR 26-NOV-2003; 2003US-00723434.  
 XX PR (ABMA-) ABMAXIS INC.

XX  
PI Zhong P, Luo P, Wang KC, Heieh M, Li Y;  
XX  
XX WPI; 2005-435361/44.  
DR  
XX New monoclonal antibody that specifically binds to human vascular  
XX  
XX endothelial growth factor, useful for treating diseases associated with  
PT abnormal angiogenesis such as cancer, rheumatoid arthritis, psoriasis,  
PT diabetic retinopathy.  
XX  
XX Claim 18; SEQ ID NO 3; 111pp; English.  
XX  
XX The invention relates to a monoclonal antibody that specifically binds to  
CC a human vascular endothelial growth factor (VEGF) with dissociation  
CC constant Kd equal to or lower than 0.2 nM. The monoclonal antibody is  
CC useful for diagnosing and treating diseases associated with abnormal  
CC angiogenesis such as cancer, rheumatoid arthritis, ischemic-reperfusion  
CC related brain edema and injury, cortical ischemia, ovarian hyperplasia  
CC and hypervascularity, endometriosis, psoriasis, diabetic retinopathy, and  
CC other ocular angiogenic diseases. The present sequence represents the  
CC amino acid sequence of the light chain variable region of an anti-VEGF  
CC antibody.  
XX  
XX Sequence 107 AA;  
SQ

Query Match 100.0%; Score 54; DB 9; Length 107;  
Best Local Similarity 100.0%; Pred. No. 0.07;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SASQDISNYLN 11  
Db 24 SASQDISNYLN 34  
|||||

RESULT 29  
AAW70620  
ID AAW70620 standard; peptide; 108 AA.  
XX  
AC AAW70620;  
XX  
XX 27-JAN-1999 (first entry)  
XX  
XX Anti-VEGF murine antibody A4.6.1 variable light domain.  
XX  
XX Light variable domain; murine; humanised antibody;  
XX anti-vascular endothelial growth factor antibody; anti-VEGF antibody;  
KW VEGF-induced angiogenesis; tumour; retinal disorder;  
KW age-related macular degeneration; diabetic retinopathy;  
KW rheumatoid arthritis; psoriasis; atherosclerosis; Grave's disease.  
XX  
XX Mus sp.  
XX  
XX WO9845331-A2.  
XX  
XX 15-OCT-1998.  
XX  
XX 03-APR-1998; 98WO-US006604.  
XX  
XX 07-APR-1997; 97US-00833504.  
XX  
XX 06-AUG-1997; 97US-00908469.  
XX  
XX (GETH ) GENENTECH INC.  
XX  
XX Baca M, Wells JA, Presta LG, Lowman HB, Chen YM;  
XX  
XX WPI; 1998-568337/48.  
XX  
XX New humanised antibody with affinity for vascular endothelial growth  
XX factor - for treatment of tumours, retinal disease and other angiogenic  
XX states, also related nucleic acid, vectors and transformed cells.  
XX  
XX Example 1; Fig 1B; 100pp; English.  
XX

CC The present sequence represents a variable light domain of the murine  
CC anti-vascular endothelial growth factor (anti-VEGF) antibody A4.6.1.. The  
CC sequence is used to construct the humanised anti-VEGF antibody of the  
CC invention. The humanised antibodies are used to inhibit VEGF-induced  
CC angiogenesis, particularly for treating or preventing tumours (of any  
CC type) and retinal disorders (e.g. age-related macular degeneration or  
CC diabetic retinopathy). They can also be used to treat other conditions  
CC that involve angiogenesis, e.g. rheumatoid arthritis, psoriasis,  
CC atherosclerosis, Grave's disease, etc  
XX  
XX Sequence 108 AA;  
SQ

Query Match 100.0%; Score 54; DB 2; Length 108;  
Best Local Similarity 100.0%; Pred. No. 0.07;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SASQDISNYLN 11  
Db 24 SASQDISNYLN 34  
|||||

RESULT 30  
AAW70618  
ID AAW70618 standard; peptide; 108 AA.  
XX  
AC AAW70618;  
XX  
XX 27-JAN-1999 (first entry)  
XX  
XX Anti-VEGF humanised antibody F(ab)-12 variable light domain.  
XX  
XX Light variable domain; murine; humanised antibody;  
XX anti-vascular endothelial growth factor antibody; anti-VEGF antibody;  
KW VEGF-induced angiogenesis; tumour; retinal disorder;  
KW age-related macular degeneration; diabetic retinopathy;  
KW rheumatoid arthritis; psoriasis; atherosclerosis; Grave's disease.  
XX  
XX Synthetic.  
XX  
XX Mus sp.  
XX  
XX Homo sapiens.  
XX  
XX WO9845331-A2.  
XX  
XX 15-OCT-1998.  
XX  
XX 03-APR-1998; 98WO-US006604.  
XX  
XX 07-APR-1997; 97US-00833504.  
XX  
XX 06-AUG-1997; 97US-00908469.  
XX  
XX (GETH ) GENENTECH INC.  
XX  
XX Baca M, Wells JA, Presta LG, Lowman HB, Chen YM;  
XX  
XX WPI; 1998-568337/48.  
XX  
XX New humanised antibody with affinity for vascular endothelial growth  
XX factor - for treatment of tumours, retinal disease and other angiogenic  
XX states, also related nucleic acid, vectors and transformed cells.  
XX  
XX Claim 10; Fig 1B; 100pp; English.  
XX  
XX The present sequence represents a variable light domain of the humanised  
CC anti-vascular endothelial growth factor (anti-VEGF) antibody F(ab)-12.  
CC The sequence is used to construct the humanised anti-VEGF antibody of the  
CC invention. The humanised antibodies are used to inhibit VEGF-induced  
CC angiogenesis, particularly for treating or preventing tumours (of any  
CC type) and retinal disorders (e.g. age-related macular degeneration or  
CC diabetic retinopathy). They can also be used to treat other conditions  
CC that involve angiogenesis, e.g. rheumatoid arthritis, psoriasis,  
CC atherosclerosis, Grave's disease, etc  
XX  
XX Sequence 108 AA;  
SQ

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Query Match      100.0%; Score 54; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.07;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SASQDISNYLN 11
      ||| ||| ||| ||| |||
DB      24 SASQDISNYLN 34

RESULT 31
AAW70696
ID AAW70696 standard; peptide; 108 AA.
XX
AC AAW70696;
XX
DT 27-JAN-1999 (first entry)
XX
DE Anti-VEGF humanised antibody F(ab)-12 variable light domain.
XX
KW Light variable domain; murine; humanised antibody;
KW anti-vascular endothelial growth factor antibody; anti-VEGF antibody;
KW VEGF-induced angiogenesis; tumour; retinal disorder;
KW age-related macular degeneration; diabetic retinopathy;
KW rheumatoid arthritis; psoriasis; atherosclerosis; Grave's disease.
XX
OS Synthetic.
OS Mus sp.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 4 /note= "Met or Leu"
FT
XX
PN WO9845331-A2.
XX
PD 15-OCT-1998.
XX
PF 03-APR-1998; 98WO-US006604.
XX
PR 07-APR-1997; 97US-00833504.
PR 06-AUG-1997; 97US-00908469.
XX
PA (GETH ) GENENTECH INC.
XX
PI Baca M, Wells JA, Presta LG, Lowman HB, Chen YM;
PI WPI; 1998-568337/48.
XX
DR
XX
PT New humanised antibody with affinity for vascular endothelial growth
PT factor - for treatment of tumours, retinal disease and other angiogenic
PT states, also related nucleic acid, vectors and transformed cells.
XX
PS Claim 12; Page 4; 100pp; English.
XX
CC The present sequence represents a variable light domain of the humanised
CC anti-vascular endothelial growth factor (anti-VEGF) antibody. The
CC sequence is used to construct the humanised anti-VEGF antibody of the
CC invention. The humanised antibodies are used to inhibit VEGF-induced
CC angiogenesis, particularly for treating or preventing tumours (of any
CC type) and retinal disorders (e.g. age-related macular degeneration or
CC diabetic retinopathy). They can also be used to treat other conditions
CC that involve angiogenesis, e.g. rheumatoid arthritis, psoriasis,
CC atherosclerosis, Grave's disease, etc
XX
SQ Sequence 108 AA;

Query Match      100.0%; Score 54; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.07;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SASQDISNYLN 11
      ||| ||| ||| ||| |||
DB      24 SASQDISNYLN 34

RESULT 32
AAB81988
ID AAB81988 standard; protein; 108 AA.
XX
AC AAB81988;
XX
DT 03-JUL-2001 (first entry)
XX
DE Ganglioside GD3 specific antibody related protein SEQ ID NO: 54.
XX
KW Ganglioside; GD3; complementarity determining region; CDR; antibody;
KW cancer.
XX
OS Synthetic.
XX
PN WO200123432-A1.
XX
PD 05-APR-2001.
XX
PF 29-SEP-2000; 2000WO-JP006774.
PR 30-SEP-1999; 95JP-00278291.
PR 06-APR-2000; 2000JP-00105088.
XX
PA (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI Hanai N, Shitara K, Nakamura K, Niwa R;
XX
PD WPI; 2001-266143/27.
XX
PT New human type complementation-determining region-transplanted antibody
PT and derivatives against ganglioside GD3, useful in diagnosis and therapy
PT of e.g. tumors, with low antigenicity, little side effects but potent
PT activity in cancer.
XX
PS Claim 22; Page 172-173; 183pp; Japanese.
XX
CC The present invention describes a monoclonal antibody which can react
CC specifically with ganglioside GD3. The antibody and its derivatives are
CC useful in the diagnosis and therapy of tumours, particularly cancer
CC diagnosis. The present sequence is a protein used in the exemplification
CC of the invention
XX
SQ Sequence 108 AA;

Query Match      100.0%; Score 54; DB 4; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.07;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SASQDISNYLN 11
      ||| ||| ||| ||| |||
DB      24 SASQDISNYLN 34

RESULT 33
AAB81986
ID AAB81986 standard; protein; 108 AA.
XX
AC AAB81986;
XX
DT 03-JUL-2001 (first entry)
XX
DE Ganglioside GD3 specific antibody related protein SEQ ID NO: 10.
XX
KW Ganglioside; GD3; complementarity determining region; CDR; antibody;
KW cancer.
XX
OS Synthetic.
XX
PN WO200123432-A1.

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XX PD 05-APR-2001.
XX
XX PF 29-SEP-2000; 2000WO-JP006774.
XX
XX PR 30-SEP-1999; 99JP-00278291.
XX
XX PR 06-APR-2000; 2000JP-00105088.
XX
XX PA (KYOW ) KYOWA HAKKO KOGYO KK.
XX
XX PI Hanai N, Shitara K, Nakamura K, Niwa R;
XX
XX WPI; 2001-266143/27.
XX
XX PT New human type complementation-determining region-transplanted antibody
XX and derivatives against ganglioside GD3, useful in diagnosis and therapy
XX of e.g. tumors, with low antigenicity, little side effects but potent
XX activity in cancer.
XX
XX PS Example 1; Page 143-144; 183pp; Japanese.
XX
XX CC The present invention describes a monoclonal antibody which can react
XX specifically with ganglioside GD3. The antibody and its derivatives are
XX useful in the diagnosis and therapy of tumours, particularly cancer
XX diagnosis. The present sequence is a protein used in the exemplification
XX of the invention
XX
XX SQ Sequence 108 AA;
XX
XX Query Match 100.0%; Score 54; DB 4; Length 108;
XX Best Local Similarity 100.0%; Pred. No. 0.07;
XX Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 SASQDISNYLN 11
XX Db 24 SASQDISNYLN 34
XX
XX RESULT 35
XX ABP61189
XX ID ABP61189 standard; protein; 108 AA.
XX
XX AC ABP61189;
XX
XX DT 20-SEP-2002 (first entry)
XX
XX DE Murine anti-VEGF muMabVEGF A.4.6.1 antibody variable light domain.
XX
XX KW Cytostatic; ophthalmological; humanised; antibody; anti-VEGF; VEGF;
XX vascular endothelial growth factor; angiogenesis inhibitor; tumour;
XX retinal disorder; intraocular neovascular disorder; murine; light chain;
XX variable domain; muMabVEGF A.4.6.1.
XX
XX OS Mus sp.
XX
XX PN US2002032315-A1.
XX
XX PD 14-MAR-2002.
XX
XX PF 06-APR-1998; 98US-00056160.
XX
XX PR 06-AUG-1997; 97US-0054856P.
XX
XX PA (BACA/) BACA M.
XX PA (WELL/) WELLS J A.
XX PA (PRES/) PRESTA L G.
XX PA (LOWM/) LOWMAN H B.
XX PA (CHEN/) CHEN Y M.
XX
XX PI Baca M, Wells JA, Presta LG, Lowman HB, Chen YM;
XX
XX DR WPI; 2002-517920/55.
XX
XX PT New humanized anti-VEGF (vascular endothelial growth factor) antibodies
XX or their variants, useful for inhibiting VEGF-induced angiogenesis in a
XX mammal, particularly for treating tumor or retinal disorders.
XX
XX PS Example 1; Fig 1; 47pp; English.
XX
XX CC The present invention relates to humanised anti-VEGF (vascular
XX endothelial growth factor) antibodies or a variant of a parent anti-VEGF
XX antibody, which binds human VEGF. The anti-VEGF antibodies are useful for
XX inhibiting VEGF-induced angiogenesis in a mammal (particularly a human),
XX particularly those having a tumour or a retinal disorder e.g. intraocular
XX neovascular disorders. The present sequence is the light chain variable
XX domain of murine anti-VEGF muMabVEGF A.4.6.1 antibody, which was used to
XX generate the humanised anti-VEGF antibodies of the invention
XX
XX SQ Sequence 108 AA;
XX
XX Query Match 100.0%; Score 54; DB 5; Length 108;
XX Best Local Similarity 100.0%; Pred. No. 0.07;

```

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASQDISNYLN 11  
 DB 24 SASQDISNYLN 34

RESULT 36  
 ABP61265  
 ID ABP61265 standard; protein; 108 AA.  
 AC ABP61265;  
 XX 20-SEP-2002 (first entry)  
 DT  
 DE Humanised anti-VEGF antibody variable light domain.  
 DE OS Mus sapiens.  
 DE OS Synthetic.  
 KW Cytostatic; ophthalmological; humanised; antibody; anti-VEGF; VEGF;  
 KW vascular endothelial growth factor; angiogenesis inhibitor; tumour;  
 KW retinal disorder; intraocular neovascular disorder; light chain;  
 KW variable domain.  
 XX Homo sapiens.  
 OS Mus sp.  
 OS Synthetic.  
 XX Key Location/Qualifiers  
 FT Misc-difference 4 /label= Met, Leu  
 FT  
 XX US2002032315-A1.  
 XX PD 14-MAR-2002.  
 XX PF 06-APR-1998; 98US-00056160.  
 XX PR 06-AUG-1997; 97US-0054856P.  
 XX PA (BACA/) BACA M.  
 XX PA (WELL/) WELLS J A.  
 XX PA (PRES/) PRESTA L G.  
 XX PA (LOWM/) LOWMAN H B.  
 XX PA (CHEN/) CHEN Y M.  
 XX Baca M, Wells JA, Presta LG, Lowman HB, Chen YM;  
 XX WPI; 2002-517920/55.  
 XX New humanized anti-VEGF (vascular endothelial growth factor) antibodies  
 PT or their variants, useful for inhibiting VEGF-induced angiogenesis in a  
 PT mammal, particularly for treating tumor or retinal disorders.  
 XX Claim 12; Page 31; 47pp; English.  
 XX The present invention relates to humanised anti-VEGF (vascular  
 CC endothelial growth factor) antibodies or a variant of a parent anti-VEGF  
 CC antibody, which binds human VEGF. The anti-VEGF antibodies are useful for  
 CC inhibiting VEGF-induced angiogenesis in a mammal (particularly a human),  
 CC particularly those having a tumour or a retinal disorder e.g. intraocular  
 CC neovascular disorders. The present sequence is an exemplary light chain  
 CC variable domain of the humanised anti-VEGF antibody of the invention

Query Match 100.0%; Score 54; DB 5; Length 108;  
 Best Local Similarity 100.0%; Pred. No. 0.07; Mismatches 0; Gaps 0;  
 Matches 11; Conservative 0; Indels 0; Gaps 0;

QY 1 SASQDISNYLN 11  
 DB 24 SASQDISNYLN 34

RESULT 37  
 ABP61187  
 ID ABP61187 standard; protein; 108 AA.  
 AC ABP61187;  
 XX 20-SEP-2002 (first entry)  
 DT  
 DE Humanised anti-VEGF F(ab) (F(ab)-12) antibody variable light domain.  
 DE OS Mus sapiens.  
 DE OS Synthetic.  
 KW Cytostatic; ophthalmological; humanised; antibody; anti-VEGF; VEGF;  
 KW vascular endothelial growth factor; angiogenesis inhibitor; tumour;  
 KW retinal disorder; intraocular neovascular disorder; F(ab) (F(ab)-12);  
 KW light chain; variable domain.  
 XX Homo sapiens.  
 OS Mus sp.  
 OS Synthetic.  
 XX US2002032315-A1.  
 XX PD 14-MAR-2002.  
 XX PF 06-APR-1998; 98US-00056160.  
 XX PR 06-AUG-1997; 97US-0054856P.  
 XX PA (BACA/) BACA M.  
 XX PA (WELL/) WELLS J A.  
 XX PA (PRES/) PRESTA L G.  
 XX PA (LOWM/) LOWMAN H B.  
 XX PA (CHEN/) CHEN Y M.  
 XX Baca M, Wells JA, Presta LG, Lowman HB, Chen YM;  
 XX WPI; 2002-517920/55.  
 XX New humanized anti-VEGF (vascular endothelial growth factor) antibodies  
 PT or their variants, useful for inhibiting VEGF-induced angiogenesis in a  
 PT mammal, particularly for treating tumor or retinal disorders.  
 XX Claim 10; Fig 1; 47pp; English.  
 XX The present invention relates to humanised anti-VEGF (vascular  
 CC endothelial growth factor) antibodies or a variant of a parent anti-VEGF  
 CC antibody, which binds human VEGF. The anti-VEGF antibodies are useful for  
 CC inhibiting VEGF-induced angiogenesis in a mammal (particularly a human),  
 CC particularly those having a tumour or a retinal disorder e.g. intraocular  
 CC neovascular disorders. The present sequence is an exemplary light chain  
 CC variable domain of the humanised anti-VEGF antibody of the invention

Query Match 100.0%; Score 54; DB 5; Length 108;  
 Best Local Similarity 100.0%; Pred. No. 0.07; Mismatches 0; Gaps 0;  
 Matches 11; Conservative 0; Indels 0; Gaps 0;

QY 1 SASQDISNYLN 11  
 DB 24 SASQDISNYLN 34

RESULT 38  
 ABU11011  
 ID ABU11011 standard; protein; 108 AA.  
 AC ABU11011;  
 XX 04-FEB-2003 (first entry)  
 DT  
 DE Modified ganglioside GD3 antibody associated protein #4.  
 XX Ganglioside GD3; anti-ganglioside GD3 antibody; tumour; melanoma.

```

XX OS Synthetic.
XX PN WO200278739-A1.
XX PD 10-OCT-2002.
XX PF 29-MAR-2002; 2002WO-JP0031170.
XX PR 29-MAR-2001; 2001JP-00097483.
XX PA (KYOW ) KYOWA HAKKO KOGYO KK.
XX PI Shitara K, Niwa R, Kanazawa J, Asada M;
XX DR WPI; 2003-067410/06.
XX PT Drugs containing genetically-modified antibody against ganglioside GD3,
XX its fragment, immunocompetent cell activators or/and antitumor agents in
XX combination, applicable in treating malignant tumor like melanoma.
XX PS Claim 8; Page 100; 121pp; Japanese.
XX CC The invention describes drugs contain a genetically-modified antibody
XX against ganglioside GD3 or its fragment and at least 1 of a substance
XX capable of activating immunocompetent cells and a substance having an
XX antitumor activity in combination. The drugs can be used to treat tumour
XX like melanoma and can provide a treatment with enhanced therapeutic
XX effect and little side-reactions, particularly to relieve problems of
XX side-effects during the conventional single administration. This sequence
XX represents a protein associated with the anti- ganglioside GD3 antibody
XX SQ Sequence 108 AA;

Query Match 100.0%; Score 54; DB 6; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.07;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SASQDISNYLN 11
Db 24 SASQDISNYLN 34

RESULT 39
ABU11013
ID ABU11013 standard; protein; 108 AA.
XX AC ABU11013;
XX DT 04-FEB-2003 (first entry)
XX DE Modified ganglioside GD3 antibody associated protein #6.
XX KW Ganglioside GD3; anti-ganglioside GD3 antibody; tumour; melanoma.
XX OS Mus musculus.
XX PN WO200278739-A1.
XX PD 10-OCT-2002.
XX PF 29-MAR-2002; 2002WO-JP0031170.
XX PR 29-MAR-2001; 2001JP-00097483.
XX PA (KYOW ) KYOWA HAKKO KOGYO KK.
XX PI Shitara K, Niwa R, Kanazawa J, Asada M;
XX DR WPI; 2003-067410/06.
XX PT Drugs containing genetically-modified antibody against ganglioside GD3,
XX its fragment, immunocompetent cell activators or/and antitumor agents in
XX combination, applicable in treating malignant tumor like melanoma.

Query Match 100.0%; Score 54; DB 6; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.07;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SASQDISNYLN 11
Db 24 SASQDISNYLN 34

RESULT 39
ABU11013
ID ABU11013 standard; protein; 108 AA.
XX AC ABU11013;
XX DT 04-FEB-2003 (first entry)
XX DE Modified ganglioside GD3 antibody associated protein #6.
XX KW Ganglioside GD3; anti-ganglioside GD3 antibody; tumour; melanoma.
XX OS Mus musculus.
XX PN WO200278739-A1.
XX PD 10-OCT-2002.
XX PF 29-MAR-2002; 2002WO-JP0031170.
XX PR 29-MAR-2001; 2001JP-00097483.
XX PA (KYOW ) KYOWA HAKKO KOGYO KK.
XX PI Shitara K, Niwa R, Kanazawa J, Asada M;
XX DR WPI; 2003-067410/06.
XX PT Drugs containing genetically-modified antibody against ganglioside GD3,
XX its fragment, immunocompetent cell activators or/and antitumor agents in
XX combination, applicable in treating malignant tumor like melanoma.

Query Match 100.0%; Score 54; DB 6; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.07;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SASQDISNYLN 11
Db 24 SASQDISNYLN 34

RESULT 40
ADG31770
ID ADG31770 standard; protein; 108 AA.
XX AC ADG31770;
XX DT 26-FEB-2004 (first entry)
XX DE V(L) domain of matured humanised murine anti-VEGF antibody SeqID4.
XX KW protein library; in silico; VEGF; vascular endothelial growth factor;
XX antibody; computational prediction; V(H) domain; mouse; murine.
XX OS Synthetic.
XX OS Mus sp.
XX PN WO2003099999-A2.
XX PD 04-DEC-2003.
XX PF 20-MAY-2003; 2003WO-US016037.
XX PR 20-MAY-2002; 2002US-00153159.
XX PR 20-MAY-2002; 2002US-00153176.
XX PA (ABMA-) ABMAXIS INC.
XX PI Luo P, Hsieh M, Zhong P, Wang C, Cao Y, Liu S;
XX DR WPI; 2004-035117/03.
XX PT Constructing antibody libraries for generating protein libraries with
XX improved biological function comprising selecting from tester protein
XX sequences two peptide segments having 15% sequence identity with the lead
XX sequence.
XX PS Disclosure; SEQ ID NO 4; 354pp; English.
XX CC This invention relates to a novel method for the generation and screening
XX of a protein library in silico. Specifically, it refers to a high-
XX throughput method optimised for the identification of anti-VEGF (vascular
XX endothelial growth factor) antibodies with improved binding affinities
XX for their target antigen (VEGF), using computational prediction. The
XX present invention describes selecting proteins with a desirable function
XX based on their structural similarity to the target structural or
XX functional motif of a lead protein of interest. Accordingly, these
XX protein libraries are functionally biased with increased diversity so as
XX to increase the chance of identifying novel hits or combinations of
XX mutants with enhanced binding affinity. Furthermore, the sequence profile

```



CC based on the multiple structure alignment of the available lead structure  
 CC allows the sampling of a larger sequence space than by traditional.  
 CC multiple sequence alignment approaches. This polypeptide sequence is the  
 CC V(L) domain of affinity matured humanised murine anti-VEGF antibody, used  
 CC in an exemplification of the invention.

XX SQ Sequence 108 AA;

Query Match 100.0%; Score 54; DB 8; Length 108;  
 Best Local Similarity 100.0%; Pred. No. 0.07;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASQDISNYLN 11  
 |||||  
 DB 24 SASQDISNYLN 34

# RESULT 41

ADG31782  
 ID ADG31782 standard; protein; 108 AA.

XX AC ADG31782;

XX DT 26-FEB-2004 (first entry)

XX DE V(L) domain of the anti-VEGF two chain antibody AM2 protein SeqID 16.

XX KW protein library; in silico; VEGF; vascular endothelial growth factor;  
 KW antibody; computational prediction; V(H) domain; flexon; AM2;  
 KW two chain antibody; murine; mouse.

XX OS Synthetic.

XX OS Unidentified.

XX OS Mus sp.

XX PN WO2003099999-A2.

XX PD 04-DEC-2003.

XX PF 20-MAY-2003; 2003WO-US016037.

XX PR 20-MAY-2002; 2002US-00153159.

XX PR 20-MAY-2002; 2002US-00153176.

XX PA (ABMA-) ABMAXIS INC.

XX PI Luo P, Hsieh M, Zhong P, Wang C, Cao Y, Liu S;

XX DR WPI; 2004-035117/03.

XX DR N-PSDB; ADG31781.

XX PT Constructing antibody libraries for generating protein libraries with  
 PT improved biological function comprising selecting from tester protein  
 PT sequences two peptide segments having 15% sequence identity with the lead  
 PT sequence.

XX PS Disclosure; SEQ ID NO 16; 354pp; English.

XX CC This invention relates to a novel method for the generation and screening  
 CC of a protein library in silico. Specifically, it refers to a high-  
 CC throughput method optimised for the identification of anti-VEGF (vascular  
 CC endothelial growth factor) antibodies with improved binding affinities  
 CC for their target antigen (VEGF), using computational prediction. The  
 CC present invention describes selecting proteins with a desirable function  
 CC based on their structural similarity to the target structural or  
 CC functional motif of a lead protein of interest. Accordingly, these  
 CC protein libraries are functionally biased with increased diversity so as  
 CC to increase the chance of identifying novel hits or combinations of  
 CC mutants with enhanced binding affinity. Furthermore, the sequence profile  
 CC based on the multiple structure alignment of the available lead structure  
 CC allows the sampling of a larger sequence space than by traditional.  
 CC multiple sequence alignment approaches. This polypeptide sequence is the  
 CC V(L) domain of the anti-VEGF two chain antibody AM2 protein, used in an

CC exemplification of the invention.

XX SQ Sequence 108 AA;

Query Match 100.0%; Score 54; DB 8; Length 108;  
 Best Local Similarity 100.0%; Pred. No. 0.07;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASQDISNYLN 11  
 |||||  
 DB 24 SASQDISNYLN 34

# RESULT 42

ADG31768  
 ID ADG31768 standard; protein; 108 AA.

XX AC ADG31768;

XX DT 26-FEB-2004 (first entry)

XX DE V(L) domain of parental humanised murine anti-VEGF antibody SeqID2.

XX KW protein library; in silico; VEGF; vascular endothelial growth factor;  
 KW antibody; computational prediction; V(H) domain; mouse; murine.

XX OS Synthetic.

XX OS Mus sp.

XX PN WO2003099999-A2.

XX PD 04-DEC-2003.

XX PF 20-MAY-2003; 2003WO-US016037.

XX PR 20-MAY-2002; 2002US-00153159.

XX PR 20-MAY-2002; 2002US-00153176.

XX PA (ABMA-) ABMAXIS INC.

XX PI Luo P, Hsieh M, Zhong P, Wang C, Cao Y, Liu S;

XX DR WPI; 2004-035117/03.

XX PT Constructing antibody libraries for generating protein libraries with  
 PT improved biological function comprising selecting from tester protein  
 PT sequences two peptide segments having 15% sequence identity with the lead  
 PT sequence.

XX PS Disclosure; SEQ ID NO 2; 354pp; English.

XX CC This invention relates to a novel method for the generation and screening  
 CC of a protein library in silico. Specifically, it refers to a high-  
 CC throughput method optimised for the identification of anti-VEGF (vascular  
 CC endothelial growth factor) antibodies with improved binding affinities  
 CC for their target antigen (VEGF), using computational prediction. The  
 CC present invention describes selecting proteins with a desirable function  
 CC based on their structural similarity to the target structural or  
 CC functional motif of a lead protein of interest. Accordingly, these  
 CC protein libraries are functionally biased with increased diversity so as  
 CC to increase the chance of identifying novel hits or combinations of  
 CC mutants with enhanced binding affinity. Furthermore, the sequence profile  
 CC based on the multiple structure alignment of the available lead structure  
 CC allows the sampling of a larger sequence space than by traditional.  
 CC multiple sequence alignment approaches. This polypeptide sequence is the  
 CC V(L) domain of parental humanised murine anti-VEGF antibody, used in an  
 CC exemplification of the invention.

XX SQ Sequence 108 AA;

Query Match 100.0%; Score 54; DB 8; Length 108;  
 Best Local Similarity 100.0%; Pred. No. 0.07;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASQDISNYLN 11  
 DB 24 SASQDISNYLN 34

RESULT 43  
 ADG31893

ID ADG31893 standard; peptide; 108 AA.  
 AC  
 XX  
 DT 26-FEB-2004 (first entry)  
 XX  
 DE V(L) protein sequence of various anti-VEGF antibodies SeqID 127.  
 XX  
 KW protein library; in silico; VEGF; vascular endothelial growth factor;  
 KW antibody; computational prediction; V(L) domain.  
 XX  
 OS Unidentified.  
 XX  
 PN WO2003099999-A2.  
 XX  
 PD 04-DEC-2003.  
 XX  
 PF 20-MAY-2003; 2003WO-US016037.  
 XX  
 PR 20-MAY-2002; 2002US-00153159.  
 PR 20-MAY-2002; 2002US-00153176.  
 XX  
 PA (ABMA-) ABMAXIS INC.  
 XX  
 PI Luo P, Hsieh M, Zhong P, Wang C, Cao Y, Liu S;  
 XX WPI; 2004-035117/03.  
 DR  
 XX Constructing antibody libraries for generating protein libraries with  
 PT improved biological function comprising selecting from tester protein  
 PT sequences two peptide segments having 15% sequence identity with the lead  
 PT sequence.  
 XX  
 PS Disclosure; SEQ ID NO 127; 354pp; English.  
 XX  
 CC This invention relates to a novel method for the generation and screening  
 CC of a protein library in silico. Specifically, it refers to a high-  
 CC throughput method optimised for the identification of anti-VEGF (vascular  
 CC endothelial growth factor) antibodies with improved binding affinities  
 CC for their target antigen (VEGF), using computational prediction. The  
 CC present invention describes selecting proteins with a desirable function  
 CC based on their structural similarity to the target structural or  
 CC functional motif of a lead protein of interest. Accordingly, these  
 CC protein libraries are functionally biased with increased diversity so as  
 CC to increase the chance of identifying novel hits or combinations of  
 CC mutants with enhanced binding affinity. Furthermore, the sequence profile  
 CC based on the multiple structure alignment of the available lead structure  
 CC allows the sampling of a larger sequence space than by traditional,  
 CC multiple sequence alignment approaches. This polypeptide sequence is the  
 CC V(L) protein sequence of various anti-VEGF antibodies, used in an  
 CC exemplification of the invention.  
 XX  
 SQ Sequence 108 AA;

Query Match 100.0%; Score 54; DB 8; Length 108;  
 Best Local Similarity 100.0%; Pred. No. 0.07;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASQDISNYLN 11  
 DB 24 SASQDISNYLN 34

RESULT 44  
 ADX80647

ID ADX80647 standard; protein; 108 AA.  
 AC  
 XX  
 DT 05-MAY-2005 (first entry)  
 XX  
 DE Humanized VEGF variable light chain amino acid sequence, seq id 7.  
 XX  
 KW Protein purification; leaching; protein A affinity chromatography; VEGF;  
 KW antibody.  
 XX  
 OS Synthetic.  
 XX  
 PN US2005038231-A1.  
 XX  
 PD 17-FEB-2005.  
 XX  
 PF 24-JUN-2004; 2004US-00877532.  
 XX  
 PR 28-JUL-2003; 2003US-0490500P.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Fahrner RL, Laverdiere A, McDonald PJ, O'leary RM;  
 XX WPI; 2005-172327/18.  
 DR  
 XX Purifying a protein, e.g. antibody or immunoadhesin, comprises reducing  
 PT the temperature of a composition subjected to protein A affinity  
 PT chromatography to 3-20 degrees C, where protein A leaching is reduced.  
 XX  
 PS Disclosure; SEQ ID NO 7; 27pp; English.  
 XX  
 CC The invention relates to a method of purifying a protein which comprises  
 CC a CH2/CH3 region by protein A affinity chromatography. The method  
 CC involves reducing the temperature of a composition comprising the protein  
 CC and one or more impurities subjected to protein A affinity chromatography  
 CC to 3-20 degrees Celsius, where protein A leaching is reduced. Preferably  
 CC the protein is antibody. The antibody is selected from Traatzumab,  
 CC humanized 2C4, humanized CD11a antibody, and humanized VEGF antibody.  
 CC Preferably, the antibody binds HER2 antigen, where the antibody is  
 CC Trastuzumab or humanized 2C4. The protein is an immunoadhesin,  
 CC specifically a TNF receptor immunoadhesin. The methods are useful for  
 CC purifying a protein, which comprises a CH2/CH3 region by protein A  
 CC affinity chromatography and for reducing leaching of protein A during  
 CC protein A affinity chromatography. The current sequence represents the  
 CC variable light chain amino acid sequence of VEGF.  
 XX  
 SQ Sequence 108 AA;

Query Match 100.0%; Score 54; DB 9; Length 108;  
 Best Local Similarity 100.0%; Pred. No. 0.07;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASQDISNYLN 11  
 DB 24 SASQDISNYLN 34

RESULT 45  
 ADZ57819

ID ADZ57819 standard; protein; 108 AA.  
 AC  
 XX  
 DT 30-JUN-2005 (first entry)  
 XX  
 DE Ganglioside GD3 binding antibody associated protein SEQ ID NO 23.  
 XX  
 KW cytostatic; antibody engineering; cancer; neoplasia; ganglioside; GD3;  
 KW pharmaceutical.  
 XX  
 OS Synthetic.

[illegible]

XX Iida S, Satoh M, Urakubo M, Wakitani M, Uchida K, Niwa R;  
 PI Shitara K;  
 XX WPI; 2005-346195/35.  
 XX  
 XX Antibody composition for treating ganglioside GD3 associated disease e.g.  
 PT cancer, comprises genetically modified antibody molecule, which  
 PT specifically binds to ganglioside GD3 and has N-glycoside-binding sugar  
 PT chain in its Fc domain.  
 XX  
 XX Claim 25; SEQ ID NO 27; 124pp; Japanese.  
 PS  
 XX The invention describes an antibody molecule which specifically binds to  
 CC ganglioside GD3 and has an N-glycoside-binding complex sugar chain in its  
 CC Fc domain, where the N-glycoside-binding complex sugar chain is a sugar  
 CC chain having no fucose attached to N-acetylglucosamine at the reducing  
 CC end of the sugar chain. Also described are: a transformant (II) capable  
 CC of producing (I), obtained by introducing DNA that encodes the antibody  
 CC molecule which specifically binds with ganglioside GD3, to a host cell;  
 CC producing (I), involving cultivating (I) in a culture medium, such that  
 CC C1 (sic) is produced and accumulated in the culture, extracting and  
 CC purifying C1 from the culture medium; a pharmaceutical (III) containing  
 CC C1 as an active ingredient; and a therapeutic agent (A1) for ganglioside  
 CC GD3 associated disease, comprising C1 as an active ingredient. (I) is  
 CC useful for treating GD3 associated disease, which involves administering  
 CC (I), where the GD3 associated disease is cancer. (A1) is also useful for  
 CC treating GD3 associated disease. (II) is useful for producing (I). (I) is  
 CC useful for manufacturing a therapeutic agent for GD3 associated disease.  
 CC This sequence represents a ganglioside GD3 binding antibody associated  
 CC protein.  
 XX  
 XX Sequence 108 AA;  
 SQ  
 Query Match 100.0%; Score 54; DB 9; Length 108;  
 Best Local Similarity 100.0%; Pred. No. 0.07; Mismatches 0; Indels 0; Gaps 0;  
 Matches 11; Conservative 0;  
 QY 1 SASQDISNYLN 11  
 DB 24 SASQDISNYLN 34  
 RESULT 48  
 ADZ57817  
 ID ADZ57817 standard; protein; 108 AA.  
 AC  
 AC ADZ57817;  
 DT 30-JUN-2005 (first entry)  
 XX  
 XX Ganglioside GD3 binding antibody associated protein SEQ ID NO 21.  
 DE  
 XX Cytostatic; antibody engineering; cancer; neoplasm; ganglioside; GD3;  
 KW pharmaceutical.  
 KW  
 XX Mus musculus.  
 OS  
 XX WO2005035577-A1.  
 PN  
 XX 21-APR-2005.  
 PD  
 XX 08-OCT-2004; 2004WO-JP015314.  
 PF  
 XX 08-OCT-2003; 2003JP-00350161.  
 PR  
 XX (KYOW ) KYOWA HAKKO KOGYO KK.  
 PA  
 XX Iida S, Satoh M, Urakubo M, Wakitani M, Uchida K, Niwa R;  
 PI Shitara K;  
 XX WPI; 2005-346195/35.  
 DR

XX Antibody composition for treating ganglioside GD3 associated disease e.g.  
 PT cancer, comprises genetically modified antibody molecule, which  
 PT specifically binds to ganglioside GD3 and has N-glycoside-binding sugar  
 PT chain in its Fc domain.  
 XX  
 XX Claim 14; SEQ ID NO 21; 124pp; Japanese.  
 PS  
 XX The invention describes an antibody molecule which specifically binds to  
 CC ganglioside GD3 and has an N-glycoside-binding complex sugar chain in its  
 CC Fc domain, where the N-glycoside-binding complex sugar chain is a sugar  
 CC chain having no fucose attached to N-acetylglucosamine at the reducing  
 CC end of the sugar chain. Also described are: a transformant (II) capable  
 CC of producing (I), obtained by introducing DNA that encodes the antibody  
 CC molecule which specifically binds with ganglioside GD3, to a host cell;  
 CC producing (I), involving cultivating (I) in a culture medium, such that  
 CC C1 (sic) is produced and accumulated in the culture, extracting and  
 CC purifying C1 from the culture medium; a pharmaceutical (III) containing  
 CC C1 as an active ingredient; and a therapeutic agent (A1) for ganglioside  
 CC GD3 associated disease, comprising C1 as an active ingredient. (I) is  
 CC useful for treating GD3 associated disease, which involves administering  
 CC (I), where the GD3 associated disease is cancer. (A1) is also useful for  
 CC treating GD3 associated disease. (II) is useful for producing (I). (I) is  
 CC useful for manufacturing a therapeutic agent for GD3 associated disease.  
 CC This sequence represents a ganglioside GD3 binding antibody associated  
 CC protein.  
 XX  
 XX Sequence 108 AA;  
 SQ  
 Query Match 100.0%; Score 54; DB 9; Length 108;  
 Best Local Similarity 100.0%; Pred. No. 0.07; Mismatches 0; Indels 0; Gaps 0;  
 Matches 11; Conservative 0;  
 QY 1 SASQDISNYLN 11  
 DB 24 SASQDISNYLN 34  
 RESULT 49  
 ADZ57820  
 ID ADZ57820 standard; protein; 108 AA.  
 AC  
 AC ADZ57820;  
 DT 30-JUN-2005 (first entry)  
 XX  
 XX Ganglioside GD3 binding antibody associated protein SEQ ID NO 24.  
 DE  
 XX Cytostatic; antibody engineering; cancer; neoplasm; ganglioside; GD3;  
 KW pharmaceutical.  
 KW  
 XX Synthetic.  
 OS  
 XX WO2005035577-A1.  
 PN  
 XX 21-APR-2005.  
 PD  
 XX 08-OCT-2004; 2004WO-JP015314.  
 PF  
 XX 08-OCT-2003; 2003JP-00350161.  
 PR  
 XX (KYOW ) KYOWA HAKKO KOGYO KK.  
 PA  
 XX Iida S, Satoh M, Urakubo M, Wakitani M, Uchida K, Niwa R;  
 PI Shitara K;  
 XX WPI; 2005-346195/35.  
 DR  
 XX Antibody composition for treating ganglioside GD3 associated disease e.g.  
 PT cancer, comprises genetically modified antibody molecule, which  
 PT specifically binds to ganglioside GD3 and has N-glycoside-binding sugar  
 PT chain in its Fc domain.  
 XX

XX PS Claim 21; SEQ ID NO 24; 124pp; Japanese.

XX CC The invention describes an antibody composition (I), comprising a

CC CC genetically modified antibody molecule which specifically binds to

CC CC ganglioside GD3 and has an N-glycoside-binding complex sugar chain in its

CC CC Fc domain, where the N-glycoside-binding complex sugar chain is a sugar

CC CC chain having no fucose attached to N-acetylglucosamine at the reducing

CC CC end of the sugar chain. Also described are: a transformant (II) capable

CC CC of producing (I), obtained by introducing DNA that encodes the antibody

CC CC molecule which specifically binds with ganglioside GD3, to a host cell;

CC CC producing (I), involving cultivating (I) in a culture medium, such that

CC CC Cl (sic) is produced and accumulated in the culture, extracting and

CC CC purifying Cl from the culture medium; a pharmaceutical (III) containing

CC CC Cl as an active ingredient; and a therapeutic agent (A1) for ganglioside

CC CC GD3 associated disease, comprising Cl as an active ingredient. (I) is

CC CC useful for treating GD3 associated disease, which involves administering

CC CC (I), where the GD3 associated diseases is cancer. (A1) is also useful for

CC CC treating GD3 associated disease. (II) is useful for producing (I). (I) is

CC CC useful for manufacturing a therapeutic agent for GD3 associated disease.

CC CC This sequence represents a ganglioside GD3 binding antibody associated

CC CC protein.

XX SQ Sequence 108 AA;

Query Match 100.0%; Score 54; DB 9; Length 108;

Best Local Similarity 100.0%; Pred. No. 0.07;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASQDISNYLN 11

DB 24 SASQDISNYLN 34

RESULT 50

AAW70673

ID AAW70673 standard; peptide; 110 AA.

XX AC AAW70673;

XX DT 27-JAN-1999 (first entry)

XX DE Anti-VEGF humanised antibody variable light domain of template MB1.6.

XX KW Light variable domain; murine; humanised antibody;

XX KW anti-vascular endothelial growth factor antibody; anti-VEGF antibody;

XX KW VEGF-induced angiogenesis; tumour; retinal disorder;

XX KW age-related macular degeneration; diabetic retinopathy;

XX KW rheumatoid arthritis; psoriasis; atherosclerosis; Grave's disease.

XX OS Synthetic.

OS Mus sp.

OS Homo sapiens.

XX PN WO9845331-A2.

XX PD 15-OCT-1998.

XX PF 03-APR-1998; 98WO-US006604.

XX PR 07-APR-1997; 97US-00833504.

XX PR 06-AUG-1997; 97US-00908469.

XX PA (GETH ) GENENTECH INC.

XX PI Baca M, Wells JA, Presta LG, Lowman HB, Chen YM;

XX DR WPI; 1998-568337/48.

XX PT New humanised antibody with affinity for vascular endothelial growth

XX PT factor - for treatment of tumours, retinal disease and other angiogenic

XX PT states, also related nucleic acid, vectors and transformed cells.

PS Example 3; Fig 9A; 100pp; English.

XX CC The present sequence represents a variable light domain of the template

CC CC molecule of the affinity-matured anti-vascular endothelial growth factor

CC CC (anti-VEGF) antibody. The sequence is used in the course of the invention

CC CC to produce the humanised anti-VEGF antibody of the invention. The

CC CC humanised antibodies are used to inhibit VEGF-induced angiogenesis,

CC CC particularly for treating or preventing tumours (of any type) and retinal

CC CC disorders (e.g. age-related macular degeneration or diabetic

CC CC retinopathy). They can also be used to treat other conditions that

CC CC involve angiogenesis, e.g. rheumatoid arthritis, psoriasis,

CC CC atherosclerosis, Grave's disease, etc

XX SQ Sequence 110 AA;

Query Match 100.0%; Score 54; DB 2; Length 110;

Best Local Similarity 100.0%; Pred. No. 0.072;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASQDISNYLN 11

DB 24 SASQDISNYLN 34

Search completed: April 6, 2006, 09:04:46

Job time : 90.661 secs

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GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: April 6, 2006, 08:56:41 ; Search time 11 Seconds  
(without alignments)  
96.217 Million cell updates/sec

Title: US-10-089-500-6  
Perfect score: 54  
Sequence: 1 SASQDISNYLN 11

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database : PIR 80.\*

1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	50	92.6	62	2 S42265	Ig kappa chain v r
2	50	92.6	87	2 IS2592	Ig kappa chain v r
3	50	92.6	88	2 S34087	Ig kappa chain v r
4	50	92.6	88	2 S34088	Ig kappa chain v r
5	50	92.6	93	2 S38564	Ig kappa chain v r
6	50	92.6	95	2 PH0862	Ig kappa chain v r
7	50	92.6	107	2 S69901	Ig kappa chain (cl
8	50	92.6	107	2 A28044	Ig kappa chain v r
9	50	92.6	107	2 D48677	Ig kappa chain v-j
10	50	92.6	107	2 B28044	Ig kappa chain v r
11	50	92.6	107	2 B49026	Ig kappa chain v r
12	50	92.6	107	2 S69906	Ig kappa chain (cl
13	50	92.6	108	1 KVM5AR	Ig kappa chain v r
14	50	92.6	108	2 PL0282	Ig kappa chain v r
15	50	92.6	108	2 C26405	Ig kappa chain v r
16	50	92.6	108	2 S38662	Ig kappa chain v r
17	50	92.6	108	2 S69902	Ig kappa chain (cl
18	50	92.6	108	2 S69900	Ig kappa chain (cl
19	50	92.6	108	2 S69903	Ig kappa chain (cl
20	50	92.6	110	2 S44118	Ig kappa chain v-j
21	50	92.6	115	2 A53276	Ig kappa chain v r
22	50	92.6	115	2 JL0080	Ig kappa chain pre
23	50	92.6	117	2 S42263	Ig kappa chain v r
24	50	92.6	117	2 S43528	Ig kappa chain v r
25	50	92.6	128	2 A26406	Ig kappa chain v r
26	50	92.6	129	2 S53789	Ig kappa chain v r
27	49	90.7	111	2 B37266	Ig kappa chain v r
28	49	90.7	111	2 B38740	Ig kappa chain v r
29	47	87.0	108	2 B26405	Ig kappa chain v r

30	47	87.0	111	2 A38740	Ig kappa chain v r
31	47	87.0	111	2 C38740	Ig kappa chain v r
32	47	87.0	111	2 C38740	Ig kappa chain v r
33	47	87.0	122	2 A29380	Ig kappa chain pre
34	47	87.0	126	2 A34904	Ig kappa chain v r
35	47	87.0	127	2 S52447	Ig kappa chain v r
36	46	85.2	108	2 S11124	Ig kappa chain v r
37	45	83.3	107	2 S32188	Ig kappa chain v r
38	45	83.3	108	1 KIHUAA	Ig kappa chain v-i
39	45	83.3	109	2 PH0888	Ig kappa chain v r
40	45	83.3	111	2 I38740	Ig kappa chain v r
41	45	83.3	135	2 S24320	Ig kappa chain pre
42	44	81.5	105	2 PH0087	Ig kappa chain v r
43	44	81.5	109	2 S19674	Ig kappa chain v r
44	44	81.5	108	2 S1981	Ig kappa chain - h
45	44	81.5	127	2 S40367	Ig kappa chain v-j
46	44	81.5	129	1 KIHUWK	Ig kappa chain pre
47	43	79.6	108	2 B30551	Ig kappa chain v r
48	43	79.6	139	2 S40365	Ig kappa chain - h
49	42	77.8	98	2 PH1065	Ig kappa chain v r
50	42	77.8	106	2 S20652	Ig kappa chain v r
51	42	77.8	107	2 B48677	Ig kappa chain v-j
52	42	77.8	107	2 C48677	Ig light chain v-j
53	42	77.8	107	2 A48677	Ig kappa chain v-j
54	42	77.8	108	1 KIHUAG	Ig kappa chain v-i
55	42	77.8	108	2 S19970	Ig kappa chain v r
56	42	77.8	127	2 PH1224	Ig kappa chain pre
57	41	75.9	92	2 D28840	Ig kappa chain v r
58	41	75.9	101	2 C28840	Ig kappa chain v r
59	41	75.9	101	2 B28840	Ig kappa chain v r
60	41	75.9	108	1 KVM573	Ig kappa chain v r
61	41	75.9	122	2 S40314	Ig kappa chain - h
62	40	74.1	95	2 PH0864	Ig kappa chain v r
63	40	74.1	1178	2 S30431	MSP-300 protein -
64	39	72.2	86	2 S34086	Ig kappa chain v r
65	39	72.2	87	2 S34084	Ig kappa chain v r
66	39	72.2	87	2 S34083	Ig kappa chain v r
67	39	72.2	88	2 S21522	Ig kappa chain v r
68	39	72.2	88	2 S21528	Ig kappa chain v r
69	39	72.2	95	2 PH0865	Ig kappa chain v r
70	39	72.2	106	2 PL0267	Ig kappa chain v r
71	39	72.2	107	2 S36264	Ig lambda chain v
72	39	72.2	108	2 S44122	Ig kappa chain v r
73	39	72.2	108	2 S39154	Ig kappa chain (BR
74	39	72.2	108	2 S47182	Ig kappa chain - h
75	39	72.2	108	2 B49047	Ig kappa chain v r
76	39	72.2	116	2 A27594	Ig kappa chain pre
77	39	72.2	117	1 KVM53B	Ig kappa chain pre
78	39	72.2	117	2 S4206	Ig kappa chain v r
79	39	72.2	123	2 S40331	Ig kappa chain - h
80	39	72.2	123	2 S35479	Ig kappa chain pre
81	39	72.2	230	2 S33161	Ig kappa chain - s
82	38	70.4	67	2 AC1954	hypothetical prote
83	38	70.4	106	2 PC2397	anti-tetanus toxin
84	38	70.4	108	1 KIHURE	Ig kappa chain v-i
85	38	70.4	904	2 G90563	lipoprotein (impor
86	37	68.5	71	2 S21526	Ig kappa chain v r
87	37	68.5	88	2 S21525	Ig kappa chain v r
88	37	68.5	95	2 PH0866	Ig kappa chain v r
89	37	68.5	95	2 PH0863	Ig kappa chain v r
90	37	68.5	101	2 S44117	Ig kappa chain v-j
91	37	68.5	106	2 PC4282	Ig kappa chain (an
92	37	68.5	107	2 S36275	Ig lambda chain v
93	37	68.5	107	2 S40366	Ig kappa chain v-j
94	37	68.5	108	1 KIHURY	Ig kappa chain v-i
95	37	68.5	115	1 KVM5L6	Ig kappa chain pre
96	37	68.5	117	2 C21056	Ig kappa chain pre
97	37	68.5	128	2 PL0101	Ig kappa chain pre
98	37	68.5	131	2 S40352	Ig kappa chain v-j
99	37	68.5	234	2 S14237	Ig kappa chain pre
100	37	68.5	346	2 A12266	hypothetical prote
101	37	68.5	709	2 A37218	uncharacterized co
102	37	68.5	835	2 T35763	probable aminopept

103	37	68.5	1711	2	T31337	176	34	63.0	2188	2	A70984	probable polyketid
104	37	68.5	1742	2	T17120	177	33	61.1	72	2	H36025	Ig heavy chain V r
105	37	68.5	4128	2	JC6306	178	33	61.1	81	2	F36025	Ig light chain V r
106	36	66.7	88	2	S38562	179	33	61.1	85	2	F36025	Ig light chain V r
107	36	66.7	89	2	A22775	180	33	61.1	94	2	F33730	Ig kappa chain V r
108	36	66.7	101	2	S13701	181	33	61.1	97	2	PH1064	Ig light chain V r
109	36	66.7	104	2	S13700	182	33	61.1	103	2	S44121	Ig kappa chain V-J
110	36	66.7	108	1	KWSAA	183	33	61.1	104	2	S26310	Ig kappa chain V r
111	36	66.7	108	2	S31977	184	33	61.1	104	2	S26329	Ig kappa chain V r
112	36	66.7	109	2	S31998	185	33	61.1	107	2	S47183	Ig kappa chain - h
113	36	66.7	125	2	S40350	186	33	61.1	108	1	KIHULY	Ig kappa chain V-I
114	36	66.7	128	1	KWNT1	187	33	61.1	108	1	KIHUOU	Ig kappa chain V-I
115	36	66.7	285	1	T15133	188	33	61.1	109	2	S31978	Ig kappa chain - h
116	36	66.7	359	2	F86683	189	33	61.1	115	2	D70338	hypothetical prote
117	36	66.7	554	2	E90601	190	33	61.1	117	1	K4RBF2	Ig kappa chain pre
118	36	66.7	4450	2	JX0340	191	33	61.1	125	2	S09365	Ig kappa chain - m
119	36	66.7	4452	1	YGBSG2	192	33	61.1	154	2	B69969	conserved hypoteth
120	35,5	65.7	2261	1	A42548	193	33	61.1	179	2	I40594	DNA-directed DNA p
121	35	64.8	82	2	C69013	194	33	61.1	185	2	C82711	hypothetical prote
122	35	64.8	91	2	S17622	195	33	61.1	210	2	D70459	hypothetical prote
123	35	64.8	98	2	PH1062	196	33	61.1	219	2	AG2036	hypothetical prote
124	35	64.8	102	2	A23620	197	33	61.1	294	2	D82393	hypothetical prote
125	35	64.8	103	2	S13703	198	33	61.1	366	2	F82376	hypothetical prote
126	35	64.8	106	2	C33936	199	33	61.1	344	2	D86597	major outer membra
127	35	64.8	109	2	S32001	200	33	61.1	344	2	H72027	hypothetical prote
128	35	64.8	109	2	S31980	201	33	61.1	352	2	T49396	hypothetical prote
129	35	64.8	109	2	S31979	202	33	61.1	359	2	T24539	hypothetical prote
130	35	64.8	124	2	S40348	203	33	61.1	404	2	A42677	DNA polymerase III
131	35	64.8	129	2	S52792	204	33	61.1	420	2	H90356	interleukin-1 beta
132	35	64.8	129	2	S32806	205	33	61.1	445	2	C71636	conserved hypoteth
133	35	64.8	157	2	I40553	206	33	61.1	452	2	AE1592	probable thiophene
134	35	64.8	200	2	D70865	207	33	61.1	452	2	AE1592	B. subtilis PBX p
135	35	64.8	358	2	H87267	208	33	61.1	470	2	TI5946	hypothetical prote
136	35	64.8	413	2	F96743	209	33	61.1	483	2	S69894	major DNA-binding
137	35	64.8	450	2	T39088	210	33	61.1	520	2	JC5356	laccase (EC 1.10.3
138	35	64.8	490	2	T28382	211	33	61.1	520	2	S59533	laccase (EC 1.10.3
139	35	64.8	512	2	C96517	212	33	61.1	532	1	CPBYV	carboxypeptidase C
140	35	64.8	520	2	B96517	213	33	61.1	635	2	T27014	hypothetical prote
141	35	64.8	549	2	G84996	214	33	61.1	692	2	H90045	hypothetical prote
142	35	64.8	557	2	AB1540	215	33	61.1	709	2	AD2843	hypothetical prote
143	35	64.8	586	2	B83790	216	33	61.1	715	2	E71073	hypothetical prote
144	35	64.8	666	2	C82932	217	33	61.1	717	2	E97620	hypothetical prote
145	35	64.8	830	1	RNEGB2	218	33	61.1	799	2	F83549	probable ATP-depen
146	35	64.8	986	2	S12021	219	33	61.1	1028	2	T34360	hypothetical prote
147	35	64.8	1042	2	S42511	220	33	61.1	1068	2	AB1082	B. subtilis xueB p
148	35	64.8	1043	2	B33754	221	33	61.1	1463	2	T30290	AAS surface protei
149	35	64.8	1043	2	A33754	222	33	61.1	1616	2	S62504	conserved hypoteth
150	35	64.8	1103	2	T42022	223	33	61.1	1996	2	F71405	probable TMV resis
151	34	63.0	43	2	S21065	224	33	61.1	2478	2	AH2140	polyketide synthas
152	34	63.0	96	2	G33730	225	32	59.3	39	2	PH0878	Ig kappa chain V r
153	34	63.0	101	2	AD0272	226	32	59.3	78	2	S34102	Ig kappa chain V r
154	34	63.0	103	2	S19975	227	32	59.3	82	2	S34090	Ig kappa chain V r
155	34	63.0	107	2	S12954	228	32	59.3	86	2	S16837	Ig kappa chain V r
156	34	63.0	108	1	KIHUHU	229	32	59.3	86	2	S16830	Ig kappa chain V r
157	34	63.0	108	1	KIHUSW	230	32	59.3	86	2	S16833	Ig kappa chain V-I
158	34	63.0	108	1	KIHUSW	231	32	59.3	86	2	S16826	Ig kappa chain V r
159	34	63.0	117	2	S21668	232	32	59.3	87	1	GCFFS	glucagon precursor
160	34	63.0	117	2	S46376	233	32	59.3	87	2	S21523	Ig kappa chain V r
161	34	63.0	117	2	S24207	234	32	59.3	88	2	S21520	Ig kappa chain V r
162	34	63.0	120	2	S21667	235	32	59.3	88	2	S34104	Ig kappa chain V r
163	34	63.0	120	2	S21666	236	32	59.3	88	2	S21524	Ig kappa chain V r
164	34	63.0	129	2	S40317	237	32	59.3	88	2	PL0261	Ig kappa chain V r
165	34	63.0	129	2	S52793	238	32	59.3	89	2	C69801	hypothetical prote
166	34	63.0	157	2	E64433	239	32	59.3	92	2	S37506	Ig kappa chain V r
167	34	63.0	162	2	T18855	240	32	59.3	92	2	S37512	Ig kappa chain V r
168	34	63.0	338	2	T47427	241	32	59.3	92	2	S37522	Ig kappa chain V r
169	34	63.0	367	2	T10352	242	32	59.3	92	2	S37516	Ig kappa chain V r
170	34	63.0	417	2	T28670	243	32	59.3	95	2	T45409	hypothetical prote
171	34	63.0	433	2	E81744	244	32	59.3	105	2	G89993	Ig kappa chain V r
172	34	63.0	443	2	I40793	245	32	59.3	106	2	PL0260	hypothetical prote
173	34	63.0	502	2	B90103	246	32	59.3	108	1	KVRB2K	Ig kappa chain V r
174	34	63.0	578	1	I40794	247	32	59.3	108	2	G44151	Ig kappa chain V r
175	34	63.0	660	2	C86877	248	32	59.3	108	2	G44151	Ig kappa chain V r



249	32	59.3	108	2	S34007	Ig kappa chain V r	322	32	59.3	887	2	F85494	pyruvate dehydroge
250	32	59.3	108	2	S30521	Ig kappa chain V r	323	32	59.3	887	2	F90643	pyruvate dehydroge
251	32	59.3	109	2	S31983	Ig kappa chain - h	324	32	59.3	922	2	T37256	metalloproteinase
252	32	59.3	111	2	S23628	Ig kappa chain V r	325	32	59.3	1077	2	D71660	hypothetical prote
253	32	59.3	114	2	S54905	Ig kappa chain V r	326	32	59.3	1117	2	S63399	probable membrane
254	32	59.3	115	1	K3HUVG	Ig kappa chain pre	327	32	59.3	1231	2	S30185	insulin receptor a
255	32	59.3	117	2	S41814	Ig kappa chain V r	328	32	59.3	1239	2	T13809	probable disintegr
256	32	59.3	117	2	S41810	Ig kappa chain V r	329	32	59.3	1417	2	T18418	hypothetical prote
257	32	59.3	124	2	S40318	Ig kappa chain V r	330	32	59.3	1486	2	E85618	hypothetical prote
258	32	59.3	124	2	S40336	Ig kappa chain V-J	331	32	59.3	1486	2	G90754	hypothetical prote
259	32	59.3	127	2	A23986	Ig kappa chain pre	332	32	59.3	1486	2	C64832	kinesin-like cell
260	32	59.3	128	2	S46372	Ig light chain var	333	32	59.3	1505	2	S28079	DNA-directed DNA p
261	32	59.3	128	2	A56701	Ig kappa chain V r	334	32	59.3	1534	2	JH0228	cell division prot
262	32	59.3	128	2	S40379	Ig kappa chain V-J	335	32	59.3	1783	2	AC2091	serine/threonine k
263	32	59.3	129	2	S40363	Ig kappa chain - h	336	32	59.3	2236	1	QZFF	rudimentary protei
264	32	59.3	130	1	KVMSM4	Ig kappa chain pre	337	32	59.3	2491	2	A57036	talin - slime mold
265	32	59.3	132	2	S38646	Ig kappa chain V r	338	32	59.3	3110	2	AC0116	probable virulence
266	32	59.3	139	2	T23371	hypothetical prote	339	32	59.3	3187	2	JC5837	364k Golgi complex
267	32	59.3	144	2	PL0106	Ig kappa chain pre	340	31.5	58.3	1877	2	T40550	probable phosphat
268	32	59.3	146	2	S60698	gag protein - huma	341	31	57.4	89	2	T17518	hypothetical prote
269	32	59.3	146	2	S60704	gag protein - huma	342	31	57.4	93	2	D89997	hypothetical prote
270	32	59.3	146	2	S60702	gag protein - huma	343	31	57.4	102	1	NRPLTB	ribonuclease T1 (B
271	32	59.3	146	2	S60703	gag protein - huma	344	31	57.4	106	2	PL0259	Ig kappa chain V r
272	32	59.3	174	1	A49689	pancreatitis-assoc	345	31	57.4	106	2	PL0262	Ig kappa chain V r
273	32	59.3	174	2	I83377	regenerating prote	346	31	57.4	107	2	S57444	Ig kappa chain V-J
274	32	59.3	201	2	D81919	hypothetical prote	347	31	57.4	108	1	KJHUKA	Ig kappa chain V-J
275	32	59.3	201	2	G81182	hypothetical prote	348	31	57.4	108	4	B47271	nitrophenyl phosph
276	32	59.3	222	2	A81084	O-methyltransferas	349	31	57.4	115	2	S11697	Ig kappa chain pre
277	32	59.3	222	2	A81860	probable methyltra	350	31	57.4	115	2	T04972	hypothetical prote
278	32	59.3	320	2	T28379	ORF MSV218 hypothe	351	31	57.4	120	2	S46370	Ig kappa chain V-J
279	32	59.3	324	2	AB1269	delta-aminolevulin	352	31	57.4	125	2	S40344	Ig kappa chain V-J
280	32	59.3	334	2	AI2003	hypothetical prote	353	31	57.4	132	2	C72200	conserved hypothet
281	32	59.3	346	2	JC1376	alcohol dehydrogen	354	31	57.4	158	2	G90332	hypothetical prote
282	32	59.3	346	2	H70860	alcohol dehydrogen	355	31	57.4	169	2	T48402	hypothetical prote
283	32	59.3	348	1	R5HS10	ribosomal protein	356	31	57.4	172	2	S59113	hypothetical prote
284	32	59.3	359	2	A90525	peptide chain rele	357	31	57.4	175	2	A41719	pancreatic stone p
285	32	59.3	362	2	D87125	alcohol dehydrogen	358	31	57.4	191	2	H90078	hypothetical prote
286	32	59.3	366	2	C84931	DNA-directed DNA p	359	31	57.4	237	2	C90159	uroporphyrogen I
287	32	59.3	366	2	H82859	DNA polymerase III	360	31	57.4	244	2	T07068	beta-fructofuranos
288	32	59.3	367	1	DJPS3P	DNA-directed DNA p	361	31	57.4	245	2	S70176	yeR protein - Yer
289	32	59.3	367	2	F83644	DNA polymerase III	362	31	57.4	245	2	AB0300	quorum-sensing tra
290	32	59.3	373	2	A68859	hypothetical prote	363	31	57.4	255	2	H97004	ortholog ygid E.co
291	32	59.3	391	2	S23507	pyruvate dehydroge	364	31	57.4	270	1	JQ1747	membrane protein -
292	32	59.3	391	2	JC6193	tumor suppressor p	365	31	57.4	273	2	G83403	conserved hypothet
293	32	59.3	402	2	T39591	cyclin - fission y	366	31	57.4	275	2	G83522	conserved hypothet
294	32	59.3	403	2	C72546	probable coenzyme	367	31	57.4	279	2	A11189	B. subtilis YcGQ p
295	32	59.3	421	2	H81843	conserved hypothet	368	31	57.4	279	2	AB1548	B. subtilis YcGQ p
296	32	59.3	421	2	D81098	gcpE protein NM813	369	31	57.4	279	2	H86213	protein F24B9.6 li
297	32	59.3	436	2	F86859	aminopeptidase C l	370	31	57.4	286	2	A82159	hypothetical prote
298	32	59.3	436	2	B48957	cysteine aminopept	371	31	57.4	287	2	T28367	hypothetical prote
299	32	59.3	443	2	G64234	hypothetical prote	372	31	57.4	288	2	T17664	probable aspartate
300	32	59.3	491	1	AI1980	glutamyl-tRNA (Gln	373	31	57.4	304	2	D96952	glycerol-3-phospha
301	32	59.3	497	1	FOLJND	gag polyprotein -	374	31	57.4	308	2	E81288	hypothetical prote
302	32	59.3	502	1	FOYWA2	gag polyprotein -	375	31	57.4	308	2	AD3154	nucleotidyltransfe
303	32	59.3	509	2	S74935	hypothetical prote	376	31	57.4	312	1	S29756	nitrogen fixation
304	32	59.3	519	1	S75850	pet112 protein - S	377	31	57.4	318	2	S76773	hypothetical prote
305	32	59.3	520	2	A35883	laccase (EC 1.10.3	378	31	57.4	325	2	JC2008	actin homolog prot
306	32	59.3	520	2	B35883	ligninolytic pheno	379	31	57.4	332	2	C95150	SAP domain protein
307	32	59.3	524	2	E71881	hypothetical prote	380	31	57.4	332	2	G88640	protein F52C12.3 (
308	32	59.3	527	2	B64633	hypothetical prote	381	31	57.4	337	2	S44187	regulator protein
309	32	59.3	548	2	S18746	laccase (EC 1.10.3	382	31	57.4	339	1	KHMSB	cathepsin B (EC 3.
310	32	59.3	593	2	S64360	probable membrane	383	31	57.4	342	2	E70463	conserved hypothet
311	32	59.3	614	2	T09902	hypothetical prote	384	31	57.4	348	2	D82114	flagellar motor sw
312	32	59.3	617	2	T46319	hypothetical prote	385	31	57.4	351	2	D31983	hypothetical prote
313	32	59.3	652	1	S39409	nitrous-oxide redu	386	31	57.4	354	2	D31751	protein kinase cat
314	32	59.3	657	2	G86799	hypothetical prote	387	31	57.4	365	2	E98133	hypothetical prote
315	32	59.3	658	2	AI1385	exonuclease ABC (	388	31	57.4	366	1	DJEC38	DNA polymerase III
316	32	59.3	658	2	AC1761	exonuclease ABC (	389	31	57.4	366	2	AB0958	DNA polymerase III
317	32	59.3	697	2	C71850	probable outer mem	390	31	57.4	366	2	D91208	DNA polymerase III
318	32	59.3	808	2	T25748	hypothetical prote	391	31	57.4	366	2	F86054	DNA polymerase III
319	32	59.3	838	2	E89473	protein F52D2.6 li	392	31	57.4	366	2	AF0497	DNA-directed DNA p
320	32	59.3	865	2	B69074	probable formate d	393	31	57.4	366	2	AC1537	exonuclease ABC,
321	32	59.3	887	1	DESCPV	pyruvate dehydroge	394	31	57.4	367	1	JQ0734	DNA-directed DNA p

395	31	57.4	367	2	A81974	probable DNA-dirac	468	31	57.4	2713	2	A55713	inositol 1,4,5-tri
396	31	57.4	367	2	C81030	DNA polymerase III	489	31	57.4	2734	2	B36579	inositol 1,4,5-tri
397	31	57.4	368	2	F64017	hypothetical prote	470	31	57.4	2749	1	ACMSIT	inositol 1,4,5-tri
398	31	57.4	373	2	AG3400	5-amino-6-(5-phosp	471	31	57.4	2749	2	A36579	inositol 1,4,5-tri
399	31	57.4	375	2	D84606	alcohol dehydrogen	472	31	57.4	3972	2	S75251	hypothetical prote
400	31	57.4	376	2	E84604	alcohol dehydrogen	473	31	57.4	4558	2	C82199	Rtx toxin RtxA Vc1
401	31	57.4	378	2	T25558	hypothetical prote	474	30	55.6	75	2	B98256	hypothetical prote
402	31	57.4	383	2	AG1216	hypothetical prote	475	30	55.6	84	2	A13028	hypothetical prote
403	31	57.4	388	2	B82317	hypothetical prote	476	30	55.6	87	2	B97134	hypothetical prote
404	31	57.4	392	2	A81107	unknown protein ho	477	30	55.6	92	1	KVRB38	Ig kappa chain V r
405	31	57.4	397	2	T38701	hypothetical prote	478	30	55.6	99	1	A39296	monocyte chemoattr
406	31	57.4	401	2	T23490	hypothetical prote	479	30	55.6	99	2	JC2336	monocyte chemoattr
407	31	57.4	425	2	D90535	DNA-damage repair	480	30	55.6	100	2	E90330	Ig kappa chain V r
408	31	57.4	440	2	S50947	Tya protein - yeas	481	30	55.6	102	2	S26346	Ig kappa chain V r
409	31	57.4	450	2	C88700	protein K0ZB2.1 li	482	30	55.6	104	2	B43413	Ig kappa chain V r
410	31	57.4	460	2	T45968	hypothetical prote	483	30	55.6	107	2	B45722	anti-Hiv1 envelope
411	31	57.4	461	2	A90512	chromosomal replic	484	30	55.6	107	2	A45722	anti-glycoprotein
412	31	57.4	475	2	S54511	hypothetical prote	485	30	55.6	107	2	AF0352	conserved hypot het
413	31	57.4	516	2	T23827	hypothetical prote	486	30	55.6	107	2	AF0352	conserved hypot het
414	31	57.4	521	2	C88827	protein M7.2 limpo	487	30	55.6	108	1	KLHUBI	Ig kappa chain V-I
415	31	57.4	536	2	S62110	lysophospholipase	488	30	55.6	108	1	KLHUBE	Ig kappa chain V-I
416	31	57.4	538	2	D70204	hypothetical prote	489	30	55.6	109	2	JN0296	Ig kappa chain V-J
417	31	57.4	546	2	D89813	alpha-glucosidase	490	30	55.6	111	2	E90111	hypothetical prote
418	31	57.4	573	2	D90202	methionyl-tRNA syn	491	30	55.6	115	2	S10146	Ig kappa chain pre
419	31	57.4	574	2	C82301	endoglucanase-rela	492	30	55.6	122	2	S34566	hypothetical 13.7K
420	31	57.4	575	2	T38640	hypothetical prote	493	30	55.6	123	2	AH1998	hypothetical prote
421	31	57.4	579	2	S51528	D-lactate dehydrog	494	30	55.6	124	1	NRPG	pancreatic ribonuc
422	31	57.4	602	2	T19898	aryl hydrocarbon r	495	30	55.6	125	2	S40315	Ig kappa chain - h
423	31	57.4	605	2	D84687	hypothetical prote	496	30	55.6	128	2	B64764	hypothetical prote
424	31	57.4	650	2	G87883	protein C41G7.5 li	497	30	55.6	132	2	F97165	hypothetical prote
425	31	57.4	653	2	H96630	hypothetical prote	498	30	55.6	138	2	A26471	Ig kappa chain pre
426	31	57.4	661	2	S50734	WH13 protein - yea	499	30	55.6	148	2	F86615	cytosine deaminase
427	31	57.4	667	2	B96575	hypothetical prote	500	30	55.6	151	2	H90035	tear transcription
428	31	57.4	680	2	T39858	hypothetical prote	501	30	55.6	155	2	E72007	cytosine deaminase
429	31	57.4	683	1	Q0BEM8	gene 29 protein -	502	30	55.6	155	2	T07708	hypothetical prote
430	31	57.4	693	2	D90441	ABC transporter, p	503	30	55.6	158	2	A97262	uncharacterized co
431	31	57.4	715	2	B75135	DNA helicase relat	504	30	55.6	175	2	D90137	ubiquitin fusion d
432	31	57.4	765	2	S72278	ATP-dependent Clp	505	30	55.6	190	1	F90425	phosphoesterase-re
433	31	57.4	787	2	S54535	hypothetical prote	506	30	55.6	190	2	A86275	unknown protein -
434	31	57.4	802	2	AF1227	phenylalanyl-tRNA	507	30	55.6	207	2	H71168	probable flagellin
435	31	57.4	802	2	A13880	phenylalanyl-tRNA	508	30	55.6	208	2	C82927	hypothetical prote
436	31	57.4	835	1	P3XRSR	minor inner core p	509	30	55.6	221	2	T47592	hypothetical prote
437	31	57.4	860	2	T15778	hypothetical prote	510	30	55.6	227	2	F71898	hypothetical prote
438	31	57.4	876	2	A23767	myosin heavy chain	511	30	55.6	227	2	B64617	hypothetical prote
439	31	57.4	887	2	S57430	probable formate d	512	30	55.6	229	2	S39155	xyanase 2 - fungu
440	31	57.4	896	2	H86762	ABC transporter pe	513	30	55.6	229	2	AF2926	hypothetical prote
441	31	57.4	896	2	G96946	hypothetical prote	514	30	55.6	253	2	C81287	probable methyltra
442	31	57.4	939	2	C81730	metalloproteinase,	515	30	55.6	257	2	T29183	hypothetical prote
443	31	57.4	953	2	S55156	probable membrane	516	30	55.6	262	2	D82918	conserved hypot het
444	31	57.4	1009	2	C89910	hypothetical prote	517	30	55.6	263	2	JC5283	proomiomalocorti
445	31	57.4	1018	2	T30853	antigenic heat-ata	518	30	55.6	263	2	T16399	hypothetical prote
446	31	57.4	1022	2	E84792	probable kinesin h	519	30	55.6	266	2	S34943	nucM protein - Brw
447	31	57.4	1026	2	C97783	cell surface anti g	520	30	55.6	274	2	A54419	neutrophil inhibit
448	31	57.4	1036	2	B69368	hypothetical prote	521	30	55.6	277	2	B71160	probable methyl-ac
449	31	57.4	1040	2	AH1926	hypothetical prote	522	30	55.6	286	2	T38670	inorganic pyrophos
450	31	57.4	1058	2	T47525	kinesin-related pr	523	30	55.6	286	2	A38088	conserved hypot het
451	31	57.4	1076	2	F96831	hypothetical prote	524	30	55.6	288	2	T28209	triacylglycerol li
452	31	57.4	1083	2	T18298	hypothetical prote	525	30	55.6	303	2	AC0392	probable lysar-fami
453	31	57.4	1084	2	T18292	pyridine nucleotid	526	30	55.6	306	2	T50120	hypothetical prote
454	31	57.4	1124	2	G91055	nicotinamide nucle	527	30	55.6	307	2	AF2402	hypothetical prote
455	31	57.4	1124	2	C85900	hypothetical prote	528	30	55.6	308	2	H96827	protein F20B17.12
456	31	57.4	1124	2	D65032	hypothetical prote	529	30	55.6	308	2	C75097	hypothetical prote
457	31	57.4	1164	2	C86238	protein T10O24.5 (	530	30	55.6	309	2	S12986	phosphoprotein pho
458	31	57.4	1191	2	A53491	bumetanide-sensiti	531	30	55.6	311	2	D86409	hypothetical prote
459	31	57.4	1210	2	H84513	probable disease r	532	30	55.6	314	2	A71614	syntaxin PFB0480w
460	31	57.4	1225	2	T48928	disease resistance	533	30	55.6	315	2	D72229	phosphoribosyl pyr
461	31	57.4	1263	2	T15496	hypothetical prote	534	30	55.6	321	1	Q0BE04	G protein-coupled
462	31	57.4	1291	1	A48940	bontoxilysin (EC 3	535	30	55.6	323	2	F89845	hypothetical prote
463	31	57.4	1291	2	I40631	non-proteolytic bo	536	30	55.6	334	2	S52723	qpobB protein - Co
464	31	57.4	1335	2	AD2220	hypothetical prote	537	30	55.6	338	2	F90129	hypothetical prote
465	31	57.4	1696	2	T00057	hypothetical prote	538	30	55.6	339	1	KHRTB	cathepsin B (EC 3
466	31	57.4	2693	2	A40743	IP3 receptor, XIP3	539	30	55.6	346	2	T44327	hypothetical prote
467	31	57.4	2695	2	S54974	type 1 inositol 1,	540	30	55.6	346	2	AG3292	metA/colG/exbB pro

541	30	55.6	347	2	S40733	hypothetical prote	614	30	55.6	710	2	A25657	hypothetical prote
542	30	55.6	351	2	P61044	rod shape-determ	615	30	55.6	715	2	T211402	hypothetical prote
543	30	55.6	356	2	S71179	cinnamyl-alcohol d	616	30	55.6	720	2	T50475	hypothetical prote
544	30	55.6	357	2	A70188	TPR repeats contai	617	30	55.6	733	2	S61984	probable membrane
545	30	55.6	360	2	T08581	cinnamyl-alcohol d	618	30	55.6	764	2	S75407	probable DNA-direc
546	30	55.6	367	2	A82571	heat-inducible tra	619	30	55.6	771	2	T45967	hypothetical prote
547	30	55.6	373	2	S48915	hypothetical prote	620	30	55.6	791	2	E81906	probable ribonucle
548	30	55.6	374	2	H75002	methyl-accepting c	621	30	55.6	791	2	G81109	ribonuclease II fa
549	30	55.6	377	2	T21170	hypothetical prote	622	30	55.6	815	2	F71880	probable iron-regu
550	30	55.6	380	2	T47176	chymosin (EC 3.4.2	623	30	55.6	818	1	JC4397	peroxinectin precu
551	30	55.6	389	2	H90413	conserved hypoteth	624	30	55.6	844	2	C86339	protein F2D10.12 (
552	30	55.6	391	2	C69673	penicillin-binding	625	30	55.6	849	2	E82038	GGDEF family prote
553	30	55.6	403	2	T17501	major capsid-like	626	30	55.6	873	2	T25442	hypothetical prote
554	30	55.6	406	2	H83074	GTP-binding protei	627	30	55.6	878	2	I51940	gene VAV2 protein
555	30	55.6	412	2	T48405	myb-like protein -	628	30	55.6	889	2	E87304	tons-dependent rec
556	30	55.6	414	2	B96808	protein F28K19.2 (	629	30	55.6	897	2	T43628	phosphatidylinosit
557	30	55.6	421	2	A90003	hypothetical prote	630	30	55.6	905	2	E64058	hemopexin-heme com
558	30	55.6	425	2	G75361	glycolate oxidase,	631	30	55.6	911	1	HXADB3	hexon protein - bo
559	30	55.6	428	2	A43741	terminus protein -	632	30	55.6	919	2	S33942	hexon protein - hu
560	30	55.6	436	2	A69662	UDP-N-acetylglucos	633	30	55.6	923	1	HXAD40	hexon protein - hu
561	30	55.6	438	2	T45602	glucosyltransferas	634	30	55.6	925	1	TVHUBB	transforming prote
562	30	55.6	442	2	D71481	probable trigger f	635	30	55.6	925	1	HXAD41	hexon protein - hu
563	30	55.6	443	2	C70392	gamma-glutamyl pho	636	30	55.6	926	2	T24923	hypothetical prote
564	30	55.6	443	2	G90388	thermopsine precu	637	30	55.6	936	2	S57637	hexon protein - hu
565	30	55.6	457	2	C95017	peptidase, M20/M25	638	30	55.6	937	2	S55504	hexon protein - hu
566	30	55.6	457	2	D97890	succinyl-diaminopi	639	30	55.6	937	2	S39301	hexon protein - hu
567	30	55.6	461	2	B89972	fumarate hydratase	640	30	55.6	940	2	S37216	hexon protein - hu
568	30	55.6	462	2	AH1130	glutamate decarbox	641	30	55.6	942	2	S39298	hexon protein - hu
569	30	55.6	464	2	F89828	conserved hypoteth	642	30	55.6	1018	2	E64451	type I restriction
570	30	55.6	467	2	AB1379	glutamate decarbox	643	30	55.6	1023	2	AG3023	AcRb/AcrD/AcrF fam
571	30	55.6	467	2	AC1748	glutamate decarbox	644	30	55.6	1023	2	B98261	probable rnd efflu
572	30	55.6	471	1	S12732	6-phosphofructo-2-	645	30	55.6	1042	2	E95103	DNA polymerase III
573	30	55.6	471	2	D95356	probable amidase (	646	30	55.6	1042	2	C97971	DNA-directed DNA p
574	30	55.6	474	2	T50258	hypothetical coile	647	30	55.6	1049	2	B90124	second-largest sub
575	30	55.6	481	2	C71079	hypothetical prote	648	30	55.6	1058	2	T19282	hypothetical prote
576	30	55.6	482	2	AB1421	beta-glucosidase h	649	30	55.6	1088	2	D82246	probable chitinase
577	30	55.6	485	2	A96736	hypothetical prote	650	30	55.6	1107	1	JQ1658	genome polyprotein
578	30	55.6	491	2	C96585	hypothetical prote	651	30	55.6	1116	2	T30828	RNA-directed RNA p
579	30	55.6	495	2	F89818	lysyl-tRNA synthet	652	30	55.6	1165	2	T30731	probable DNA-direc
580	30	55.6	501	2	T06653	ammonium transport	653	30	55.6	1231	2	E90182	hypothetical prote
581	30	55.6	505	2	F71218	hypothetical prote	654	30	55.6	1268	2	S33411	botulinum neurotox
582	30	55.6	506	2	T41623	probable protein k	655	30	55.6	1297	2	S39791	neurotoxin - Clost
583	30	55.6	511	2	JH0173	alpha-bungarotoxin	656	30	55.6	1308	2	T05178	hypothetical prote
584	30	55.6	515	2	T43152	hypothetical prote	657	30	55.6	1338	2	T40993	protein kinase csk
585	30	55.6	534	2	S57974	hypothetical prote	658	30	55.6	1367	2	H82874	conserved hypoteth
586	30	55.6	541	1	WZEPY7	pectate lyase (EC	659	30	55.6	1433	1	A36734	bacillopeptidase F
587	30	55.6	552	2	S39297	fiber protein - hu	660	30	55.6	1433	2	A46053	bullous pemphigoid
588	30	55.6	557	2	A32694	interferon alpha/b	661	30	55.6	1581	2	T30832	pentafunctional en
589	30	55.6	560	2	S27387	interferon alpha r	662	30	55.6	1582	2	A56248	aulfonylurea recep
590	30	55.6	562	2	C64634	iron-regulated out	663	30	55.6	1740	2	T43215	ribonucleotide red
591	30	55.6	564	2	T41503	alpha-amylase - fi	664	30	55.6	1997	2	F71607	DNA helicase II BR
592	30	55.6	566	2	A72254	methyl-accepting c	665	30	55.6	2348	2	AD1841	hypothetical prote
593	30	55.6	572	2	AC0486	pectate lyase (EC	666	30	55.6	2391	2	G89779	hypothetical prote
594	30	55.6	573	2	E84687	hypothetical prote	667	30	55.6	2599	2	F90608	ABC transporter pe
595	30	55.6	575	2	B97188	phosphomannomutase	668	30	55.6	2895	2	H85382	hypothetical prote
596	30	55.6	579	2	T16237	hypothetical prote	669	30	55.6	3655	2	T38084	TRAP-like protein
597	30	55.6	590	2	A45283	interferon alpha/b	670	30	55.6	10797	2	T30152	probable peptide s
598	30	55.6	591	2	S50972	RIB2 protein - yea	671	29.5	54.6	327	2	S61660	probable membrane
599	30	55.6	593	2	D97806	penicillin-binding	672	29.5	54.6	442	2	C81370	probable thiophene
600	30	55.6	607	2	T40906	probable ATP-depen	673	29	53.7	51	2	D97830	hypothetical prote
601	30	55.6	619	2	S30780	hexose metabolism-	674	29	53.7	53	2	PH0881	Ig kappa chain V r
602	30	55.6	631	2	A64578	conserved hypoteth	675	29	53.7	62	2	H95154	hypothetical prote
603	30	55.6	634	2	T48418	ABC transporter-li	676	29	53.7	66	2	T37773	very hypotethical
604	30	55.6	640	2	B90590	hypothetical prote	677	29	53.7	72	2	T39894	integrin PS2 alpha
605	30	55.6	662	2	D54078	methyl-accepting c	678	29	53.7	77	2	C33335	hypothetical prote
606	30	55.6	672	1	KIHUCA	protein kinase C (	679	29	53.7	79	2	B90014	nonstructural prot
607	30	55.6	672	1	KINSCA	protein kinase C (	680	29	53.7	80	2	T03453	hypothetical prote
608	30	55.6	672	1	KINBC	protein kinase C (	681	29	53.7	86	2	S78488	Ig kappa chain V r
609	30	55.6	672	1	KIRTC	protein kinase C (	682	29	53.7	107	1	K1HUAR	Ig kappa chain V-I
610	30	55.6	692	2	B64381	hypothetical prote	683	29	53.7	107	2	C45722	anti-glycoprotein
611	30	55.6	692	2	T41240	hypothetical zinc	684	29	53.7	109	1	CCDBK	cytochrome c [vali
612	30	55.6	701	2	F90038	hypothetical prote	685	29	53.7	110	2	D70610	probable PS protei
613	30	55.6	710	2	T50469	hypothetical prote	686	29	53.7	115	1	K3HU15	Ig kappa chain pre

687	29	53.7	117	2	G70127	hypothetical prote	760	29	53.7	331	2	JN0886	ribose-phosphate d
688	29	53.7	118	2	C97092	probable transcrip	761	29	53.7	333	1	HLHUC	T-cell surface gly
689	29	53.7	121	2	AG2510	hypothetical prote	762	29	53.7	333	2	S76680	hypothetical prote
690	29	53.7	122	2	S40370	ig kappa chain - h	763	29	53.7	337	2	T06196	hypothetical prote
691	29	53.7	123	2	B97140	phage related tran	764	29	53.7	338	2	T19816	ferric anguibactin
692	29	53.7	124	2	B82444	hypothetical prote	765	29	53.7	341	2	G82880	protein containing
693	29	53.7	125	2	S04936	ig kappa chain pre	766	29	53.7	345	2	E97326	transcription regu
694	29	53.7	130	2	PL0113	ig kappa chain pre	767	29	53.7	346	2	E86715	protein FA0A5.26 (
695	29	53.7	130	2	S40368	ig kappa chain - h	768	29	53.7	346	2	F96785	type I restriction
696	29	53.7	132	2	S40334	ig kappa chain - h	769	29	53.7	348	2	E82933	hypothetical prote
697	29	53.7	132	2	C90131	hypothetical prote	770	29	53.7	348	2	T22065	hypothetical prote
698	29	53.7	134	2	T05469	heat shock protein	771	29	53.7	352	2	B84524	translation initia
699	29	53.7	141	2	B65057	hypothetical prote	772	29	53.7	353	2	C69863	glycoprotein gp41
700	29	53.7	144	2	F64004	hypothetical prote	773	29	53.7	354	1	WNV41	3-dehydroquinate s
701	29	53.7	156	2	G91210	hypothetical prote	774	29	53.7	354	2	A89925	probable permease
702	29	53.7	173	2	G89852	hypothetical prote	775	29	53.7	354	2	C82110	DNA repair protein
703	29	53.7	175	2	S29822	pancreatitis-assoc	776	29	53.7	354	2	T43507	hypothetical prote
704	29	53.7	175	2	G86845	H+-transporting tw	777	29	53.7	361	2	T13450	phosphoserine tran
705	29	53.7	176	1	F69370	conserved hypothet	778	29	53.7	362	2	S71439	acyl-CoA dehydroge
706	29	53.7	176	2	T47036	hypothetical prote	779	29	53.7	363	2	A81134	probable ABC trans
707	29	53.7	176	2	AP0234	fimbrial protein (	780	29	53.7	370	2	F95950	moxR-like ATPase (
708	29	53.7	183	2	A11562	hypothetical prote	781	29	53.7	373	2	S22635	ADP,ATP carrier pr
709	29	53.7	202	2	T06994	hypothetical prote	782	29	53.7	377	2	C97129	biz-1 protein - ba
710	29	53.7	206	2	A69712	mutants block spor	783	29	53.7	385	1	S29852	glycoprotein gp41
711	29	53.7	193	2	T28200	hypothetical prote	784	29	53.7	391	2	T04477	nuclear protein EM
712	29	53.7	194	2	T06993	proyestatin PR01 -	785	29	53.7	397	2	S36696	specificity determ
713	29	53.7	196	2	T32001	hypothetical prote	786	29	53.7	397	2	T09579	penicillin-binding
714	29	53.7	201	2	F83441	hypothetical prote	787	29	53.7	397	2	AC1498	tetracycline resis
715	29	53.7	202	2	T06994	proyestatin PR02 -	788	29	53.7	401	1	AB1142	yop targeting prot
716	29	53.7	206	2	A69712	hypothetical prote	789	29	53.7	401	1	YTEC70	specificity determ
717	29	53.7	207	2	T32331	gene 31 protein -	790	29	53.7	401	2	T43596	nitrogen fixation
718	29	53.7	208	1	Q8BEM9	hypothetical prote	791	29	53.7	401	2	AE1498	GP41/P40 orf80 - B
719	29	53.7	208	2	T42945	AT-rich DNA-bindin	792	29	53.7	402	2	D82890	hypothetical prote
720	29	53.7	214	2	H97233	ribosomal protein	793	29	53.7	403	2	T41823	probable zinc-meta
721	29	53.7	221	2	S53649	ATP-dependent Clp	794	29	53.7	405	2	C90194	zinc metalloprotei
722	29	53.7	224	2	A87094	hexon-associated p	795	29	53.7	407	2	D71862	hypothetical prote
723	29	53.7	224	2	D45574	hypothetical prote	796	29	53.7	407	2	F64567	occlusion-derived
724	29	53.7	226	2	G95247	hypothetical prote	797	29	53.7	409	2	T20847	hypothetical prote
725	29	53.7	227	2	C89808	exotoxin 15 (impor	798	29	53.7	409	2	A72860	hypothetical prote
726	29	53.7	228	2	C87184	conserved hypothet	799	29	53.7	409	2	T40633	exonuclease sbcd (
727	29	53.7	233	1	SDAD41	hexon-associated p	800	29	53.7	414	2	AF0389	protein T1N15.3 (i
728	29	53.7	242	2	S05453	transcription fact	801	29	53.7	414	2	D96524	hypothetical prote
729	29	53.7	246	2	D98112	hypothetical prote	802	29	53.7	414	2	B96905	UNP-N-acetylglucos
730	29	53.7	251	2	C97789	hypothetical prote	803	29	53.7	418	2	E97334	histidyl-tRNA synt
731	29	53.7	253	2	C97026	thioesterase II of	804	29	53.7	425	2	AH1284	Carbon catabolite
732	29	53.7	256	2	H83002	imidazoleglycerol-	805	29	53.7	425	2	A70394	hypothetical prote
733	29	53.7	256	2	F80255	conserved hypothet	806	29	53.7	427	2	JN0785	hypothetical prote
734	29	53.7	257	2	F82499	hypothetical prote	807	29	53.7	427	2	AE2512	hypothetical prote
735	29	53.7	258	2	H75027	sy v-atpase proteo	808	29	53.7	429	2	F66240	hypothetical prote
736	29	53.7	260	1	CTXLPB	corticotropin / li	809	29	53.7	436	2	D64028	methyl-accepting c
737	29	53.7	261	2	AD0171	probable methyltra	810	29	53.7	441	2	B96953	tryptophan 5-monoo
738	29	53.7	264	1	C70470	myo-inositol-1(or	811	29	53.7	444	2	S51199	cysteine aminopept
739	29	53.7	266	2	AB1827	hypothetical prote	812	29	53.7	445	2	S48143	probable proteinase
740	29	53.7	276	2	D41044	octopine-binding p	813	29	53.7	451	2	C81820	probable DNA-bindi
741	29	53.7	278	2	D96513	unknown protein, 6	814	29	53.7	452	2	S46054	replication initia
742	29	53.7	290	2	D90075	intercellular adhe	815	29	53.7	460	2	E86529	chromosomal replic
743	29	53.7	292	2	S25818	hypothetical prote	816	29	53.7	460	2	F72052	cruciferin 4 precu
744	29	53.7	292	2	D91229	probable aldolase	817	29	53.7	465	1	S14762	glutamate decarbox
745	29	53.7	293	2	T09758	probable aldolase	818	29	53.7	466	2	B86786	probable outer mem
746	29	53.7	296	2	A34543	myb-related protei	819	29	53.7	467	2	F81825	multidrug efflux p
747	29	53.7	300	2	F71616	spectact precursor	820	29	53.7	467	2	D81051	Na+/H+-exchanging
748	29	53.7	300	2	D64436	RNA-binding protei	821	29	53.7	468	2	L64182	probable pap2 pro
749	29	53.7	310	2	S52504	nifB homolog - Met	822	29	53.7	468	2	H70521	penicillin-binding
750	29	53.7	312	2	QJ1318	probable membrane	823	29	53.7	473	2	S36241	hypothetical prote
751	29	53.7	314	2	E84970	pectin lyase (EC 4	824	29	53.7	474	2	S73677	hypothetical prote
752	29	53.7	315	2	S76596	pseudouridylate sy	825	29	53.7	474	2	T31064	hypothetical prote
753	29	53.7	319	2	S06367	hypothetical prote	826	29	53.7	481	2	AB1927	hypothetical prote
754	29	53.7	320	2	G97016	ND1 intron 1 prote	827	29	53.7	481	2	A70091	probable phosphoe
755	29	53.7	324	2	AD1631	comE-like protein,	828	29	53.7	487	2	B95059	hypothetical prote
756	29	53.7	325	2	C90282	delta-aminolevulin	829	29	53.7	487	2	A97928	type I site-specif
757	29	53.7	328	2	C97268	hypothetical prote	830	29	53.7	487	2	E83120	probable outer mem
758	29	53.7	331	2	B64545	uncharacterized pr	831	29	53.7	487	2	A30909	bactericidal/perme
759	29	53.7	331	2	C71962	beta-ketoacyl-acyl	832	29	53.7	497	2	E90061	hypothetical prote

833	29	53.7	507	2	JC7855	pyridoxine 4-oxida	906	29	53.7	971	2	T43656	matng-type switch
834	29	53.7	511	2	F70110	conserved hypothet	907	29	53.7	982	1	VCLJVS	env polyprotein pr
835	29	53.7	513	2	S58200	probable membrane	908	29	53.7	983	1	E45390	env polyprotein pr
836	29	53.7	514	2	AB0120	conserved hypothet	909	29	53.7	1032	2	B86224	hypothetical prote
837	29	53.7	520	2	T18124	probable capsid pr	910	29	53.7	1035	2	G97273	isoleucyl-tRNA syn
838	29	53.7	526	2	E71422	hypothetical prote	911	29	53.7	1036	2	E96682	hypothetical prote
839	29	53.7	529	2	T27922	hypothetical prote	912	29	53.7	1046	2	S39630	multidrug-efflux t
840	29	53.7	540	2	T49074	hypothetical prote	913	29	53.7	1046	2	E83593	RND multidrug effl
841	29	53.7	543	2	T16015	hypothetical prote	914	29	53.7	1077	2	A44067	serine-rich protei
842	29	53.7	544	2	A98591	hypothetical prote	915	29	53.7	1104	1	A36866	microbial collagen
843	29	53.7	546	2	T25257	hypothetical prote	916	29	53.7	1105	2	C87622	T0NB-dependent rec
844	29	53.7	549	2	T16016	hypothetical prote	917	29	53.7	1114	2	T30819	RNA-directed RNA p
845	29	53.7	550	1	FGRTA	fibrinogen alpha c	918	29	53.7	1119	2	T15842	hypothetical prote
846	29	53.7	552	2	A41035	chitinase (EC 3.2.	919	29	53.7	1140	2	S73786	hypothetical prote
847	29	53.7	560	2	AD2389	serine/threonine.k	920	29	53.7	1148	2	T00016	minor outer capsid
848	29	53.7	562	2	A41035	chitinase (EC 3.2.	921	29	53.7	1163	2	I56126	lymphocyte function
849	29	53.7	562	2	S50371	chitinase (EC 3.2.	922	29	53.7	1188	2	T13933	pol polyprotein -
850	29	53.7	569	2	G95418	probable KdPA pota	923	29	53.7	1206	2	A64207	hypothetical prote
851	29	53.7	574	1	VGNZHB	cell fusion glycop	924	29	53.7	1238	2	AH0038	probable exported
852	29	53.7	577	2	S64250	probable membrane	925	29	53.7	1263	2	T19472	hypothetical prote
853	29	53.7	579	2	AD1664	adenine deaminases	926	29	53.7	1274	2	I40813	neurotoxin type F
854	29	53.7	579	2	T01160	hypothetical prote	927	29	53.7	1275	2	T33369	hypothetical prote
855	29	53.7	580	2	AF1292	adenine deaminases	928	29	53.7	1284	2	T40578	hypothetical prote
856	29	53.7	584	2	S62198	formylmethanofuran	929	29	53.7	1303	2	E96805	hypothetical prote
857	29	53.7	587	1	E69171	phosphoesterase-re	930	29	53.7	1339	2	A55301	1,3-beta-D-glucan-
858	29	53.7	601	2	T21329	hypothetical prote	931	29	53.7	1449	2	T20181	hypothetical prote
859	29	53.7	603	2	C90426	phosphoenolpyruvat	932	29	53.7	1502	1	RGBYH1	CYC1/CFP3 transcri
860	29	53.7	608	2	S51790	centromere protein	933	29	53.7	1571	2	T14155	zinc finger protei
861	29	53.7	609	2	F90160	membrane conserved	934	29	53.7	1584	2	T20180	hypothetical prote
862	29	53.7	649	2	T47609	hypothetical prote	935	29	53.7	1586	2	T20179	hypothetical prote
863	29	53.7	649	2	T39826	probable clathrin	936	29	53.7	1638	2	T25352	hypothetical prote
864	29	53.7	651	2	A96591	NPXI-related prote	937	29	53.7	1670	2	T06754	DNA-directed RNA p
865	29	53.7	655	2	A12556	hypothetical prote	938	29	53.7	1737	2	T17101	probable voltage-a
866	29	53.7	655	2	A57681	hypothetical prote	939	29	53.7	1747	2	AC1842	WD-40 repeat prote
867	29	53.7	660	1	G6BPT4	baseplate protein	940	29	53.7	1854	2	T35766	hypothetical prote
868	29	53.7	663	2	S67259	MNEI protein - yea	941	29	53.7	1857	2	T50513	hypothetical prote
869	29	53.7	679	2	A83488	hypothetical prote	942	29	53.7	1950	2	S12332	ubiquitin-protein
870	29	53.7	681	2	F71814	probable ATP-depen	943	29	53.7	2076	2	T28915	genome polyprotein
871	29	53.7	682	2	F64704	DNA helicase II -	944	29	53.7	2156	1	RRVUNE	acetyl-CoA carboxy
872	29	53.7	686	2	D96930	methyl-accepting c	945	29	53.7	2288	2	T30568	hypothetical prote
873	29	53.7	718	2	C53292	penicillin-binding	946	29	53.7	2523	2	T18477	hypothetical prote
874	29	53.7	720	2	S73267	phenylalanine-tRNA	947	29	53.7	2670	2	A46719	inositol 1,4,5-tri
875	29	53.7	743	2	A29232	101K malaria anti	948	29	53.7	2671	2	A49873	inositol 1,4,5-tri
876	29	53.7	792	1	A24050	ribonucleoside-dip	949	29	53.7	2701	2	S17796	inositol-triphosph
877	29	53.7	792	2	S16680	ribonucleoside-dip	950	29	53.7	3839	2	T49799	related to TOM1 pr
878	29	53.7	796	2	A97731	bifunctional penic	951	28.5	52.8	350	2	AD1749	internalin protein
879	29	53.7	801	2	A47744	diacylglycerol kin	952	28.5	52.8	425	2	D71965	apolipoprotein n-a
880	29	53.7	809	2	S67665	ubiquitin-specific	953	28.5	52.8	512	2	G96753	Similar to disease
881	29	53.7	825	2	H82885	hypothetical prote	954	28.5	52.8	944	2	S26710	spindle pole body
882	29	53.7	827	2	S25949	gene coxII intron	955	28.5	52.8	1173	2	T43527	sp8 protein - flas
883	29	53.7	834	1	QXB31	gene coxI intron 1	956	28.5	52.8	1727	2	T50073	myosin-like coiled
884	29	53.7	834	2	S78642	invasin - Yersinia	957	28	51.9	21	2	A60684	L-ascorbate peroxi
885	29	53.7	835	1	S54216	invasin - Yersinia	958	28	51.9	47	2	S54221	flagellar hook for
886	29	53.7	835	2	S11442	invasin - Yersinia	959	28	51.9	57	2	A60516	pepsin A (EC 3.4.2
887	29	53.7	839	2	S35319	nucleoporin-intera	960	28	51.9	57	2	B89981	truncated transpos
888	29	53.7	862	2	D70199	DNA mismatch repai	961	28	51.9	62	2	C49570	plasma membrane ca
889	29	53.7	866	2	T23551	hypothetical prote	962	28	51.9	66	2	T16820	hypothetical prote
890	29	53.7	878	2	S42707	preprotein translo	963	28	51.9	86	2	S16825	ig kappa chain v r
891	29	53.7	885	2	T71608	ATP-dept. acyl-CoA	964	28	51.9	86	2	S16840	ig kappa chain v r
892	29	53.7	889	2	T11742	egg sperm receptor	965	28	51.9	87	2	AH1828	hypothetical prote
893	29	53.7	900	2	C64232	alanine-tRNA ligas	966	28	51.9	91	2	E86183	hypothetical prote
894	29	53.7	905	2	T38980	hypothetical prote	967	28	51.9	92	2	S37504	ig kappa chain v r
895	29	53.7	920	2	T43263	cell division prot	968	28	51.9	98	2	S41813	ig kappa chain v r
896	29	53.7	925	2	D59105	hypothetical prote	969	28	51.9	98	2	PH1083	ig light chain v r
897	29	53.7	930	2	D71617	SERA antigen/papai	970	28	51.9	98	2	T32160	hypothetical prote
898	29	53.7	940	2	S49087	lactoferrin-bindin	971	28	51.9	100	2	T13176	hypothetical prote
899	29	53.7	943	2	C81070	lactoferrin-bindin	972	28	51.9	105	2	E97862	hypothetical prote
900	29	53.7	944	2	C81798	lactoferrin-bindin	973	28	51.9	106	2	S26345	ig light chain v r
901	29	53.7	946	1	A29550	methylentetrahidr	974	28	51.9	109	1	K1HUBN	ig kappa chain v-I
902	29	53.7	956	2	B71468	probable insulinas	975	28	51.9	109	2	S31619	Gene X protein - B
903	29	53.7	964	2	T21865	hypothetical prote	976	28	51.9	110	2	PN0535	ig kappa chain v r
904	29	53.7	966	2	D96662	hypothetical prote	977	28	51.9	113	2	C90083	hypothetical prote
905	29	53.7	971	2	T39912	conserved hypothet	978	28	51.9	115	1	K3HUCU	ig kappa chain pre

979 28 51.9 115 2 A30553 Ig kappa chain pre  
980 28 51.9 117 1 K1HU12 Ig kappa chain pre  
981 28 51.9 117 2 S41812 Ig kappa chain V r  
982 28 51.9 117 2 S10227 Ig kappa chain pre  
983 28 51.9 119 2 D97127 probable transcript  
984 28 51.9 121 2 G90550 hypothetical prote  
985 28 51.9 124 1 NRCM pancreatic ribonuc  
986 28 51.9 124 1 NRCMB pancreatic ribonuc  
987 28 51.9 124 1 NRCMW pancreatic ribonuc  
988 28 51.9 125 2 S40333 Ig kappa chain V-J  
989 28 51.9 127 2 S04574 Ig kappa chain pre  
990 28 51.9 129 2 S29627 Ig kappa chain V r  
991 28 51.9 130 1 WRBPF5 early protein gpl5  
992 28 51.9 130 2 JC2506 colonic lysozyme 2  
993 28 51.9 142 2 F64033 hypothetical prote  
994 28 51.9 142 2 T45803 hypothetical prote  
995 28 51.9 146 2 S60700 gag protein - huma  
996 28 51.9 146 2 S60697 gag protein - huma  
997 28 51.9 146 2 S60708 gag protein - huma  
998 28 51.9 146 2 S60699 gag protein - huma  
999 28 51.9 148 2 T32810 hypothetical prote  
1000 28 51.9 154 2 AC2062 two-component resp

## ALIGNMENTS

RESULT 1  
S42265  
Ig kappa chain V region (018) - human  
C:Species: Homo sapiens (man)  
C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 17-Mar-1999  
C:Accession: S42265  
R:Scott, M.G.; Crimmins, D.L.; McCourt, D.W.; Chung, G.; Schaeble, K.F.; Thiebs, R.; Que  
J. Immunol. 147, 4007-4013, 1991  
A:Title: Clonal characterization of the human IgG antibody repertoire to Haemophilus inf  
A:Reference number: S42263; MUID:92043792; PMID:1940382  
A:Accession: S42265  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-62 <SCO>  
A:Cross-references: UNIPARC:UPI0000176D84; EMBL:M64856  
C:Genetics:  
A:Introns: 19/1  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin

Query Match 92.6%; Score 50; DB 2; Length 62;  
Best Local Similarity 100.0%; Pred. No. 0.03;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ASQDISNYLN 11  
Db 25 ASQDISNYLN 34  
RESULT 2  
I52592  
Ig kappa chain V region - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 21-Jan-2000  
C:Accession: I52592  
R:Wagner, S.D.; Martinelli, V.; Luzzatto, L.  
Blood 83, 3647-3653, 1994  
A:Title: Similar patterns of V kappa gene usage but different degrees of somatic mutat  
A:Reference number: I52592; MUID:94264318; PMID:8204889  
A:Accession: I52592  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-87 <RES>  
A:Cross-references: UNIPARC:UPI0000113P67; GB:S71057; NID:9547053; PIDN:AAB30971.1; PID:  
C:Genetics:  
A:Gene: IGKV

C:Superfamily: immunoglobulin V region; immunoglobulin homology  
F:9-83/Domain: immunoglobulin homology <IMM>

Query Match 92.6%; Score 50; DB 2; Length 87;  
Best Local Similarity 100.0%; Pred. No. 0.041;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ASQDISNYLN 11  
Db 18 ASQDISNYLN 27

## RESULT 3

S34087  
Ig kappa chain V region - human  
C:Species: Homo sapiens (man)  
C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 21-Jan-2000  
C:Accession: S34087  
R:Wagner, S.D.; Luzzatto, L.  
Eur. J. Immunol. 23, 391-397, 1993  
A:Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distribute  
A:Reference number: S34076; MUID:93170387; PMID:8436174  
A:Accession: S34087  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-88 <WAG>  
A:Cross-references: UNIPARC:UPI0000176D9B; EMBL:X67171  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:9-83/Domain: immunoglobulin homology <IMM>

Query Match 92.6%; Score 50; DB 2; Length 88;  
Best Local Similarity 100.0%; Pred. No. 0.042;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ASQDISNYLN 11  
Db 18 ASQDISNYLN 27

## RESULT 4

S34088  
Ig kappa chain V region - human  
C:Species: Homo sapiens (man)  
C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 21-Jan-2000  
C:Accession: S34088  
R:Wagner, S.D.; Luzzatto, L.  
Eur. J. Immunol. 23, 391-397, 1993  
A:Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distribute  
A:Reference number: S34076; MUID:93170387; PMID:8436174  
A:Accession: S34088  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-88 <WAG>  
A:Cross-references: UNIPARC:UPI0000176D9A; EMBL:X67172  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:9-83/Domain: immunoglobulin homology <IMM>

Query Match 92.6%; Score 50; DB 2; Length 88;  
Best Local Similarity 100.0%; Pred. No. 0.042;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ASQDISNYLN 11  
Db 18 ASQDISNYLN 27

## RESULT 5

S38564  
Ig kappa chain V region (ASWU1) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 21-Jan-2000

C;Accession: S38564  
R;Monestier, M.; Lozman, L.J.; Novick, K.E.; Aris, J.P.  
submitted to the EMBL Data Library, September 1993  
A;Description: Molecular analysis of mercury-induced anti-nucleolar antibodies in H-2a M  
A;Reference number: S38559  
A;Accession: S38564  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-93 <NON>  
A;Cross-references: UNIPARC:UPI00001161CA; EMBL:X75105; NID:g414153; PIDN:CAA52996.1; PI  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: immunoglobulin  
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 92.6%; Score 50; DB 2; Length 93;  
Best Local Similarity 100.0%; Pred. No. 0.044;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ASQDISNYLN 11  
|||||  
Db 25 ASQDISNYLN 34

RESULT 6  
PH0862  
Ig kappa chain V region (anti-DNA, III-3R) - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 09-Oct-1992 #sequence\_revision 09-Oct-1992 #text\_change 21-Jan-2000  
C;Accession: PH0862  
R;Manheimer-Lory, A.; Katz, J.B.; Pillinger, M.; Grossein, C.; Smith, A.; Diamond, B.  
J. Exp. Med. 174, 1639-1652, 1991  
A;Title: Molecular characteristics of antibodies bearing an anti-DNA-associated idiotype  
A;Reference number: PH0862; MUID:92078875; PMID:1660528  
A;Accession: PH0862  
A;Molecule type: DNA  
A;Residues: 1-95 <MAN>  
A;Cross-references: UNIPARC:UPI0000176D9C  
C;Comment: This antibody is produced by Epstein-Barr virus-transformed B cell that bears  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;1-23/Region: framework 1  
F;16-90/Domain: immunoglobulin homology <IMM>  
F;24-34/Region: complementarity-determining 1  
F;35-49/Region: framework 2  
F;50-56/Region: complementarity-determining 2  
F;57-88/Region: framework 3  
F;89-95/Region: complementarity-determining 3

Query Match 92.6%; Score 50; DB 2; Length 95;  
Best Local Similarity 100.0%; Pred. No. 0.045;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ASQDISNYLN 11  
|||||  
Db 25 ASQDISNYLN 34

RESULT 7  
S69901  
Ig kappa chain (clone KL2.21) - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 14-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 21-Jan-2000  
C;Accession: S69901  
R;Wysocki, L.J.; Creighton, G.; Lehmann, K.R.; Cambier, J.C.  
Immunology 75, 116-121, 1992  
A;Title: B-cell proliferation initiated by Ia cross-linking and sustained by interleukin  
A;Reference number: S69900; MUID:92165291; PMID:1537587  
A;Accession: S69901  
A;Status: preliminary; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-107 <WYS>  
A;Cross-references: UNIPARC:UPI0000115EA4; EMBL:X55042; NID:g511025; PIDN:CAA38882.1; PI  
C;Superfamily: immunoglobulin V region; immunoglobulin homology

F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 92.6%; Score 50; DB 2; Length 107;  
Best Local Similarity 100.0%; Pred. No. 0.051;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ASQDISNYLN 11  
|||||  
Db 25 ASQDISNYLN 34

RESULT 8  
A28044  
Ig kappa chain V region (2B5) - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 19-May-1989 #sequence\_revision 19-May-1989 #text\_change 21-Jan-2000  
C;Accession: A28044  
R;Meek, K.; Sanz, I.; Rathbun, G.; Nisonoff, A.; Capra, J.D.  
Proc. Natl. Acad. Sci. U.S.A. 84, 6244-6248, 1987  
A;Title: Identity of the V-kappa-10-Ars-A gene segments of the A/J and BALB/c strains.  
A;Reference number: A94179; MUID:87317629; PMID:3114744  
A;Accession: A28044  
A;Molecule type: mRNA  
A;Residues: 1-107 <MEB>  
A;Cross-references: UNIPARC:UPI0000176B2A  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 92.6%; Score 50; DB 2; Length 107;  
Best Local Similarity 100.0%; Pred. No. 0.051;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ASQDISNYLN 11  
|||||  
Db 25 ASQDISNYLN 34

RESULT 9  
D48677  
Ig kappa chain V-J region (24) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 19-May-1994 #sequence\_revision 19-May-1994 #text\_change 21-Jan-2000  
C;Accession: D48677  
R;Tassignon, J.; Brait, M.; Jamila, I.; Urbain, J.; Gottlieb, P.; Brown, A.; Hasemann, C.  
Proc. Natl. Acad. Sci. U.S.A. 90, 9508-9512, 1993  
A;Title: Molecular characterization of monoclonal CRI-A-positive anti-arsonate antibodies  
A;Reference number: A48677; MUID:94022404; PMID:8415731  
A;Accession: D48677  
A;Status: preliminary; not compared with conceptual translation  
A;Molecule type: mRNA  
A;Residues: 1-107 <TAS>  
A;Cross-references: UNIPARC:UPI0000176CBF  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: immunoglobulin  
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 92.6%; Score 50; DB 2; Length 107;  
Best Local Similarity 100.0%; Pred. No. 0.051;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ASQDISNYLN 11  
|||||  
Db 25 ASQDISNYLN 34

RESULT 10  
B28044  
Ig kappa chain V region (GP1) - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 19-May-1989 #sequence\_revision 19-May-1989 #text\_change 21-Jan-2000  
C;Accession: B28044  
R;Meek, K.; Sanz, I.; Rathbun, G.; Nisonoff, A.; Capra, J.D.



Proc. Natl. Acad. Sci. U.S.A. 84, 6244-6248, 1987  
A>Title: Identity of the V-kappa-10-Ars-A gene segments of the A/J and BALB/c strains.  
A/Reference number: A94179; MUID:87317629; PMID:3114744  
A/Accession: B28044  
A/Molecule type: mRNA  
A/Residues: 1-107 <ME>  
A/Cross-references: UNIPARC:UPI0000176B29  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F:16-90/Domain: immunoglobulin homology <IMM>  
  
Query Match 92.6%; Score 50; DB 2; Length 107;  
Best Local Similarity 100.0%; Pred. No. 0.051;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 2 ASQDISNYLN 11  
Db 25 ASQDISNYLN 34  
|||||  
|  
RESULT 11  
B49026  
Ig kappa chain V region, anti-idiotypic monoclonal antibody - mouse  
C/Species: Mus musculus (house mouse)  
C/Date: 19-Dec-1993 #sequence\_revision 18-Nov-1994 #text\_change 21-Jan-2000  
C/Accession: B49026; PL0220  
R/Koizumi, T.; Puccetti, A.; Migliorini, P.; Barrett, K.J.; Schwartz, R.S.  
Eur. J. Immunol. 21, 2185-2193, 1991  
A>Title: Molecular heterogeneity of auto-anti-idiotypic antibodies in MRL-lpr/lpr mice.  
A/Reference number: A49026; MUID:91364791; PMID:1903645  
A/Accession: B49026  
A/Status: preliminary; not compared with conceptual translation  
A/Molecule type: nucleic acid  
A/Residues: 1-107 <KO>  
A/Cross-references: UNIPARC:UPI0000176D3F  
A/Experimental source: MRL-lpr/lpr  
A/Note: sequence extracted from NCBI backbone (NCBIP:60876)  
R/Puccetti, A.; Koizumi, T.; Migliorini, P.; Andre-Schwartz, J.; Barrett, K.J.; Schwartz  
J. Exp. Med. 171, 1919-1930, 1990  
A>Title: An immunoglobulin light chain from a lupus-prone mouse induces autoantibodies 1  
A/Reference number: PL0220; MUID:90278348; PMID:1693654  
A/Accession: PL0220  
A/Status: nucleic acid sequence not shown  
A/Molecule type: mRNA  
A/Residues: 1-107 <PO>  
A/Cross-references: UNIPARC:UPI0000176D3F  
A/Experimental source: strain lupus-prone MRL-lpr/lpr mouse  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F:16-90/Domain: immunoglobulin homology <IMM>  
F:24-34/Region: complementarity-determining 1  
F:50-56/Region: complementarity-determining 2  
F:89-97/Region: complementarity-determining 3  
  
Query Match 92.6%; Score 50; DB 2; Length 107;  
Best Local Similarity 100.0%; Pred. No. 0.051;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 2 ASQDISNYLN 11  
Db 25 ASQDISNYLN 34  
|||||  
|  
RESULT 12  
S69906  
Ig kappa chain (clone KL4A1) - mouse  
C/Species: Mus musculus (house mouse)  
C/Date: 14-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 21-Jan-2000  
C/Accession: S69906  
R/Wysocki, L.J.; Creighton, G.; Lehmann, K.R.; Cambier, J.C.  
Immunology 75, 116-121, 1992  
A>Title: B-cell proliferation initiated by Ia cross-linking and sustained by interleukin  
A/Reference number: S69906; MUID:92165291; PMID:1537587

A/Accession: S69906  
A/Status: preliminary; translation not shown  
A/Molecule type: DNA  
A/Residues: 1-107 <WYS>  
A/Cross-references: UNIPARC:UPI0000115EA6; EMBL:X55047; NID:G511035; PIDN:CAA38887.1; PI  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
F:16-90/Domain: immunoglobulin homology <IMM>  
  
Query Match 92.6%; Score 50; DB 2; Length 107;  
Best Local Similarity 100.0%; Pred. No. 0.051;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 2 ASQDISNYLN 11  
Db 25 ASQDISNYLN 34  
|||||  
|  
RESULT 13  
KWMSAR  
Ig kappa chain V regions (anti-arsenate hybridoma proteins) - mouse  
C/Species: Mus musculus (house mouse)  
C/Date: 06-Jul-1982 #sequence\_revision 06-Jul-1982 #text\_change 09-Jul-2004  
C/Accession: A01927  
R/Siegelman, M.; Capra, J.D.  
Proc. Natl. Acad. Sci. U.S.A. 78, 7679-7683, 1981  
A>Title: Complete amino acid sequence of light chain variable regions derived from five  
A/Reference number: A01927; MUID:82150934; PMID:6801658  
A/Accession: A01927  
A/Molecule type: protein  
A/Residues: 1-108 <SIE>  
A/Cross-references: UNIPROT:P01644; UNIPARC:UPI000002A0C5  
A/Experimental source: strain A/J  
A/Note: HP 93G7 differs in having 93-Met; HP 123E6 differs in having 7-Ser, 92-Tyr, and  
Arg, 84-Ser, and 93-Ala  
C/Comment: The sequence shown is HP R16.7.  
C/Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa)  
chain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into la  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer  
F:16-90/Domain: immunoglobulin homology <IMM>  
F:23-88/Disulfide bonds: #status Predicted  
  
Query Match 92.6%; Score 50; DB 1; Length 108;  
Best Local Similarity 100.0%; Pred. No. 0.051;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 2 ASQDISNYLN 11  
Db 25 ASQDISNYLN 34  
|||||  
|  
RESULT 14  
PL0282  
Ig kappa chain V region (45-49, anti p-azophenylarsonate) - mouse (fragment)  
C/Species: Mus musculus (house mouse)  
C/Date: 24-Feb-1994 #sequence\_revision 24-Feb-1994 #text\_change 21-Jan-2000  
C/Accession: PL0282  
R/Wysocki, L.J.; Gelfer, M.L.; Margolies, M.N.  
J. Exp. Med. 172, 315-323, 1990  
A>Title: Parallel evolution of antibody variable regions by somatic processes: Consecuti  
Y point mutation and selection rather than by gene conversion.  
A/Reference number: PL0281; MUID:90293694; PMID:2358780  
A/Accession: PL0282  
A/Molecule type: mRNA  
A/Residues: 1-108 <WYS>  
A/Cross-references: UNIPARC:UPI0000176B45  
A/Experimental source: A/J mice  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: immunoglobulin  
F:16-90/Domain: immunoglobulin homology <IMM>  
  
Query Match 92.6%; Score 50; DB 2; Length 108;  
Best Local Similarity 100.0%; Pred. No. 0.051;



Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASQDISNYLN 11  
|||||  
Db 25 ASQDISNYLN 34

RESULT 15  
C26405  
Ig kappa chain V region (3D10) - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 30-Jun-1988 #sequence\_revision 30-Jun-1988 #text\_change 21-Jan-2000  
C:Accession: C26405  
R:Smith, J.A.; Margolies, M.N.  
Biochemistry 26, 604-612, 1987  
A:Title: Complete amino acid sequences of the heavy and light chain variable regions from

A:Reference number: A90518; MUID:87157677; PMID:3103682  
A:Accession: C26405  
A:Molecule type: protein  
A:Residues: 1-108 <SMI>  
A:Cross-references: UNIPARC:UPI00001769E9  
A:Experimental source: strain A/J  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 92.6%; Score 50; DB 2; Length 108;  
Best Local Similarity 100.0%; Pred. No. 0.051;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASQDISNYLN 11  
|||||  
Db 25 ASQDISNYLN 34

RESULT 16  
S38862  
Ig kappa chain V region - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 06-Feb-1995 #sequence\_revision 06-Feb-1995 #text\_change 21-Jan-2000  
C:Accession: S38862  
R:Fischer, R.; Voss, A.; Hunziker, W.; Stierhof, Y.D.; Kreuzaler, F.  
submitted to the EMBL Data Library, August 1993  
A:Description: Production and cloning of TMV-specific monoclonal antibodies.  
A:Reference number: S37200  
A:Accession: S38862  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-108 <FIS>  
A:Cross-references: UNIPARC:UPI00001161D1; EMBL:X75854; NID:g429110; PID:g429110  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 92.6%; Score 50; DB 2; Length 108;  
Best Local Similarity 100.0%; Pred. No. 0.051;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASQDISNYLN 11  
|||||  
Db 25 ASQDISNYLN 34

RESULT 17  
S69902  
Ig kappa chain (clone KL2.28) - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 14-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 21-Jan-2000  
C:Accession: S69902  
R:Wysocki, L.J.; Creadon, G.; Lehmann, K.R.; Cambier, J.C.  
Immunology 75, 116-121, 1992  
A:Title: B-cell proliferation initiated by Ia cross-linking and sustained by interleukin

A:Reference number: S69900; MUID:92165291; PMID:1537587  
A:Accession: S69902  
A>Status: preliminary; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-108 <WYS>  
A:Cross-references: UNIPARC:UPI0000115EA5; EMBL:X55043; NID:g511027; PIDN:CAA38883.1; PI  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 92.6%; Score 50; DB 2; Length 108;  
Best Local Similarity 100.0%; Pred. No. 0.051;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASQDISNYLN 11  
|||||  
Db 25 ASQDISNYLN 34

RESULT 18  
S69900  
Ig kappa chain (clone KL2.18 / KL4B10 / KL4C11) - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 14-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 21-Jan-2000  
C:Accession: S69900; S69907; S69908  
R:Wysocki, L.J.; Creadon, G.; Lehmann, K.R.; Cambier, J.C.  
Immunology 75, 116-121, 1992  
A:Title: B-cell proliferation initiated by Ia cross-linking and sustained by interleukin  
A:Reference number: S69900; MUID:92165291; PMID:1537587  
A:Accession: S69900  
A>Status: preliminary; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-108 <WYS>  
A:Cross-references: UNIPARC:UPI0000115EA3; EMBL:X55041; NID:g511023; PIDN:CAA38881.1; PI  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 92.6%; Score 50; DB 2; Length 108;  
Best Local Similarity 100.0%; Pred. No. 0.051;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASQDISNYLN 11  
|||||  
Db 25 ASQDISNYLN 34

RESULT 19  
S69903  
Ig kappa chain (clone KL2.29 / KL2.33 / KL3.8) - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 14-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 21-Jan-2000  
C:Accession: S69903; S69904; S69905  
R:Wysocki, L.J.; Creadon, G.; Lehmann, K.R.; Cambier, J.C.  
Immunology 75, 116-121, 1992  
A:Title: B-cell proliferation initiated by Ia cross-linking and sustained by interleukin  
A:Reference number: S69900; MUID:92165291; PMID:1537587  
A:Accession: S69903  
A>Status: preliminary; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-108 <WYS>  
A:Cross-references: UNIPARC:UPI0000115227; EMBL:X55044; NID:g511029; PIDN:CAA38884.1; PI  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 92.6%; Score 50; DB 2; Length 108;  
Best Local Similarity 100.0%; Pred. No. 0.051;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASQDISNYLN 11  
|||||  
Db 25 ASQDISNYLN 34



submitted to the EMBL Data Library, December 1991

A:Reference number: S43528  
A:Accession: S43528  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-117 <SCO>  
A:Cross-references: UNIPARC:UPI0000113B52; EMBL:M64856  
C:Genetics: 19/1  
A:introns: 19/1  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
F:38-112/Domain: immunoglobulin homology <IMM>

Query Match 92.6%; Score 50; DB 2; Length 117;  
Best Local Similarity 100.0%; Pred. No. 0.056; 0; Mismatches 0; Indels 0; Gaps 0;  
Matches 10; Conservative 0;

QY 2 ASQDISNYLN 11  
|||||  
Db 47 ASQDISNYLN 56

## RESULT 25

A26406  
Ig kappa chain V region (Ars-A) - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 30-Jun-1995 #sequence\_revision 30-Jun-1991 #text\_change 09-Jul-2004  
A:Accession: A26406  
R:Sanz, I.; Capra, J.D.  
Proc. Natl. Acad. Sci. U.S.A. 84, 1085-1089, 1987  
A:Title: V-K and J-K gene segments of A/J Ars-A antibodies: somatic recombination generates  
A:Reference number: A26406; MUID:87147197; PMID:3103124  
A:Accession: A26406  
A:Molecule type: DNA  
A:Residues: 1-128 <SAN>  
A:Cross-references: UNIPROT:Q91WP8; UNIPARC:UPI000017679C; GB:M15519  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:36-110/Domain: immunoglobulin homology <IMM>

Query Match 92.6%; Score 50; DB 2; Length 128;  
Best Local Similarity 100.0%; Pred. No. 0.061; 0; Mismatches 0; Indels 0; Gaps 0;  
Matches 10; Conservative 0;

QY 2 ASQDISNYLN 11  
|||||  
Db 45 ASQDISNYLN 54

## RESULT 26

S52789  
Ig kappa chain V region - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 19-May-1995 #sequence\_revision 21-Jul-1995 #text\_change 21-Jan-2000  
A:Accession: S52789  
R:Rocca, A.; Khamlichi, A.A.; Touchard, G.; Mougnot, B.; Ronco, P.; Denoroy, L.; Deret,  
submitted to the EMBL Data Library, March 1995  
A:Description: Light chain V region gene usage restriction and peculiarities in myeloma-  
A:Reference number: S52789  
A:Accession: S52789  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-129 <ROC>  
A:Cross-references: UNIPARC:UPI0000116220; EMBL:X85995; NID:g758588; PIDN:CAA59987.1; PI  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:38-112/Domain: immunoglobulin homology <IMM>

Query Match 92.6%; Score 50; DB 2; Length 129;  
Best Local Similarity 100.0%; Pred. No. 0.062; 0; Mismatches 0; Indels 0; Gaps 0;  
Matches 10; Conservative 0;

QY 2 ASQDISNYLN 11  
|||||

Db 47 ASQDISNYLN 56

## RESULT 27

B37266  
Ig kappa chain V region (2G8) - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 18-Oct-1991 #sequence\_revision 18-Oct-1991 #text\_change 21-Jan-2000  
A:Accession: B37266  
R:Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.  
J. Biol. Chem. 266, 6607-6613, 1991  
A:Title: Heavy and light chain variable region sequences and antibody properties of anti  
A:Reference number: A38740; MUID:91177923; PMID:1706720  
A:Accession: B37266  
A:Status: preliminary; not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-111 <RUF>  
A:Cross-references: UNIPARC:UPI0000176B07  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:19-93/Domain: immunoglobulin homology <IMM>

Query Match 90.7%; Score 49; DB 2; Length 111;  
Best Local Similarity 90.0%; Pred. No. 0.081; 1; Mismatches 0; Indels 0; Gaps 0;  
Matches 9; Conservative 1;

QY 2 ASQDISNYLN 11  
|||||  
Db 28 ASQDISNYLN 37

## RESULT 28

G38740  
Ig kappa chain V region (Py69) - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 18-Oct-1991 #sequence\_revision 18-Oct-1991 #text\_change 09-Jul-2004  
A:Accession: G38740  
R:Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.  
J. Biol. Chem. 266, 6607-6613, 1991  
A:Title: Heavy and light chain variable region sequences and antibody properties of anti  
A:Reference number: A38740; MUID:91177923; PMID:1706720  
A:Accession: G38740  
A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra  
A:Molecule type: mRNA  
A:Residues: 1-111 <RUF>  
A:Cross-references: UNIPROT:Q91WS9; UNIPARC:UPI0000176CDA  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:19-93/Domain: immunoglobulin homology <IMM>

Query Match 90.7%; Score 49; DB 2; Length 111;  
Best Local Similarity 90.9%; Pred. No. 0.081; 0; Mismatches 1; Indels 0; Gaps 0;  
Matches 10; Conservative 0;

QY 1 SASQDISNYLN 11  
|||||  
Db 27 SASQDIRNYLN 37

## RESULT 29

B26405  
Ig kappa chain V region (1F6) - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 30-Jun-1988 #sequence\_revision 30-Jun-1988 #text\_change 21-Jan-2000  
A:Accession: B26405  
R:Smith, J.A.; Margolies, M.N.  
Biochemistry 26, 604-612, 1987  
A:Title: Complete amino acid sequences of the heavy and light chain variable regions fro  
A:Reference number: A90518; MUID:87157677; PMID:3103682  
A:Accession: B26405  
A:Molecule type: protein  
A:Residues: 1-108 <SMI>

A;Cross-references: UNIPARC:UPI00001769E7  
 A;Experimental source: strain A/J  
 C;Superfamily: immunoglobulin V region; immunoglobulin homology  
 C;Keywords: heterotetramer; immunoglobulin  
 F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 87.0%; Score 47; DB 2; Length 108;  
 Best Local Similarity 90.0%; Pred. No. 0.18; Mismatches 1; Gaps 0;  
 Matches 9; Conservative 1; Indels 0; Gaps 0;

Qy 2 ASQDISNYLN 11  
 |||||:||||  
 Db 25 ASQDINNYLN 34

## RESULT 30

A38740  
 Ig kappa chain V region (Py20) - mouse  
 C;Species: Mus musculus (house mouse)  
 C;Date: 18-Oct-1991 #sequence\_revision 18-Oct-1991 #text\_change 09-Jul-2004  
 C;Accession: A38740  
 R;Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.  
 J. Biol. Chem. 266, 6607-6613, 1991  
 A;Title: Heavy and light chain variable region sequences and antibody properties of anti  
 A;Reference number: A38740; MUID:91177923; PMID:1706720  
 A;Accession: A38740  
 A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra  
 A;Molecule type: mRNA  
 A;Residues: 1-111 <RUF>  
 A;Cross-references: UNIPROT:Q91WS9; UNIPARC:UPI0000176CD9  
 C;Superfamily: immunoglobulin V region; immunoglobulin homology  
 C;Keywords: heterotetramer; immunoglobulin  
 F;19-93/Domain: immunoglobulin homology <IMM>

Query Match 87.0%; Score 47; DB 2; Length 111;  
 Best Local Similarity 90.9%; Pred. No. 0.19; Mismatches 0; Indels 1; Gaps 0;  
 Matches 10; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

Qy 1 SASQDISNYLN 11  
 |||||:||||  
 Db 27 SASQGISNYLN 37

## RESULT 31

E38740  
 Ig kappa chain V region (Py54) - mouse  
 C;Species: Mus musculus (house mouse)  
 C;Date: 18-Oct-1991 #sequence\_revision 18-Oct-1991 #text\_change 09-Jul-2004  
 C;Accession: E38740  
 R;Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.  
 J. Biol. Chem. 266, 6607-6613, 1991  
 A;Title: Heavy and light chain variable region sequences and antibody properties of anti  
 A;Reference number: A38740; MUID:91177923; PMID:1706720  
 A;Accession: E38740  
 A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra  
 A;Molecule type: mRNA  
 A;Residues: 1-111 <RUF>  
 A;Cross-references: UNIPROT:Q91WS9; UNIPARC:UPI0000176CD8  
 C;Superfamily: immunoglobulin V region; immunoglobulin homology  
 C;Keywords: heterotetramer; immunoglobulin  
 F;19-93/Domain: immunoglobulin homology <IMM>

Query Match 87.0%; Score 47; DB 2; Length 111;  
 Best Local Similarity 90.9%; Pred. No. 0.19; Mismatches 0; Indels 1; Gaps 0;  
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SASQDISNYLN 11  
 |||||:||||  
 Db 27 SASQGISNYLN 37

## RESULT 32

C38740

Ig kappa chain V region (Py2) - mouse  
 C;Species: Mus musculus (house mouse)  
 C;Date: 18-Oct-1991 #sequence\_revision 18-Oct-1991 #text\_change 09-Jul-2004  
 C;Accession: C38740  
 R;Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.  
 J. Biol. Chem. 266, 6607-6613, 1991  
 A;Title: Heavy and light chain variable region sequences and antibody properties of anti  
 A;Reference number: A38740; MUID:91177923; PMID:1706720  
 A;Accession: C38740  
 A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra  
 A;Molecule type: mRNA  
 A;Residues: 1-111 <RUF>  
 A;Cross-references: UNIPROT:Q91WS9; UNIPARC:UPI0000176CDB  
 C;Superfamily: immunoglobulin V region; immunoglobulin homology  
 C;Keywords: heterotetramer; immunoglobulin  
 F;19-93/Domain: immunoglobulin homology <IMM>

Query Match 87.0%; Score 47; DB 2; Length 111;  
 Best Local Similarity 90.9%; Pred. No. 0.19; Mismatches 0; Indels 1; Gaps 0;  
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SASQDISNYLN 11  
 |||||:||||  
 Db 27 SASQGISNYLN 37

## RESULT 33

A29380  
 Ig kappa chain precursor V region (AC-1001) - mouse (fragment)  
 C;Species: Mus musculus (house mouse)  
 C;Date: 31-Dec-1988 #sequence\_revision 31-Dec-1988 #text\_change 21-Jan-2000  
 C;Accession: A29380  
 R;Chen, H.T.; Kabat, E.A.; Lundblad, A.; Ratcliffe, R.M.  
 J. Biol. Chem. 262, 13579-13583, 1987  
 A;Title: Nucleotide and translated amino acid sequences of cDNA coding for the variable  
 A;Reference number: A92612; MUID:88007582; PMID:3115981  
 A;Accession: A29380  
 A;Molecule type: mRNA  
 A;Residues: 1-122 <CHE>  
 A;Cross-references: UNIPARC:UPI000011677C; GB:M17160; GB:J02815; NID:g196895; PIDN:AAA38  
 A;Note: the authors translated the codon TTC for residue 1 as Leu  
 C;Superfamily: immunoglobulin V region; immunoglobulin homology  
 C;Keywords: heterotetramer; immunoglobulin  
 F;30-104/Domain: immunoglobulin homology <IMM>

Query Match 87.0%; Score 47; DB 2; Length 122;  
 Best Local Similarity 90.0%; Pred. No. 0.21; Mismatches 1; Indels 0; Gaps 0;  
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ASQDISNYLN 11  
 |||||:||||  
 Db 39 ASQDINNYLN 48

## RESULT 34

A34904  
 Ig kappa chain precursor V region (5-27) - mouse  
 C;Species: Mus musculus (house mouse)  
 C;Date: 27-Jul-1990 #sequence\_revision 27-Jul-1990 #text\_change 09-Jul-2004  
 C;Accession: A34904  
 R;Bedzyk, W.D.; Herron, J.N.; Edmundson, A.B.; Voss Jr., E.W.  
 J. Biol. Chem. 265, 133-138, 1990  
 A;Title: Active site structure and antigen binding properties of idiotypically cross-re  
 A;Reference number: A34903; MUID:90094387; PMID:2104617  
 A;Accession: A34904  
 A;Status: preliminary; not compared with conceptual translation  
 A;Molecule type: mRNA  
 A;Residues: 1-126 <BED>

A;Cross-references: UNIPROT:Q91WF8; UNIPARC:UPI000017679E  
 C;Superfamily: immunoglobulin V region; immunoglobulin homology  
 C;Keywords: heterotetramer; immunoglobulin  
 F;35-109/Domain: immunoglobulin homology <IMM>

```
Query Match      87.0%; Score 47; DB 2; Length 126;
Best Local Similarity 90.0%; Pred. No. 0.21; Mismatches 1; Gaps 0;
Matches 9; Conservative 1; Indels 0;

QY      2 ASQDISNYLN 11
      |||||:||||
Db      44 ASQDINNYLN 53

RESULT 35
S52447
IG kappa chain V region - mouse
C:Species: Mus musculus (house mouse)
C>Date: 08-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
C:Accession: S52447
submitted to the EMBL Data Library, November 1994
A:Description: Specific amplification by the polymerase chain reaction of rearranged ger
A:Reference number: S52445
A:Accession: S52447
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-127 <BER>
A:Cross-references: UNIPARC:UPI0000116206; EMBL:X82688; NID:g673443; PIDN:CAA58009.1; PI
C:Genetics: 17/1
A:Introns: 17/1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:36-110/Domain: immunoglobulin homology <IMM>

Query Match      87.0%; Score 47; DB 2; Length 127;
Best Local Similarity 90.0%; Pred. No. 0.21; Mismatches 1; Gaps 0;
Matches 9; Conservative 1; Indels 0;

QY      2 ASQDISNYLN 11
      |||||:||||
Db      45 ASQDINNYLN 54

RESULT 36
S11124
IG kappa chain V region (clone N05-89.4) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 19-Mar-1997 #sequence_revision 18-Jul-1997 #text_change 21-Jan-2000
C:Accession: S11124
R:Kaartinen, M.; Griffiths, G.M.; Markham, A.F.; Milstein, C.
Nature 304, 320-324, 1983
A:Title: mRNA sequences define an unusually restricted IgG response to 2-phenyloxazolone
A:Reference number: S07331; MUID:83271467; PMID:6877353
A:Accession: S11124
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-108 <KAA>
A:Cross-references: UNIPARC:UPI0000176E7
A>Note: 87-Pne was also found
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match      85.2%; Score 46; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.28; Mismatches 0; Gaps 0;
Matches 9; Conservative 0; Indels 0;

QY      3 SQDISNYLN 11
      |||||:||||
Db      26 SQDISNYLN 34

RESULT 37
S32188
IG kappa chain V region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
C:Accession: S32188
```

```
R:Izui, S.
submitted to the EMBL Data Library, February 1993
A:Reference number: S32185
A:Accession: S32188
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-107 <IZU>
A:Cross-references: UNIPARC:UPI0000116101; EMBL:X70090; NID:g288253; PIDN:CAA49695.1; PI
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match      83.3%; Score 45; DB 2; Length 107;
Best Local Similarity 90.0%; Pred. No. 0.42; Mismatches 1; Gaps 0;
Matches 9; Conservative 1; Indels 0;

QY      2 ASQDISNYLN 11
      |||||:||||
Db      25 ASQDISNYLN 34

RESULT 38
KIHUAV
IG kappa chain V-I region (Au) - human
C:Species: Homo sapiens (man)
C>Date: 24-Apr-1984 #sequence_revision 02-Jul-1998 #text_change 09-Jul-2004
C:Accession: A91653; A01862; S02573
R:Schiechl, H.; Hilschmann, N.
Hoppe-Sevler's Z. Physiol. Chem. 353, 345-370, 1972
A:Title: Die Primaerstruktur einer monoklonalen Immunglobulin-L-Kette vom kappa-Typ. Su
A:Reference number: A91653; MUID:72189444; PMID:5028201
A:Accession: A91653
A:Molecule type: protein
A:Residues: 1-108 <SCH>
A:Cross-references: UNIPROT:P01594; UNIPARC:UPI000012E13E
A>Note: the C region of this chain has the Inv (3) marker
R:Fehlhammer, H.; Schiffer, M.; Epp, O.; Colman, P.M.; Lattman, E.E.; Schwager, P.; Stei
Biophys. Struct. Mech. 1, 139-146, 1975
A:Title: The structure determination of the variable portion of the Bence-Jones protein
A:Reference number: A90729; MUID:77022433; PMID:1234024
A:Contents: annotation; X-ray crystallography
A>Note: the structure of the V region was determined by molecular replacement methods us
R:Steiner, V.; Chang, J.Y.
FEBS Lett. 222, 6-10, 1987
A:Title: Chemical modification of the carboxyl groups of protein substrates enhances the
A:Reference number: S02572; MUID:88005152; PMID:3115831
A:Contents: annotation
C:Comment: This is a Bence Jones protein.
C:Genetics:
A:Gene: GDB:IGKV1
A:Cross-references: GDB:136264
A:Map position: 2p12-2p12
C:Complex: an immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds; in some cases, such as IGA and IGM, the subunits associate into la
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>
F:23-88/Disulfide bonds: #status predicted

Query Match      83.3%; Score 45; DB 1; Length 108;
Best Local Similarity 90.0%; Pred. No. 0.42; Mismatches 1; Gaps 0;
Matches 9; Conservative 1; Indels 0;

QY      2 ASQDISNYLN 11
      |||||:||||
Db      25 ASQDISNYLN 34

RESULT 39
PH0888
IG kappa chain V region (anti-CD3) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 21-Jan-2000
```

C;Accession: PH0888  
 R;Shalaby, M.R.; Shepard, H.M.; Presta, L.; Rodrigues, M.L.; Beverley, P.C.L.; Feldmann, J. Exp. Med. 175, 217-225, 1992  
 A;Title: Development of humanized bispecific antibodies reactive with cytotoxic lymphocytes  
 A;Reference number: PH0885; MUID:92113462; PMID:1346155  
 A;Accession: PH0888  
 A;Molecule type: mRNA  
 A;Residues: 1-109 <SHA>  
 A;Cross-references: UNIPARC:UPI0000176B2B  
 C;Superfamily: immunoglobulin V region; immunoglobulin homology  
 C;Keywords: immunoglobulin  
 F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 83.3%; Score 45; DB 2; Length 109;  
 Best Local Similarity 90.0%; Pred. No. 0.43; Mismatches 0; Gaps 0;  
 Matches 9; Conservative 0; Indels 1; Indels 0; Gaps 0;

Qy 2 ASQDISNYLN 11  
 ||||| |||||  
 Db 25 ASQDIRNYLN 34  
 ||||| |||||

RESULT 40  
 Ig kappa chain V region (Py42) - mouse  
 C;Species: Mus musculus (house mouse)  
 C;Date: 18-Oct-1991 #sequence\_revision 18-Oct-1991 #text\_change 21-Jan-2000  
 C;Accession: I38740  
 R;Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.  
 J. Biol. Chem. 266, 6607-6613, 1991  
 A;Title: Heavy and light chain variable region sequences and antibody properties of anti  
 A;Reference number: A38740; MUID:91177923; PMID:1706720  
 A;Accession: I38740  
 A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra  
 A;Molecule type: mRNA  
 A;Residues: 1-111 <RUF>  
 A;Cross-references: UNIPARC:UPI0000176D2D  
 C;Superfamily: immunoglobulin V region; immunoglobulin homology  
 C;Keywords: heterotetramer; immunoglobulin  
 F;19-93/Domain: immunoglobulin homology <IMM>

Query Match 83.3%; Score 45; DB 2; Length 111;  
 Best Local Similarity 90.0%; Pred. No. 0.43; Mismatches 0; Gaps 0;  
 Matches 9; Conservative 0; Indels 1; Indels 0; Gaps 0;

Qy 2 ASQDISNYLN 11  
 ||||| |||||  
 Db 28 ASQDASNYLN 37  
 ||||| |||||

RESULT 41  
 Ig kappa chain precursor - human  
 C;Species: Homo sapiens (man)  
 C;Date: 02-Dec-1993 #sequence\_revision 17-Nov-1995 #text\_change 21-Jan-2000  
 C;Accession: S24320  
 R;Accouturier, P.; Khamlichi, A.A.; Preud'homme, J.L.; Bauwens, M.; Touchard, G.; Cogné, Biochem. J. 285, 149-152, 1992  
 A;Title: Complementary DNA sequence of human amyloidogenic immunoglobulin light-chain pr  
 A;Reference number: S24319; MUID:92344562; PMID:1379039  
 A;Accession: S24320  
 A;Status: preliminary  
 A;Molecule type: mRNA  
 A;Residues: 1-135 <AUC>  
 A;Cross-references: UNIPARC:UPI0000116013; EMBL:X64133; NID:G32810; PIDN:CAA45494.1; PID  
 A;Note: the authors translated the codon CAA for residue 122 as Glu  
 C;Superfamily: immunoglobulin V region; immunoglobulin homology  
 C;Keywords: heterotetramer; immunoglobulin  
 F;18-112/Domain: immunoglobulin homology <IMM>

Query Match 83.3%; Score 45; DB 2; Length 135;  
 Best Local Similarity 90.0%; Pred. No. 0.53; Mismatches 1; Indels 0; Gaps 0;  
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ASQDISNYLN 11  
 ||||| |||||  
 Db 47 ASQDISDYLN 56  
 ||||| |||||

## RESULT 42

PH0087  
 Ig kappa chain V region (anti-cyclosporin C and D) - mouse (fragment)

C;Species: Mus musculus (house mouse)  
 C;Date: 15-Jan-1993 #sequence\_revision 15-Jan-1993 #text\_change 21-Jan-2000  
 C;Accession: PH0087

R;Schmitter, D.; Poch, O.; Zeder, G.; Heinrich, G.F.; Kocher, H.P.; Quesniaux, V.F.J.; V. Mol. Immunol. 27, 1029-1038, 1990  
 A;Title: Analysis of the structural diversity of monoclonal antibodies to cyclosporine.  
 A;Reference number: PH0087; MUID:91042649; PMID:2122240  
 A;Accession: PH0087  
 A;Molecule type: mRNA  
 A;Residues: 1-105 <SCH>  
 A;Cross-references: UNIPARC:UPI0000115EE7; GB:X57639; NID:G296839; PIDN:CAA40857.1; PID:  
 C;Superfamily: immunoglobulin V region; immunoglobulin homology  
 C;Keywords: heterotetramer; immunoglobulin  
 F;16-90/Domain: immunoglobulin homology <IMM>  
 F;24-34/Region: complementarity-determining 1  
 F;50-56/Region: complementarity-determining 2  
 F;89-97/Region: complementarity-determining 3

Query Match 81.5%; Score 44; DB 2; Length 105;  
 Best Local Similarity 90.0%; Pred. No. 0.63; Mismatches 0; Gaps 0;  
 Matches 9; Conservative 0; Indels 1; Indels 0; Gaps 0;

Qy 2 ASQDISNYLN 11  
 ||||| |||||  
 Db 25 ASQDISNYLN 34  
 ||||| |||||

## RESULT 43

S19674  
 Ig kappa chain V region (clone alpha-TEL9) - human

C;Species: Homo sapiens (man)  
 C;Date: 22-Jan-1993 #sequence\_revision 22-Jan-1993 #text\_change 20-Jun-2000  
 C;Accession: S19674

R;Marks, J.D.; Hoogenboom, H.R.; Bonnert, T.P.; McCafferty, J.; Griffiths, A.D.; Winter, J. Mol. Biol. 222, 581-597, 1991  
 A;Title: By-passing immunization. Human antibodies from V-gene libraries displayed on ph  
 A;Reference number: S19663; MUID:92085276; PMID:1748994  
 A;Accession: S19674  
 A;Molecule type: mRNA  
 A;Residues: 1-108 <MAR>  
 A;Cross-references: UNIPARC:UPI0000115FE1; EMBL:X61642; NID:G37860; PIDN:CAA43823.1; PID:  
 C;Superfamily: immunoglobulin V region; immunoglobulin homology  
 C;Keywords: heterotetramer; immunoglobulin  
 F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 81.5%; Score 44; DB 2; Length 108;  
 Best Local Similarity 90.0%; Pred. No. 0.64; Mismatches 0; Gaps 0;  
 Matches 9; Conservative 0; Indels 1; Indels 0; Gaps 0;

Qy 2 ASQDISNYLN 11  
 ||||| |||||  
 Db 25 ASQDISNYLN 34  
 ||||| |||||

## RESULT 44

S31981  
 Ig kappa chain - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 21-Jan-2000  
 C;Accession: S31981

R;Portolano, S.; Chazenbalk, G.D.; Hutchison, S.J.; McLachlan, S.M.; Rapoport, B. submitted to the EMBL Data Library, June 1992  
 A;Description: Lack of promiscuity in autoantigen-specific H and L chain combinations as  
 A;Reference number: S31977

A:Accession: S31981  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-109 <POR>  
A:Cross-references: UNIPARC:UPI0000116494; EMBL:Z15077; NID:G38493; PIDN:CAA78786.1; PID  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 81.5%; Score 44; DB 2; Length 109;  
Best Local Similarity 90.0%; Pred. No. 0.65;  
Matches 9; Conservative 0; Mismatches 0; Gaps 0; Indels 1; Indels 0; Gaps 0;

QY 2 ASQDISNYLN 11  
||| ||| ||| ||| |||  
DB 25 ASQDISRYLN 34

RESULT 45  
S40367  
Ig kappa chain V-J-C region - human  
C:Species: Homo sapiens (man)  
C:Date: 19-May-1994 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000  
C:Accession: S40367  
R:Klein, R.; Jaenichen, R.; Zachau, H.G.  
Eur. J. Immunol. 23, 3248-3271, 1993  
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.  
A:Reference number: S40312; MUID:94080891; PMID:8258341  
A:Accession: S40367  
A:Status: preliminary; translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-127 <KLE>  
A:Cross-references: UNIPARC:UPI0000176CB4; EMBL:X72477  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:33-107/Domain: immunoglobulin homology <IMM>

Query Match 81.5%; Score 44; DB 2; Length 127;  
Best Local Similarity 90.0%; Pred. No. 0.76;  
Matches 9; Conservative 0; Mismatches 0; Gaps 0; Indels 1; Indels 0; Gaps 0;

QY 2 ASQDISNYLN 11  
||| ||| ||| ||| |||  
DB 42 ASQDISRYLN 51

RESULT 46  
K1HWK  
Ig kappa chain precursor V-I region (Walker) - human  
C:Species: Homo sapiens (man)  
C:Date: 17-Mar-1987 #sequence\_revision 17-Mar-1987 #text\_change 09-Jul-2004  
C:Accession: A01883  
R:Klobeck, H.G.; Combrato, G.; Zachau, H.G.  
Nucleic Acids Res. 12, 6995-7006, 1984  
A:Title: Immunoglobulin genes of the kappa light chain type from two human lymphoid cell  
A:Reference number: A93534; MUID:85014148; PMID:6091049  
A:Accession: A01883  
A:Molecule type: DNA  
A:Residues: 1-129 <KLO>  
A:Cross-references: UNIPROT:P04431; UNIPARC:UPI000012E151  
A:Note: the sequence was determined from the differentiated gene  
C:Genetics:  
A:Gene: GDB:IGKV1  
A:Cross-references: GDB:136264  
A:Map position: 2p12-2p12  
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap  
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:1-22/Domain: signal sequence #status predicted <SIG>  
F:23-129/Product: Ig kappa chain V-I region (Walker) #status predicted <MAT>  
F:23-45/Region: framework 1  
F:38-112/Domain: immunoglobulin homology <IMM>

F:46-56/Region: complementarity-determining 1  
F:57-71/Region: framework 2  
F:72-78/Region: complementarity-determining 2  
F:79-110/Region: framework 3  
F:111-119/Region: complementarity-determining 3  
F:120-129/Region: framework 4  
F:45-110/Disulfide bonds: #status predicted

Query Match 81.5%; Score 44; DB 1; Length 129;  
Best Local Similarity 90.0%; Pred. No. 0.77;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ASQDISNYLN 11  
||| ||| ||| ||| |||  
DB 47 ASQDISNYLN 56

RESULT 47  
B30551  
Ig kappa chain V region (36-71) - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 03-Mar-1989 #sequence\_revision 03-Mar-1989 #text\_change 21-Jan-2000  
C:Accession: B30551  
R:Sharon, J.; Geffter, M.L.; Wysocki, L.J.; Margolies, M.N.  
J. Immunol. 142, 596-601, 1989  
A:Title: Recurrent somatic mutations in mouse antibodies to p-azophenylarsonate increase  
A:Reference number: A30551; MUID:89093946; PMID:2911012  
A:Accession: B30551  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-108 <SHA>  
A:Cross-references: UNIPARC:UPI0000114FA1  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 79.6%; Score 43; DB 2; Length 108;  
Best Local Similarity 80.0%; Pred. No. 0.98;  
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASQDISNYLN 11  
||| ||| ||| ||| |||  
DB 25 ASQDISNYLN 34

RESULT 48  
S40365  
Ig kappa chain - human  
C:Species: Homo sapiens (man)  
C:Date: 06-Mar-1994 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000  
C:Accession: S40365  
R:Klein, R.; Jaenichen, R.; Zachau, H.G.  
Eur. J. Immunol. 23, 3248-3271, 1993  
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.  
A:Reference number: S40312; MUID:94080891; PMID:8258341  
A:Accession: S40365  
A:Status: preliminary; translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-139 <KLE>  
A:Cross-references: UNIPARC:UPI0000116173; EMBL:X72475; NID:G441418; PIDN:CAAS1143.1; PI  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:31-105/Domain: immunoglobulin homology <IMM>

Query Match 79.6%; Score 43; DB 2; Length 139;  
Best Local Similarity 80.0%; Pred. No. 1.3;  
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 ASQDISNYLN 11  
||| ||| ||| ||| |||  
DB 40 ATQDIGNYLN 49

```
RESULT 49
PH1065
Ig kappa chain V region (clone 163.47) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C:Accession: PH1065
R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B c
A:Reference number: PH0971; MUID:92381444; PMID:1512540
A:Accession: PH1065
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-98 <TIL>
A:Cross-references: UNIPROT:Q9RIA5; UNIPARC:UPI0000176AB5
A:Experimental source: B cell, strain [NZB x NZW]F1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin

Query Match          77.8%; Score 42; DB 2; Length 98;
Best Local Similarity 80.0%; Pred. No. 1.4;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASQDISNYLN 11
   |||||:|
Db 25 ASQDINNYLS 34

RESULT 50
S20652
Ig kappa chain V region - mouse
C:Species: Mus musculus (house mouse)
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
C:Accession: S20652
R:Logman, M.; Fasy, T.M.; Novick, K.E.; Monestier, M.
submitted to the EMBL Data Library, February 1992
A:Description: Relationships among antinuclear antibodies from autoimmune MRL mice react
A:Reference number: S20639
A:Accession: S20652
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-106 <LOS>
A:Cross-references: UNIPARC:UPI0000116026; EMBL:X65008; NID:G52649; PIDN:CAA46141.1; PID
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match          77.8%; Score 42; DB 2; Length 106;
Best Local Similarity 80.0%; Pred. No. 1.5;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASQDISNYLN 11
   |||||:|
Db 25 ASQDINNYLS 34

Search completed: April 6, 2006, 08:58:40
Job time : 17 secs
```



GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: April 6, 2006, 08:55:21 ; Search time 73.0847 Seconds  
(without alignments)  
106.189 Million cell updates/sec

Title: US-10-089-500-6  
Perfect score: 54  
Sequence: 1 SASQDISNYLN 11

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : UniProt 05.80.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	ID	Description
1	54	100.0	1 KV5U MOUSE	P04946 mus musculus
2	50	92.6	2 Q6LHV5 HUMAN	Q6LHV5 homo sapien
3	50	92.6	1 KV5K MOUSE	P01644 mus musculus
4	50	92.6	1 KV5L MOUSE	P01645 mus musculus
5	50	92.6	1 KV5M MOUSE	P01646 mus musculus
6	47	87.0	1 KV5N MOUSE	P01647 mus musculus
7	47	87.0	1 KV5O MOUSE	P01648 mus musculus
8	45	83.3	1 KV1B HUMAN	P01594 homo sapien
9	44	81.5	1 Q9UL81 HUMAN	Q9UL81 homo sapien
10	44	81.5	1 KV1Y HUMAN	P80362 homo sapien
11	44	81.5	1 KV1W HUMAN	P04431 homo sapien
12	44	81.5	2 Q7Z3Y4 HUMAN	Q7Z3Y4 homo sapien
13	42	77.8	1 KV1A HUMAN	P01593 homo sapien
14	42	77.8	2 Q9GPF6 HUMAN	Q9GPF6 homo sapien
15	42	77.8	2 Q6GMX0 HUMAN	Q6GMX0 homo sapien
16	41	75.9	1 KV5J MOUSE	P01643 mus musculus
17	41	75.9	2 Q7PD14 PLAYO	Q7PD14 plasmodium
18	40	74.1	2 Q5ZHN4 CHICK	Q5ZHN4 gallus gall
19	40	74.1	2 Q6LZM4 METMP	Q6LZM4 methanococc
20	40	74.1	2 Q8ILX3 PLAF7	Q8ILX3 plasmodium
21	40	74.1	2 Q7RDE1 PLAYO	Q7RDE1 plasmodium
22	40	74.1	2 Q7500 2	Q7500 drosophila
23	40	74.1	2 Q9VMT8 DROME	Q9VMT8 drosophila
24	39	72.2	2 Q96SA9 HUMAN	Q96SA9 homo sapien
25	39	72.2	2 Q9UL77 HUMAN	Q9UL77 homo sapien
26	39	72.2	1 KV5H MOUSE	P01641 mus musculus
27	39	72.2	2 Q569I7 HUMAN	Q569I7 homo sapien
28	39	72.2	2 Q4XR33 PLACH	Q4XR33 plasmodium
29	39	72.2	2 Q9X556 ENTFC	Q9X556 enterococc
30	39	72.2	2 Q38Y1Y ENTFA	Q38Y1Y enterococc
31	39	72.2	2 Q9H192 THEAC	Q9H192 thermoplasm

32	39	72.2	2 Q5EAT3 XENLA	Q5EAT3 xenopus lae
33	39	72.2	2 Q5LPH3 BACFN	Q5LPH3 bacteroides
34	39	72.2	2 Q64W97 BACFN	Q64W97 bacteroides
35	39	72.2	2 Q8EV69 MYCPE	Q8EV69 mycoplasma
36	39	72.2	2 Q7PDL3 PLAYO	Q7PDL3 plasmodium
37	38	70.4	2 Q8YXNO ANASP	Q8YXNO anabaena ap
38	38	70.4	1 KV1O HUMAN	P01607 homo sapien
39	38	70.4	2 Q54P35 DICDI	Q54P35 dictyostell
40	38	70.4	2 Q7V117 PROMP	Q7V117 prochloroco
41	38	70.4	2 Q7N5S4 PHOLL	Q7N5S4 photorhabd
42	38	70.4	2 Q4N4X6 THEPA	Q4N4X6 theileria p
43	38	70.4	2 Q4UEL8 THEAN	Q4UEL8 theileria a
44	38	70.4	2 Q6N1A8 CORDI	Q6N1A8 corynebacte
45	38	70.4	2 Q4WSZ8 ASPFU	Q4WSZ8 aspergillus
46	38	70.4	2 Q7S4U7 NEUCR	Q7S4U7 neurospora
47	38	70.4	2 Q6BPM0 DEBHA	Q6BPM0 debaryomye
48	38	70.4	2 Q98QF1 MYCPU	Q98QF1 mycoplasma
49	38	70.4	2 Q5ALR7 CANAL	Q5ALR7 candida alb
50	38	70.4	2 Q5AM66 CANAL	Q5AM66 candida alb
51	38	70.4	2 Q976A4 SULTO	Q976A4 sulfolobus
52	37.5	69.4	2 Q7NAW3 MYCGA	Q7NAW3 mycoplasma
53	37	68.5	1 KV1P HUMAN	P01608 homo sapien
54	37	68.5	2 Q9UL70 HUMAN	Q9UL70 homo sapien
55	37	68.5	1 KV5F MOUSE	P01638 mus musculu
56	37	68.5	2 Q5LUX3 SILPO	Q5LUX3 silicibacte
57	37	68.5	2 Q8E1T8 STRAS	Q8E1T8 streptococc
58	37	68.5	2 Q8E7A0 STRA3	Q8E7A0 streptococc
59	37	68.5	2 Q7TS98 MOUSE	Q7TS98 mus musculu
60	37	68.5	2 Q8EUE2 MYCPE	Q8EUE2 mycoplasma
61	37	68.5	2 Q76P35 DICDI	Q76P35 dictyostell
62	37	68.5	2 Q5AS33 DICDI	Q5AS33 dictyostell
63	37	68.5	2 Q8YQX3 ANASP	Q8YQX3 anabaena ap
64	37	68.5	2 Q4YHGB PLABE	Q4YHGB plasmodium
65	37	68.5	2 Q4HJZ3 CAMLA	Q4HJZ3 campylobact
66	37	68.5	2 Q97FZ1 CLOAB	Q97FZ1 clostridium
67	37	68.5	2 Q8T458 DROME	Q8T458 drosophila
68	37	68.5	2 Q8MEL1 DROME	Q8MEL1 drosophila
69	37	68.5	2 Q8S215 STRCO	Q8S215 streptomyc
70	37	68.5	2 Q7RJT3 PLAYO	Q7RJT3 plasmodium
71	37	68.5	2 Q8IEB5 PLAF7	Q8IEB5 plasmodium
72	37	68.5	2 Q9GR06 PLAF7	Q9GR06 plasmodium
73	37	68.5	2 Q4Z6R8 PLABE	Q4Z6R8 plasmodium
74	37	68.5	2 Q9W1Z6 DROME	Q9W1Z6 drosophila
75	37	68.5	2 Q89ZH9 BACTN	Q89ZH9 bacteroides
76	37	68.5	2 Q8EV71 MYCPE	Q8EV71 mycoplasma
77	37	68.5	2 P96311 ANATH	P96311 anaerocellu
78	37	68.5	1 GUNA CALSA	P22534 caldocellum
79	37	68.5	1 PRKDC MOUSE	P97313 mus musculu
80	36	66.7	2 Q5HNB1 STAEQ	Q5HNB1 staphylococ
81	36	66.7	2 Q8CS20 STAEQ	Q8CS20 staphylococ
82	36	66.7	1 KV5P MOUSE	P01637 mus musculu
83	36	66.7	2 KV5E MOUSE	P01637 mus musculu
84	36	66.7	2 Q4YP21 PLABE	Q4YP21 plasmodium
85	36	66.7	2 Q71D85 DROYA	Q71D85 drosophila
86	36	66.7	2 Q5EFE6 HUMAN	Q5EFE6 homo sapien
87	36	66.7	2 Q8EDG4 SHEON	Q8EDG4 shewanella
88	36	66.7	2 Q51QC1 MAGGR	Q51QC1 magnaporthe
89	36	66.7	2 Q7P1F8 CHRVO	Q7P1F8 chromobacte
90	36	66.7	2 Q8AVX5 XENLA	Q8AVX5 xenopus lae
91	36	66.7	2 Q9AZM4 SCAUD	Q9AZM4 bacterioph
92	36	66.7	2 Q9C196 LACLA	Q9C196 lactococcu
93	36	66.7	2 Q7QM95 ANOGA	Q7QM95 anophales g
94	36	66.7	2 Q8D316 WIGBR	Q8D316 wiggleswort
95	36	66.7	2 Q64B15 ARCH	Q64B15 uncultured
96	36	66.7	2 Q7S0T9 NEUCR	Q7S0T9 neurospora
97	36	66.7	2 Q8A4T4 BACTN	Q8A4T4 bacteroides
98	36	66.7	2 Q8YXZ6 ORYSA	Q8YXZ6 oryza sativ
99	36	66.7	2 Q8ERX1 OCEIH	Q8ERX1 oceanobacil
100	36	66.7	2 Q98PK5 MYCPU	Q98PK5 mycoplasma
101	36	66.7	2 Q91GC6 NPVEP	Q91GC6 epiphyas po
102	36	66.7	2 Q87WJ0 PSESM	Q87WJ0 pseudomonas
103	36	66.7	2 Q50W74 ENTHN	Q50W74 entamoeba h
104	36	66.7	2 Q8A4J7 BACTN	Q8A4J7 bacteroides

105	36	66.7	614	2	Q5CYX9	CRYPV	Q5CYX9	cryptospori	178	35	64.8	464	1	Y1713	FUSNN	Q8r5z8	fusobacteri
106	36	66.7	815	2	Q4UDJ1	THEAN	Q4udj1	theileria a	179	35	64.8	480	2	Q8HXA0	ATEFU	Q8hxa0	ateles fusc
107	36	66.7	1061	2	Q4WBY1	ASPFU	Q4wby1	aspergillus	180	35	64.8	480	2	Q8HXA3	ALOBE	Q8hxa3	alouatta be
108	36	66.7	1072	2	Q59SK9	CANAL	Q59sk9	candida alb	181	35	64.8	480	2	Q8HYD3	PRIM	Q8hyd3	alouatta gu
109	36	66.7	1097	2	Q8A8X5	BACTN	Q8a8x5	bacteroides	182	35	64.8	480	2	Q8HYD4	ATEGE	Q8hyd4	ateles geof
110	36	66.7	1110	2	Q4P945	USTMA	Q4p945	ustilago ma	183	35	64.8	480	2	Q8HYD5	ATEGE	Q8hyd5	ateles geof
111	36	66.7	1297	2	Q4P3M1	USTMA	Q4p3m1	ustilago ma	184	35	64.8	480	2	Q8HYD6	ALOSE	Q8hyd6	alouatta se
112	36	66.7	2068	2	Q4UBV3	THEAN	Q4ubv3	theileria a	185	35	64.8	480	2	Q8HYD7	ALOPE	Q8hyd7	alouatta pa
113	36	66.7	2409	2	Q5CV41	CRYPV	Q5cv41	cryptospori	186	35	64.8	480	2	Q8HYD8	ALOPI	Q8hyd8	alouatta pi
114	36	66.7	2699	2	Q7RF08	PLAYO	Q7rf08	plasmodium	187	35	64.8	480	2	Q8HYD9	ALOPE	Q8hyd9	alouatta pa
115	36	66.7	4449	1	GRSB	BREBE	P0C064	b gramicididi	188	35	64.8	490	2	Q9YVM1	MSEPV	Q9yvm1	melanoplus
116	36	66.7	4450	1	GRSB	ANEMI	P0C063	a gramicidi	189	35	64.8	511	2	Q8PV66	METMA	Q8pv66	methanopsarc
117	35.5	65.7	2251	1	L	MUMPM	P30929	mumps virus	190	35	64.8	512	2	Q7G9K0	ARATH	Q7g9k0	arabidopsis
118	35.5	65.7	2261	2	Q5SC50	9PARA	Q5sc50	mumps virus	191	35	64.8	520	2	Q9SX35	ARATH	Q9sx35	arabidopsis
119	35.5	65.7	2261	2	Q8B4T7	9PARA	Q8b4t7	mumps virus	192	35	64.8	529	2	Q7Z8M3	PARSR	Q7z8m3	paracoccidi
120	35.5	65.7	2261	2	Q6BC94	9PARA	Q6bc94	mumps virus	193	35	64.8	540	2	Q6VER2	PSESY	Q6ver2	pseudomonas
121	35.5	65.7	2261	2	Q6EAM0	9PARA	Q6eam0	mumps virus	194	35	64.8	544	2	Q8ELI4	OCEIH	Q8eli4	oceanobacil
122	35.5	65.7	2261	2	Q77IS0	MUMPJ	Q77ie0	mumps virus	195	35	64.8	549	1	G6PI	BUCAI	P57636	buchnera ap
123	35.5	65.7	2261	2	Q783V6	9PARA	Q783v6	mumps virus	196	35	64.8	557	2	Q92DF5	LISIN	Q92df5	listeria in
124	35.5	65.7	2261	2	Q7TDZ3	9PARA	Q7tdz3	mumps virus	197	35	64.8	571	2	Q6XC74	9SCIU	Q6xc74	sciurus ign
125	35.5	65.7	2261	2	Q8QV64	MUMPJ	Q8qv64	mumps virus	198	35	64.8	573	2	Q6XC51	9SCIU	Q6xc51	paraxerus v
126	35.5	65.7	2261	2	Q8QY67	9PARA	Q8qy67	mumps virus	199	35	64.8	576	2	Q4LADI	STAHJ	Q4lad1	staphylococ
127	35.5	65.7	2261	2	Q910G6	9PARA	Q910g6	mumps virus	200	35	64.8	579	2	Q6XC78	9SCIU	Q6xc78	petaurista
128	35.5	65.7	2261	2	Q91N63	9PARA	Q91n63	mumps virus	201	35	64.8	584	2	Q6XC71	9SCIU	Q6xc71	callosciuru
129	35.5	65.7	2261	2	Q91N66	9PARA	Q91n66	mumps virus	202	35	64.8	585	2	Q9KDT9	BACHD	Q9kdt9	bacillus ba
130	35.5	65.7	2261	2	Q91N67	9PARA	Q91n67	mumps virus	203	35	64.8	589	2	Q6XC70	9SCIU	Q6xc70	tamipops swi
131	35.5	65.7	2261	2	Q9DQA0	9PARA	Q9dqa0	mumps virus	204	35	64.8	632	2	Q6AIV7	DESPP	Q6aiv7	desulfotale
132	35.5	65.7	2261	2	Q9J4L0	9PARA	Q9j4l0	mumps virus	205	35	64.8	649	2	Q6XC69	9SCIU	Q6xc69	dremomys pe
133	35	64.8	57	2	Q74VX7	YERPE	Q74vx7	yersinia pe	206	35	64.8	655	2	Q50PB6	ENTHI	Q50pb6	entamoeba h
134	35	64.8	82	2	Q26213	METTH	Q26213	methanobact	207	35	64.8	666	1	UVRB	UREPA	Q9pr24	ureaplasma
135	35	64.8	87	2	Q5ULG7	9CAUD	Q5ulg7	lactobacill	208	35	64.8	686	2	Q6XC56	9SCIU	Q6xc56	heliosciuru
136	35	64.8	102	1	RAPC	PENCH	P09647	penicillium	209	35	64.8	688	2	Q6XC59	9ARMO	Q6xc59	marmota mon
137	35	64.8	126	2	Q6MGF9	BDEBA	Q6mgp9	bdeilovibri	210	35	64.8	692	2	Q6XC79	GLAVO	Q6xc79	glaucomys v
138	35	64.8	140	2	Q8RCN0	THETN	Q8rcn0	thermoanaer	211	35	64.8	701	2	Q6XC55	9SCIU	Q6xc55	protoxerus
139	35	64.8	157	2	Q45444	BACSU	Q45444	bacillus su	212	35	64.8	702	2	Q6XC63	9SCIU	Q6xc63	sciurotamia
140	35	64.8	157	2	Q84E49	BACPU	Q84e49	bacillus pu	213	35	64.8	705	2	Q6XC72	9SCIU	Q6xc72	callosciuru
141	35	64.8	157	2	Q7BUV5	BACPU	Q7buv5	bacillus pu	214	35	64.8	706	2	Q6XC87	9RODE	Q6xc87	microtus ir
142	35	64.8	191	2	Q8BF14	XENLA	Q8bf14	xenopus lae	215	35	64.8	708	2	Q6WDI7	RHAPU	Q6wdi7	rhadomys p
143	35	64.8	200	1	CLPPI	MYCTU	P0A527	mycobacteri	216	35	64.8	708	2	Q6XC52	9SCIU	Q6xc52	paraxerus o
144	35	64.8	200	1	CLPPI	MYCTU	P0A526	mycobacteri	217	35	64.8	708	2	Q6XC66	9SCIU	Q6xc66	xerus inaur
145	35	64.8	209	2	Q6FA10	ACTAD	Q6fa10	acinetobact	218	35	64.8	708	2	Q6XC80	9SCIU	Q6xc80	sciurillus
146	35	64.8	213	2	Q4YZ57	PLABE	Q4yz57	plasmodium	219	35	64.8	710	2	Q6XC53	9SCIU	Q6xc53	paraxerus c
147	35	64.8	286	2	Q5M4X4	CANAL	Q544x4	candida alb	220	35	64.8	711	2	Q6XC54	9SCIU	Q6xc54	funiciurus
148	35	64.8	291	2	Q5SL67	CRYNE	Q5sl61	cryptococcu	221	35	64.8	711	2	Q6XC64	9SCIU	Q6xc64	spemophilo
149	35	64.8	291	2	Q5KAC0	CRYNE	Q5kac0	cryptococcu	222	35	64.8	712	2	Q5JL05	ORYSA	Q5jl05	oryza sativ
150	35	64.8	292	2	Q9LVH1	ARATH	Q9lvh1	arabidopsis	223	35	64.8	713	2	Q6WDI8	9MURI	Q6wdi8	paracomys s
151	35	64.8	300	2	Q4MG41	BACCE	Q4mg41	bacillus ce	224	35	64.8	713	2	Q6XC61	TAMAM	Q6xc61	tamias amoe
152	35	64.8	337	2	P87504	NPVAG	P87504	antiscarsia	225	35	64.8	713	2	Q6XC73	9SCIU	Q6xc73	microsciuru
153	35	64.8	337	2	Q8U604	PLAFA	Q8u6q4	plasmodium	226	35	64.8	757	2	Q99XJ6	STRPY	Q99xj6	streptococc
154	35	64.8	347	2	Q4NKS6	9MICC	Q4nks6	arthrobacte	227	35	64.8	757	2	Q8KSH9	STRP3	Q8ksh9	streptococc
155	35	64.8	354	2	Q7P2T5	FUSNV	Q7p2t5	fusobacteri	228	35	64.8	757	2	Q684D7	9VIRU	Q684d7	sulfolobus
156	35	64.8	358	1	HRC4	CAUCR	P54305	caulobacteri	229	35	64.8	767	2	Q5X9C9	STRP6	Q5xc9c9	streptococc
157	35	64.8	359	2	Q7YQ05	LOXAF	Q7yq05	loxodonta a	230	35	64.8	813	2	Q94LD6	ORYSA	Q94ld6	oryza sativ
158	35	64.8	361	2	Q7YQ04	ELEMA	Q7yq04	elephas max	231	35	64.8	819	2	Q54JX0	DICDI	Q54jx0	dictyosteli
159	35	64.8	361	2	Q7TLS2	NPVCP	Q7tl2	christoneu	232	35	64.8	830	1	RPOC2	EUGHR	P23581	euglena gra
160	35	64.8	366	2	Q1G1T1	NPVEP	Q1g1t1	epiphyas po	233	35	64.8	931	2	Q8IY72	HUMAN	Q8iy72	homo sapien
161	35	64.8	372	2	Q51FR6	ENTHI	Q51fr6	entamoeba h	234	35	64.8	938	2	Q7R6S4	GIALA	Q7r6s4	giardia iam
162	35	64.8	374	2	Q6TT53	CYNVA	Q6tt53	cynoccephalu	235	35	64.8	941	2	Q5MPM8	9PHPU	Q5mpm8	spenodon p
163	35	64.8	378	2	Q6VTR4	NPVCD	Q6vtr4	christoneu	236	35	64.8	944	2	Q9HE41	NEUCR	Q9he41	neurospora
164	35	64.8	392	2	Q5C8D3	9PEZI	Q5c8d3	chaetosphae	237	35	64.8	952	2	Q6WDH8	9RODE	Q6wdh8	tatera robu
165	35	64.8	395	2	Q6XC57	9SCIU	Q6xc57	heliosciuru	238	35	64.8	982	2	Q6WDI4	9MURI	Q6wdi4	chrotomys g
166	35	64.8	400	2	Q6XC67	9SCIU	Q6xc67	exilisciuru	239	35	64.8	985	1	GUNZ	CLOSR	P23659	clostridium
167	35	64.8	404	2	Q6XC65	9SCIU	Q6xc65	xerus rutil	240	35	64.8	993	2	Q6F2I9	MESFL	Q6f2i9	mesoplasma
168	35	64.8	405	2	Q6XC84	9RODE	Q6xc84	allactaga s	241	35	64.8	993	2	Q6WDI1	9MURI	Q6wdi1	arvicanthlis
169	35	64.8	407	2	Q6WDI6	AETNA	Q6wdi6	athomyys na	242	35	64.8	995	2	Q8IJ91	PLAF7	Q8ij91	plasmodium
170	35	64.8	408	2	Q6WDJ0	9RODE	Q6wdj0	petromyscus	243	35	64.8	997	2	Q6WDH1	CRIMI	Q6wdh1	cricetus
171	35	64.8	412	2	Q8AMZ4	ARATH	Q8amz4	arabidopsis	244	35	64.8	997	2	Q6WDH3	PHOSU	Q6wdh3	phodopus su
172	35	64.8	412	2	Q6NMU1	BDEBA	Q6nm18	bdeilovibri	245	35	64.8	998	2	Q6WDI2	PRANA	Q6wdi2	praomys nat
173	35	64.8	413	2	Q9C7G8	ARATH	Q9c7g8	arabidopsis	246	35	64.8	1000	2	Q6WDH5	CLEGA	Q6wdh5	clethrionom
174	35	64.8	444	2	Q8DVL5	STRMU	Q8dvl5	streptococc	247	35	64.8	1003	2	Q6WDG5	9RODE	Q6wdg5	irenomys ta
175	35	64.8	444	2	Q8B1Q6	STRA5	Q8b1q6	streptococc	248	35	64.8	1006	2	Q6WDG8	NEOFL	Q6wdg8	neotoma flo
176	35	64.8	444	2	Q8E770	STRA3	Q8e770	streptococc	249	35	64.8	1011	2	Q4JLH4	LACRE	Q4jlh4	lactobacill
177	35	64.8	450	1	VATH	SCHPO	O14265	schizosacch	250	35	64.8	1040	1	RAGL	MOUSE	P15919	mus musculu

251	35	64.8	1040	2	Q7BNA6_MOUSE	Q78na6	mus musculus	324	34	63.0	498	2	Q4LAD0_STAHL	Q4lad0	staphylococ
252	35	64.8	1042	1	RAG1_RABIT	P34088	oryctolagus	325	34	63.0	502	2	Q9XG35_GUTH	Q9xg35	guillardia
253	35	64.8	1043	1	RAG1_HUMAN	P15918	homo sapien	326	34	63.0	510	2	Q97251_PLAF7	Q97251	plasmodium
254	35	64.8	1047	2	Q2B463_MONDO	Q2B463	monodelphis	327	34	63.0	521	2	Q90312_9PHYC	Q90312	chlorella v
255	35	64.8	1087	2	Q4PA11_USTMA	Q4pa11	ustilago ma	328	34	63.0	522	2	Q7ZU78_BRARE	Q7zu78	brachydanio
256	35	64.8	1103	1	CHS6_USTMA	O13395	ustilago ma	329	34	63.0	528	2	Q91F84_IRV6	Q91fe4	chilo iride
257	35	64.8	1206	1	Q869X8_DICDI	Q869x8	dictyosteli	330	34	63.0	529	2	Q82NJ6_STRAW	Q82nj6	streptomyce
258	35	64.8	1213	2	Q553Z2_DICDI	Q553z2	dictyosteli	331	34	63.0	540	2	Q4P7R9_USTMA	Q4p7r9	ustilago ma
259	35	64.8	1486	1	MURK_SHIFL	Q7xam1	shigella fl	332	34	63.0	540	2	Q4P7R9_USTMA	Q4p7r9	ustilago ma
260	35	64.8	1492	2	Q6GN08_XENLA	Q6gn08	xenopus lae	333	34	63.0	547	2	Q4N8P9_THEPA	Q4n8p9	theillaria p
261	35	64.8	1499	2	Q81E92_PLAF7	Q81e92	plasmodium	334	34	63.0	549	2	Q5HKV0_STAEP	Q5hkv0	staphylococ
262	35	64.8	1501	2	Q815G0_PLAF7	Q815g0	plasmodium	335	34	63.0	549	2	Q8CQY1_STAEP	Q8cqy1	staphylococ
263	35	64.8	2093	2	Q5VIN3_PARB	Q5vin3	paracoccidi	336	34	63.0	560	1	INARI_SHEEP	Q82589	ovis aries
264	35	64.8	4433	2	Q81J15_PLAF7	Q81j15	plasmodium	337	34	63.0	567	2	Q6CY56_KLULA	Q6cy56	kluyveromyc
265	34.5	63.9	1321	2	Q6LUF4_PLAF7	Q6luf4	plasmodium	338	34	63.0	578	2	Q59298_9CLOT	Q59299	clostridium
266	34	63.0	101	2	Q6ZEE0_YERPE	Q6zee0	yersinia pe	339	34	63.0	586	2	Q73RA7_TREDE	Q73ra7	treponema d
267	34	63.0	101	2	Q6ZEE0_YERPE	Q6zee0	yersinia pe	339	34	63.0	587	2	Q81AV3_PLAF7	Q81av3	plasmodium
268	34	63.0	102	2	Q86AHS_YERPS	Q66ahs	yersinia pe	340	34	63.0	588	2	Q4Q3A4_LEIMA	Q4q3a4	leishmania
269	34	63.0	102	2	Q9R9B9_BORBU	Q9r9b9	borrelia bu	341	34	63.0	592	2	Q6MBR3_PARUW	Q6mbr3	parachlamyd
270	34	63.0	108	1	KV1H_HUMAN	P01600	homo sapien	342	34	63.0	628	2	Q54TV4_DICDI	Q54tv4	dictyosteli
271	34	63.0	108	1	KV1Q_HUMAN	P01609	homo sapien	343	34	63.0	635	2	Q54ND5_DICDI	Q54nd5	dictyosteli
272	34	63.0	108	1	KV1S_HUMAN	P01611	homo sapien	344	34	63.0	636	2	Q57Z11_9TRYP	Q57z11	trypanosoma
273	34	63.0	109	2	Q8CL60_YERPE	Q8cl60	yersinia pe	345	34	63.0	646	2	Q6AJA2_DESPS	Q6aja2	desulfotale
274	34	63.0	115	2	Q8XJC4_CLOPE	Q8xjc4	clostridium	346	34	63.0	656	2	Q6AJA3_DESPS	Q6aja3	desulfotale
275	34	63.0	119	2	Q5TSM3_ANOGA	Q5tsw3	anopheles g	347	34	63.0	660	2	Q9CE29_LACLA	Q9ce29	lactococcus
276	34	63.0	122	2	Q5XVE9_BORGA	Q5xve9	borrelia ga	348	34	63.0	667	2	Q54F11_DICDI	Q54f11	dictyosteli
277	34	63.0	129	2	Q9CQY3_MOUSE	Q9cqy3	m mus muscu	349	34	63.0	737	2	Q54XW9_DICDI	Q54xw9	dictyosteli
278	34	63.0	137	2	Q9C4T1_HALVO	Q9c4t1	halobacteri	350	34	63.0	758	2	Q8S5U0_ORYSA	Q8s5u0	oryza sativ
279	34	63.0	144	2	Q416D8_STAHL	Q416d8	staphylococ	351	34	63.0	763	2	Q4TR78_9SPHN	Q4tr78	erythrobaet
280	34	63.0	151	1	PEN3_ADEB2	Q91113	morone saxa	352	34	63.0	780	2	Q7QGS3_ANOGA	Q7qgs3	anopheles g
281	34	63.0	157	1	X1070_METJA	Q96623	bovine aden	353	34	63.0	805	2	Q60ND5_CAEBR	Q60nd5	caenorhabdi
282	34	63.0	162	2	Q17590_CABEL	Q58470	methanococc	354	34	63.0	809	2	Q6BNY8_DBBHA	Q6bny8	debaromyce
283	34	63.0	162	2	Q65MD6_BACLD	Q65md6	bacillus li	355	34	63.0	817	2	Q813Y1_PLAF7	Q813y1	plasmodium
284	34	63.0	171	2	Q7N8U1_PHOLL	Q7n8u1	photorhabdu	356	34	63.0	820	2	Q8RAM1_THETN	Q8ram1	thermoanaer
285	34	63.0	193	2	Q6UKD6_9CAUD	Q6ukd6	burkholderi	357	34	63.0	836	2	Q87QC3_VIBPA	Q87qc3	vibrio para
286	34	63.0	193	2	Q6UKD6_9CAUD	Q6ukd6	burkholderi	358	34	63.0	849	2	Q8PPH0_XANAC	Q8pph0	xanthomonas
287	34	63.0	209	2	Q5AXZ7_EMENI	Q5axz7	aspergillus	359	34	63.0	852	2	Q4P044_USTMA	Q4p044	ustilago ma
288	34	63.0	209	2	Q4XP23_PLACH	Q4xp23	plasmodium	360	34	63.0	852	2	Q4P9M5_USTMA	Q4p9m5	ustilago ma
289	34	63.0	220	2	Q8D2F4_WIGBR	Q8d2f4	wiggleswort	361	34	63.0	857	2	Q4UYN9_XANCP	Q4uyn9	xanthomonas
290	34	63.0	222	2	Q8E983_SHEON	Q8e983	shewanella	362	34	63.0	872	2	Q5VRS8_ORYSA	Q5vrs8	oryza sativ
291	34	63.0	225	2	Q5HIN9_STAAC	Q5hin9	staphylococ	363	34	63.0	901	2	Q815U5_PLAF7	Q815u5	plasmodium
292	34	63.0	232	2	Q4HL73_CAMLA	Q4hl73	campylobact	364	34	63.0	901	2	Q5QX08_IDILO	Q5qx08	idiomarina
293	34	63.0	258	2	Q87304_BORBU	Q87304	borrelia bu	365	34	63.0	906	2	Q4P352_USTMA	Q4p352	ustilago ma
294	34	63.0	258	2	Q44789_BORBU	Q44789	borrelia bu	366	34	63.0	908	2	Q7SD12_NEUCR	Q7sdi2	neurospora
295	34	63.0	263	2	Q5GVW1_XANOR	Q5gvw1	xanthomonas	367	34	63.0	932	2	Q591E2_BRARE	Q591e2	brachydanio
296	34	63.0	266	2	Q972V2_SULTO	Q972v2	sulfolobus	368	34	63.0	941	2	Q869Y0_DICDI	Q869y0	dictyosteli
297	34	63.0	270	2	Q5CHB1_CRYHO	Q5chb1	cryptospori	370	34	63.0	941	2	Q553Y8_DICDI	Q553y8	dictyosteli
298	34	63.0	271	2	Q8D3C4_WIGBR	Q8d3c4	wiggleswort	371	34	63.0	978	2	Q4PE74_USTMA	Q4pe74	ustilago ma
299	34	63.0	284	1	DNAS1_GREMO	Q42446	oreochromis	372	34	63.0	1047	2	Q7NAN4_MYCGA	Q7nan4	mycoplasma
300	34	63.0	288	2	Q5CT18_CRYPV	Q5ct18	cryptospori	373	34	63.0	1104	2	Q86AS4_DICDI	Q86as4	dictyosteli
301	34	63.0	301	1	HPRK_MYCPE	Q86aw5	mycoplasma	374	34	63.0	1105	2	Q6NU19_XENLA	Q6nu19	xenopus lae
302	34	63.0	330	2	Q5LDX5_BACFN	Q5ldx5	bacteroides	375	34	63.0	1145	2	Q5AIR7_CANAL	Q5air7	candida alb
303	34	63.0	338	2	Q9M288_ARATH	Q9m288	arabidopsis	376	34	63.0	1145	2	Q9UR03_CANAL	Q9ur03	candida alb
304	34	63.0	352	2	Q4KLE3_XENLA	Q4kle3	xenopus lae	377	34	63.0	1146	2	Q5AHV6_CANAL	Q5ahv6	candida alb
305	34	63.0	367	1	VP41_FPVOP	O10333	orygia pueu	378	34	63.0	1163	2	Q7RPB5_PLAYO	Q7rpe5	plasmodium
306	34	63.0	370	2	Q55FR7_BACLD	Q65fr7	bacillus li	379	34	63.0	1200	2	Q4P6Z0_USTMA	Q4pezo	ustilago ma
307	34	63.0	380	2	Q812A2_PLAF7	Q812a2	plasmodium	380	34	63.0	1243	2	Q6BHL5_DBBHA	Q6bhl5	debaromyce
308	34	63.0	384	2	Q6LYLO_METMP	Q6lyl0	methanococc	381	34	63.0	1291	2	Q6GR96_CLOBO	Q6gr96	clostridium
309	34	63.0	390	2	Q6RHT7_9CAUD	Q6rht7	aeromonas p	382	34	63.0	1291	2	Q933K0_CLOBO	Q933k0	clostridium
310	34	63.0	405	2	Q6FCE2_ACTAD	Q6fce2	acinetobact	383	34	63.0	1291	2	Q93G71_CLOBO	Q93g71	clostridium
311	34	63.0	417	2	P72417_9ENTR	P72417	salmonella	384	34	63.0	1291	2	Q92AJ8_CLOBO	Q92aj8	clostridium
312	34	63.0	430	2	Q81113_BACCR	Q81113	bacillus ce	385	34	63.0	1343	2	Q6BRF7_DBBHA	Q6brf7	debaromyce
313	34	63.0	433	1	TIG_CHLMU	Q9p119	chlamydia m	386	34	63.0	1397	2	Q54D75_DICDI	Q54d75	dictyosteli
314	34	63.0	441	2	Q9X708_CLOBO	Q9x708	clostridium	387	34	63.0	1431	2	Q4P110_USTMA	Q4p110	ustilago ma
315	34	63.0	443	2	Q59298_9CLOT	Q59298	clostridium	388	34	63.0	1498	2	Q4KM09_HUMAN	Q4kmq9	homo sapien
316	34	63.0	449	2	Q41F10_GTBZE	Q41f10	gibberella	389	34	63.0	1499	1	Q4PCB3_USTMA	Q4pcb3	ustilago ma
317	34	63.0	456	2	Q5CI03_CRYHO	Q5ci03	cryptospori	390	34	63.0	1507	2	Y0056_HUMAN	P4695	homo sapien
318	34	63.0	456	2	Q5CSA7_CRYPV	Q5cea7	cryptospori	391	34	63.0	1630	2	Q9V7M1_DROME	Q9v7m1	drosofila
319	34	63.0	471	2	Q994EA_9ADEN	Q994ea	porcine ade	392	34	63.0	1690	2	Q4P388_USTMA	Q4p388	ustilago ma
320	34	63.0	474	2	Q4Y210_PLACH	Q4y210	plasmodium	393	34	63.0	2042	2	Q9VJG3_DROME	Q9vjg3	drosofila
321	34	63.0	478	2	Q7M6E9_ADEB2	Q7m6e9	bovine aden	394	34	63.0	2188	2	P96202_MYCTU	P96202	mycobacteri
322	34	63.0	485	2	Q5AKA5_CANAL	Q5aka5	candida alb	395	34	63.0	2188	2	Q7TXL8_MYCBO	Q7txl8	mycobacteri
323	34	63.0	492	2	Q51Q25_MAGGR	Q51q25	magnaporthe	396	34	63.0	3317	2	Q8ENP8_MYCPE	Q8enp8	mycoplasma

397	34	63.0	4638	2	Q8IK96 PLAF7	Q8IK96 plasmodium	470	33	61.1	366	2	Q8EKT1 SHEON	Q8ekt1 shewanella
398	34	63.0	5174	2	QRTB6_PLAYO	Q7rtb6 plasmodium	471	33	61.1	366	2	Q87TQ6_VIBPA	Q87tq6 vibrio para
399	34	63.0	6735	1	Q4QHG5_LEIMA	Q4qhg5 leishmania	472	33	61.1	366	2	Q7MQJ6_VIBVY	Q7mqj6 vibrio vuln
400	33	61.1	108	1	KVIM_HUMAN	P01A05 homo sapien	473	33	61.1	367	2	Q5P4N9_AZOSE	Q5p4n9 azoarcus sp
401	33	61.1	108	1	KVIN_HUMAN	P01606 homo sapien	474	33	61.1	367	2	Q62N54_BURMA	Q62n54 burkholderi
402	33	61.1	115	1	Y420_AQUAE	Q68736 aquifex aeo	475	33	61.1	367	2	Q63YW6_BURMA	Q63yw6 burkholderi
403	33	61.1	117	1	KV10_RABIT	P01691 oryctolagus	476	33	61.1	367	2	Q5QV38_IDILO	Q5qy38 idiomarina
404	33	61.1	121	2	Q5G6P0_SCHJA	Q586p0 schistosoma	477	33	61.1	368	2	Q4LH76_BURK	Q4lht6 burkholderi
405	33	61.1	129	2	Q4Z7H6_PLABE	Q4z7h6 plasmodium	478	33	61.1	368	2	Q5NSX4_BURML	Q5nsx4 burkholderi
406	33	61.1	146	2	Q6TY36_HPV05	Q6ty36 human papil	479	33	61.1	369	2	Q7VSE1_BORPE	Q7vse1 bordetella
407	33	61.1	154	2	Q32023_BACSU	Q32023 bacillus su	480	33	61.1	371	1	DPO3B_BUCBP	Q7vse1 bordetella
408	33	61.1	156	1	RS7_AZOSE	Q53236 azoarcus sp	481	33	61.1	371	2	Q7WDK0_BORBR	Q7wdk0 bordetella
409	33	61.1	158	2	Q512EH_ENTHI	Q512eh entamoeba h	482	33	61.1	371	2	Q8XTV5_RALSO	Q8xtv5 ralstonia s
410	33	61.1	158	2	Q512FP_ENTHI	Q512fp entamoeba h	483	33	61.1	371	2	Q76218_TETTH	Q76218 tetrahymena
411	33	61.1	159	2	Q6BY04_DEBHA	Q6by04 debaryomyce	484	33	61.1	377	2	Q613G8_CAEBR	Q613g8 caenorhabdi
412	33	61.1	160	2	Q4YMV8_PLABE	Q4ymv8 plasmodium	485	33	61.1	384	2	Q8PUN6_METWA	Q8pun6 metanosarc
413	33	61.1	166	2	Q66051_9GAMA	Q66051 herpesvirus	486	33	61.1	392	2	Q4YV81_PLABE	Q4yve1 plasmodium
414	33	61.1	167	2	Q7GUG1_GIALA	Q7gug1 giardia lam	487	33	61.1	396	2	Q84BS9_9BACT	Q84bs9 gram-negati
415	33	61.1	170	2	Q5CV74_CRYPV	Q5cv74 cryptospori	488	33	61.1	401	2	Q84BT3_9BACT	Q84bt3 gram-negati
416	33	61.1	170	2	Q5IL09_DROME	Q5il09 drosophila	489	33	61.1	401	2	Q84BT4_9BACT	Q84bt4 gram-negati
417	33	61.1	170	2	Q5CIMO_CRYHO	Q5cimo cryptospori	490	33	61.1	401	2	Q84BS7_9PSED	Q84bs7 pseudomonas
418	33	61.1	179	2	Q628L7_CAEBR	Q628l7 caenorhabdi	491	33	61.1	401	2	Q84BS8_9VIBR	Q84bs8 vibrio sp.
419	33	61.1	180	2	Q7ND08_GLOVI	Q7nd08 giceobacter	492	33	61.1	401	2	Q84BT2_9GAMM	Q84bt2 photobacter
420	33	61.1	182	1	Y3064_BACCC	Q63816 bacillus ce	493	33	61.1	401	2	Q84BT5_9GAMM	Q84bt5 photobacter
421	33	61.1	182	1	Y3154_BACHK	Q6hg49 bacillus th	494	33	61.1	401	2	CASPI_HUMAN	P29466 homo sapien
422	33	61.1	182	1	Y3353_BACCR	Q81b38 bacillus ce	495	33	61.1	404	1	Q53EY6_HUMAN	Q53ey6 homo sapien
423	33	61.1	182	1	Y3390_BACC1	P61546 bacillus ce	496	33	61.1	404	2	Q54BQ5_DICDI	Q54bq5 dictyosteli
424	33	61.1	182	1	Y3420_BACAN	P81m29 bacillus an	497	33	61.1	415	2	Q9X737_SULSO	Q9x737 sulfolobus
425	33	61.1	182	1	Q4MXT1_BACCE	Q4mxt1 bacillus ce	498	33	61.1	420	2	Q6P4J4_XENTR	Q6p4j4 xenopus tro
426	33	61.1	185	2	Q4SP25_BRANA	Q9p25 brassicica na	499	33	61.1	424	2	Q83D10_COXBU	Q83d10 coxiella bu
427	33	61.1	185	2	Q87E39_XYLFT	Q87e39 xyella fas	500	33	61.1	434	1	TRME_RICPR	Q83d10 coxiella bu
428	33	61.1	185	2	Q9PE24_XYLFA	Q9pe24 xyella fas	501	33	61.1	445	1	Q68VZ0_RICTY	Q68vz0 rickettsia
429	33	61.1	186	1	PTH_MESFL	Q6f240 mesoplasma	502	33	61.1	445	2	Q92CB1_LISIN	Q92cb1 listeria in
430	33	61.1	192	2	Q6P8D5_XENTR	Q6p8d5 xenopus tro	503	33	61.1	452	2	Q5WRY0_LEGPL	Q5wry0 legionella
431	33	61.1	210	1	Y1850_AQUAE	Q67702 aquifex aeo	504	33	61.1	454	2	Q6G5G4_BARHE	Q6g5g4 bartonella
432	33	61.1	219	1	TRMB_ANASP	Q8yvxx4 anabaena sp	505	33	61.1	455	2	Q5EBY5_PAPHY	Q5ebv5 lentinus ti
433	33	61.1	231	2	Q71B70_9HIV1	Q71b70 human immun	506	33	61.1	463	2	Q5CJ35_CRYHO	Q5cjj5 cryptospori
434	33	61.1	233	1	DPO3E_BUCAP	Q8880 buchnera ap	507	33	61.1	467	2	Q7YYO6_CRYPV	Q7yyo6 cryptospori
435	33	61.1	237	1	TRPC_THEAC	Q91k02 thermoplas	508	33	61.1	470	1	DNPEP_CAELP	Q91087 caenorhabdi
436	33	61.1	237	2	Q8Y3C7_RALSO	Q8y3c7 ralstonia s	509	33	61.1	471	2	Q61L53_CAEBR	Q61l53 caenorhabdi
437	33	61.1	241	2	Q92LA6_MOUSE	Q92la6 mus musculu	510	33	61.1	472	2	Q74D65_GEOSL	Q74d65 geobacter s
438	33	61.1	241	2	Q4TZW7_BRARE	Q4tzw7 brachydanio	511	33	61.1	479	2	Q6MNV4_DDEBA	Q6mnv4 bdellovibri
439	33	61.1	242	2	Q511Z7_FLABR	Q511z7 flaveria br	512	33	61.1	480	2	Q4UK70_RICPE	Q4uk70 rickettsia
440	33	61.1	245	2	Q7U4U9_SYNPX	Q7u4u9 synechococc	513	33	61.1	483	2	Q82172_9GAMA	Q82172 pseudomonas
441	33	61.1	258	2	Q8RG82_FUSNN	Q8rg82 fusobacteri	514	33	61.1	501	2	Q72ZS0_BACCI	Q72ze0 bacillus ce
442	33	61.1	268	2	Q4UH86_THEAN	Q4uh86 theileria a	515	33	61.1	505	2	Q6FU41_CANGA	Q6fu41 candida gla
443	33	61.1	279	2	Q6D8A6_ERWCT	Q6d8a6 erwinia car	516	33	61.1	520	1	LAC4_TRAVE	Q12719 trameetes ve
444	33	61.1	283	2	Q6FMX7_CANGA	Q6fmx7 candida gla	517	33	61.1	520	1	LAC4_TRAVE	Q99055 trameetes vi
445	33	61.1	283	2	Q72U37_LEPIC	Q72u37 leptospira	518	33	61.1	520	2	Q50JG4_TRAVE	Q50jg4 trameetes ve
446	33	61.1	283	2	Q8F114_LEPIN	Q8f114 leptospira	519	33	61.1	524	2	Q6TH77_PAPHY	Q6th77 trameetes ap
447	33	61.1	292	2	Q6F7M8_ACIAD	Q6f7m8 acinetobact	520	33	61.1	526	2	Q5ACZ9_CANAL	Q5acz9 candida alb
448	33	61.1	294	2	Q9KKX1_VIBCH	Q9kxx1 vibrio chol	521	33	61.1	532	1	CBPY_YEAST	P00729 saccharomyc
449	33	61.1	296	2	Q8HQY9_STAEO	Q8hqy9 staphylococ	522	33	61.1	548	2	Q9Y049_CAELP	Q9y049 caenorhabdi
450	33	61.1	296	2	Q8CTG0_STAEP	Q8ctg0 staphylococ	523	33	61.1	550	2	Q7MTF4_PORGI	Q7mtf4 porphyromon
451	33	61.1	303	2	Q8RGN8_STAOU	Q8rgn8 staphylococ	524	33	61.1	559	2	Q74IM5_LACJO	Q74im5 lactobacill
452	33	61.1	323	2	Q87825_STAOU	Q87825 staphylococ	525	33	61.1	565	2	Q83DB5_COXBU	Q83db5 coxiella bu
453	33	61.1	326	2	Q4Y7Q5_PLACH	Q4y7q5 plasmodium	526	33	61.1	581	2	Q5SPR1_BRARE	Q5spr1 brachydanio
454	33	61.1	339	2	Q6KB01_TRAVE	Q6kb01 trameetes p	527	33	61.1	581	2	Q8A7H6_BACTN	Q8a7h6 bacteroides
455	33	61.1	344	1	OMP2_CHLPN	Q97f52 chlamydia v	528	33	61.1	590	1	NP44_YLDV	Q9dhr2 yaba-like d
456	33	61.1	346	2	Q77363_PLAF7	Q77363 plasmodium	529	33	61.1	595	2	Q4Y678_PLACH	Q4y678 plasmodium
457	33	61.1	348	2	Q5WYT8_LEGPL	Q5wyt8 legionella	530	33	61.1	595	2	Q8CWK4_STRMU	Q8cwx4 streptococc
458	33	61.1	348	2	Q5X7E2_LEGPA	Q5x7e2 legionella	531	33	61.1	599	2	Q4V108_BACCC	Q4v108 bacillus ce
459	33	61.1	348	2	Q5ZXW9_LEGPH	Q5zxw9 legionella	532	33	61.1	608	2	Q4IGT1_GIBZE	Q4igt1 gibberella
460	33	61.1	352	2	Q9P671_NEUCR	Q9p671 neurospora	533	33	61.1	618	2	Q54CJ0_DICDI	Q54cj0 dictyosteli
461	33	61.1	354	2	Q8XH37_CLOPE	Q8xh37 clostridium	534	33	61.1	618	2	Q55FC8_DICDI	Q55fc8 dictyosteli
462	33	61.1	356	2	Q6JTA7_CAPAN	Q6jta7 capsicum an	535	33	61.1	623	2	Q9V3T6_DROME	Q9v3t6 drosophila
463	33	61.1	359	2	Q9XUR3_CAELP	Q9xur3 caenorhabdi	536	33	61.1	625	2	Q4YJ93_PLABE	Q4y93 plasmodium
464	33	61.1	365	2	Q6DMQ1_HUMAN	Q6dmq1 homo sapien	537	33	61.1	648	2	Q4I706_GIBZE	Q4i706 gibberella
465	33	61.1	365	2	Q5LC71_BACFN	Q5lc71 bacteroides	538	33	61.1	656	2	Q7Y4Y1_BPR69	Q7y4y1 bacterioph
466	33	61.1	366	1	DPO3B_VIBCH	Q9kvx5 vibrio chol	539	33	61.1	663	2	Q4Z6T0_PLABE	Q4z6t0 plasmodium
467	33	61.1	366	1	Q5E8Z1_VIBF1	Q5e8z1 vibrio fiesc	540	33	61.1	665	2	Q894K5_CLOTE	Q894k5 clostridium
468	33	61.1	366	2	Q7NB61_MYCGA	Q7nb61 mycoplasma	541	33	61.1	668	2	Q553D7_DICDI	Q553d7 dictyosteli
469	33	61.1	366	2	Q8DDJ0_VIBVU	Q8ddj0 vibrio vuln	542	33	61.1				

543	33	61.1	668	2	Q86HC6_DICDI	Q86hc6 dictyosteli	616	33	61.1	1996	2	Q23293_ARATH	Q23293 arabidopels
544	33	61.1	669	2	Q54DY0_DICDI	Q54dy0 dictyosteli	617	33	61.1	1997	2	Q8LRM7_CHLRE	Q8lrn7 chlamydomon
545	33	61.1	670	2	Q6KIS9_MYCWO	Q6kis9 mycoplasma	618	33	61.1	2008	2	Q4ZD65_9VIRU	Q4zdn5 bacteriophon
546	33	61.1	671	2	Q6XC82_PROCIU	Q6xc82 ratufa bico	619	33	61.1	2055	1	DOCK9_MOUSE	Q8bik4 mus musculu
547	33	61.1	672	2	Q6A6B4_PRCIAC	Q6a6b4 propionibac	620	33	61.1	2063	2	Q8VOC2_9ENTO	Q8voc2 human polio
548	33	61.1	673	2	Q5HDB4_STAAC	Q5hdb4 staphylococ	621	33	61.1	2063	2	Q8VOC3_9ENTO	Q8voc3 human polio
549	33	61.1	674	2	Q6G6N1_STAAC	Q6g6n1 staphylococ	622	33	61.1	2063	2	Q8VOC4_9ENTO	Q8voc4 human polio
550	33	61.1	675	2	Q6GDZ1_STAAR	Q6gdz3 staphylococ	623	33	61.1	2105	2	Q4Y4H6_PLACH	Q4y4h6 plasmodium
551	33	61.1	676	2	Q7A3Q7_STAAN	Q7a3q7 staphylococ	624	33	61.1	2188	2	Q7D6F1_MYCTU	Q7d6f1 mycobacteri
552	33	61.1	677	2	Q8NUZ5_STAAN	Q8nuz5 staphylococ	625	33	61.1	2478	2	Q8YTN5_ASTAP	Q8ytn5 anabaena sp
553	33	61.1	678	2	Q99RJ2_STAAM	Q99rj2 staphylococ	626	33	61.1	2483	2	Q8XQB2_RALSO	Q8xqb2 ralestonia s
554	33	61.1	679	2	Q7NXU6_CHRVO	Q7nxu6 chromobacte	627	33	61.1	4811	2	Q4YV05_PLABE	Q4yv05 plasmodium
555	33	61.1	702	2	Q5B6G0_EMENI	Q5b6g0 aspergillus	628	33	61.1	5432	2	Q7RXP5_PLAYO	Q7rxp5 plasmodium
556	33	61.1	704	2	Q8I3L5_PLAF7	Q8i3l5 plasmodium	629	32.5	60.2	82	2	Q4XXY6_PLACH	Q4xy6 plasmodium
557	33	61.1	709	2	Q8UDF4_AGR15	Q8udf4 agrobacteri	630	32.5	60.2	251	2	Q4XFL7_PLACH	Q4xfl7 plasmodium
558	33	61.1	710	2	Q5CG67_CRYHO	Q5cg67 cryptospori	631	32.5	60.2	416	1	HGD_LEGPH	Q9x4t0 legionella
559	33	61.1	715	1	HELS_PYRHO	Q59025 pyrococcus	632	32.5	60.2	416	2	Q5WX50_LEGPL	Q5wx50 legionella
560	33	61.1	716	2	Q6C4H9_YARLI	Q6c4h9 yarrowia li	633	32.5	60.2	416	2	Q5X5S2_LRGPA	Q5x5s2 legionella
561	33	61.1	717	2	Q7CKP8_AGR15	Q7ckp8 agrobacteri	634	32.5	60.2	1167	2	Q5CTS9_CRYPV	Q5cte9 cryptospori
562	33	61.1	721	2	Q7SXG9_BRARE	Q7sxg9 brachydanio	635	32	59.3	74	2	Q8K671_STRP3	Q8k671 streptococ
563	33	61.1	731	2	Q5A4H5_CANAL	Q5a4h5 candida alb	636	32	59.3	86	2	Q9CQ84_MOUSE	Q9cqe4 m mus muscu
564	33	61.1	777	2	Q6BKX5_DEBHA	Q6bkx5 debaryomyce	637	32	59.3	87	2	Q58S11_9HIV1	Q58s11 human immun
565	33	61.1	789	2	Q7PDP0_PLAYO	Q7pdp0 plasmodium	638	32	59.3	88	2	Q5XAK6_STRP6	Q5xak6 streptococ
566	33	61.1	799	2	Q915F9_PSEAE	Q915f9 pseudomonas	639	32	59.3	88	2	Q9YJ4_STRPY	Q9yjk4 streptococ
567	33	61.1	800	2	Q4J678_AZOV1	Q4j678 azotobacter	640	32	59.3	88	2	Q8NZX5_STRP8	Q8nzz5 streptococ
568	33	61.1	802	2	Q4WL16_ASPFU	Q4wl16 aspergillus	641	32	59.3	89	2	Q31578_BACSU	Q31578 bacillus su
569	33	61.1	805	2	Q42PE8_PSEFU	Q42pe8 pseudomonas	642	32	59.3	92	2	Q33108_MYCLE	Q33108 mycobacteri
570	33	61.1	805	2	Q88MX5_PSEPK	Q88mx5 pseudomonas	643	32	59.3	92	2	P88660_9HIV1	P88660 human immun
571	33	61.1	805	2	Q87XG8_PSEPM	Q87xg8 pseudomonas	644	32	59.3	96	1	GLUC_MYOSC	Q9wt5 myoxocephal
572	33	61.1	806	2	Q4K6Y0_PSEF5	Q4k6y0 pseudomonas	645	32	59.3	97	2	Q9WJ75_9HIV1	Q9wt5 human immun
573	33	61.1	812	2	Q6FX93_CANGA	Q6fx93 candida gla	646	32	59.3	100	2	Q5BTA7_SCHJA	Q5bta7 schistosoma
574	33	61.1	825	2	Q55F59_DICDI	Q55f59 dictyosteli	647	32	59.3	101	2	Q4XCR0_PLACH	Q4xcr0 plasmodium
575	33	61.1	828	2	Q8L274_PROVU	Q8l274 proteus vul	648	32	59.3	104	2	Q99C95_9HIV1	Q99c95 human immun
576	33	61.1	835	2	Q9VAR0_DROME	Q9var0 drosophila	649	32	59.3	104	2	Q99C97_9HIV1	Q99c97 human immun
577	33	61.1	857	2	Q7T9Q5_GVAO	Q7t9q5 adoxophyes	650	32	59.3	104	2	Q99C99_9HIV1	Q99c99 human immun
578	33	61.1	880	2	Q61SG7_CAEER	Q61sg7 caenorhabdi	651	32	59.3	104	2	Q99CA1_9HIV1	Q99ca1 human immun
579	33	61.1	881	2	Q8JED9_9HIV1	Q8jed9 human immun	652	32	59.3	104	2	Q99CA4_9HIV1	Q99ca4 human immun
580	33	61.1	900	2	Q6FVQ0_CANGA	Q6fvq0 candida gla	653	32	59.3	104	2	Q99CA6_9HIV1	Q99ca6 human immun
581	33	61.1	917	2	Q95XQ4_CAEEL	Q95xq4 caenorhabdi	654	32	59.3	104	2	Q99CA9_9HIV1	Q99ca9 human immun
582	33	61.1	918	2	Q858F8_9CAUD	Q858f8 enterobacte	655	32	59.3	104	2	Q99CB0_9HIV1	Q99cb0 human immun
583	33	61.1	929	2	Q5LDR6_BACFN	Q5ldr6 bacteroides	656	32	59.3	104	2	Q99CB1_9HIV1	Q99cb1 human immun
584	33	61.1	929	2	Q64U00_BACFR	Q64u00 bacteroides	657	32	59.3	104	2	Q99CB2_9HIV1	Q99cb2 human immun
585	33	61.1	938	2	Q81EE6_PLAF7	Q81ee6 plasmodium	658	32	59.3	104	2	Q99CB4_9HIV1	Q99cb4 human immun
586	33	61.1	953	2	Q6BRA4_DEBHA	Q6bra4 debaryomyce	659	32	59.3	104	2	Q99CB6_9HIV1	Q99cb6 human immun
587	33	61.1	992	2	Q4XR12_PLACH	Q4xr12 plasmodium	660	32	59.3	104	2	Q99CB8_9HIV1	Q99cb8 human immun
588	33	61.1	1019	2	Q83CM1_COXBU	Q83cm1 coxiella bu	661	32	59.3	104	2	Q99CB9_9HIV1	Q99cb9 human immun
589	33	61.1	1024	2	Q6BQT8_DEBHA	Q6bqt8 debaryomyce	662	32	59.3	104	2	Q99CC0_9HIV1	Q99cc0 human immun
590	33	61.1	1028	2	Q76836_CAEEL	Q76836 caenorhabdi	663	32	59.3	104	2	Q99CC1_9HIV1	Q99cc1 human immun
591	33	61.1	1033	2	Q8D4H9_VIBVU	Q8d4h9 vibrio vuln	664	32	59.3	104	2	Q99CC3_9HIV1	Q99cc3 human immun
592	33	61.1	1033	2	Q7MG13_VIBVY	Q7mg13 vibrio vuln	665	32	59.3	104	2	Q99CC4_9HIV1	Q99cc4 human immun
593	33	61.1	1039	2	Q5X0E8_LEGPL	Q5x0e8 legionella	666	32	59.3	104	2	Q99CC5_9HIV1	Q99cc5 human immun
594	33	61.1	1068	2	Q725A5_LISMF	Q725a5 listeria mo	667	32	59.3	104	2	Q99CC6_9HIV1	Q99cc6 human immun
595	33	61.1	1068	2	Q8YAO9_LISMO	Q8yao9 listeria mo	668	32	59.3	104	2	Q99CC7_9HIV1	Q99cc7 human immun
596	33	61.1	1092	2	Q7OTU0_GIALA	Q7otu0 giardia lam	669	32	59.3	104	2	Q99CC8_9HIV1	Q99cc8 human immun
597	33	61.1	1144	2	Q8I2Z0_PLAF7	Q8i2zo plasmodium	670	32	59.3	104	2	Q99CC9_9HIV1	Q99cc9 human immun
598	33	61.1	1198	2	Q6CSR5_KLUUL	Q6csr5 kluyveromyc	671	32	59.3	104	2	Q99CD0_9HIV1	Q99cd0 human immun
599	33	61.1	1246	2	Q8T2L7_DICDI	Q8t2l7 dictyosteli	672	32	59.3	104	2	Q99CD1_9HIV1	Q99cd1 human immun
600	33	61.1	1255	2	Q4YVF1_PLABE	Q4yvf1 plasmodium	673	32	59.3	104	2	Q99CD2_9HIV1	Q99cd2 human immun
601	33	61.1	1270	2	Q5SAI8_DICDI	Q5sai8 dictyosteli	674	32	59.3	104	2	Q99CD4_9HIV1	Q99cd4 human immun
602	33	61.1	1342	2	Q8I2I8_PLAF7	Q8i2i8 plasmodium	675	32	59.3	104	2	Q99CD5_9HIV1	Q99cd5 human immun
603	33	61.1	1355	2	Q5B2F9_EMENI	Q5b2f9 aspergillus	676	32	59.3	104	2	Q99CD6_9HIV1	Q99cd6 human immun
604	33	61.1	1404	2	Q8RJN9_MYCHO	Q8rjn9 mycoplasma	677	32	59.3	104	2	Q99CD7_9HIV1	Q99cd7 human immun
605	33	61.1	1413	2	Q4PCS7_USTMA	Q4pcs7 ustilago ma	678	32	59.3	104	2	Q99CD8_9HIV1	Q99cd8 human immun
606	33	61.1	1418	2	Q9GSZ6_PLACH	Q9gsz6 plasmodium	679	32	59.3	104	2	Q99CD9_9HIV1	Q99cd9 human immun
607	33	61.1	1432	2	Q7R0U4_GIALA	Q7rou4 giardia lam	680	32	59.3	104	2	Q99CE1_9HIV1	Q99ce1 human immun
608	33	61.1	1463	2	Q86919_STASA	Q86919 staphylococ	681	32	59.3	104	2	Q99CE2_9HIV1	Q99ce2 human immun
609	33	61.1	1525	2	Q5AR27_DICDI	Q5ar27 dictyosteli	682	32	59.3	104	2	Q99CE3_9HIV1	Q99ce3 human immun
610	33	61.1	1562	2	Q7RKN2_PLAYO	Q7rkn2 plasmodium	683	32	59.3	104	2	Q99CE4_9HIV1	Q99ce4 human immun
611	33	61.1	1616	1	YARD_SCHPO	Q99853 schizosacch	684	32	59.3	104	2	Q99CE5_9HIV1	Q99ce5 human immun
612	33	61.1	1687	2	Q81BA8_PLAF7	Q81ba8 plasmodium	685	32	59.3	104	2	Q99CE6_9HIV1	Q99ce6 human immun
613	33	61.1	1807	2	Q55GM7_DICDI	Q55gm7 dictyosteli	686	32	59.3	104	2	Q99CE7_9HIV1	Q99ce7 human immun
614	33	61.1	1841	2	Q7RTA2_PLAYO	Q7rta2 plasmodium	687	32	59.3	104	2	Q99CE9_9HIV1	Q99ce9 human immun
615	33	61.1	1920	2	Q7TN11_MOUSE	Q7tn11 mus musculu	688	32	59.3	104	2	Q99CF0_9HIV1	Q99cf0 human immun

689	32	59.3	104	2	Q9SCF1_9HIV1	Q9SCf1 human immun	762	32	59.3	124	2	Q7SIR4_9HIV1	Q7sir4 human immun
690	32	58.3	104	2	Q9SCF2_9HIV1	Q9SCf2 human immun	763	32	59.3	125	2	Q8C1F5_MOUSE	Q8c1f5 mus musculus
691	32	59.3	104	2	Q9SCF3_9HIV1	Q9SCf3 human immun	764	32	59.3	127	2	Q9YF58_9HIV1	Q9yf58 human immun
692	32	59.3	104	2	Q9SCF6_9HIV1	Q9SCf6 human immun	765	32	59.3	128	2	Q5YD99_BIOMPHARI	Q5y999 Biomphalaria
693	32	59.3	104	2	Q9SCF7_9HIV1	Q9SCf7 human immun	766	32	59.3	128	2	Q8I130_CAEEL	Q8i130 caenorhabdi
694	32	59.3	104	2	Q9SCF8_9HIV1	Q9SCf8 human immun	767	32	59.3	129	2	Q4Y952_PLACH	Q4y952 plasmodium
695	32	59.3	104	2	Q9SCG0_9HIV1	Q9SCg0 human immun	768	32	59.3	129	2	Q4YEH3_PLABE	Q4yeh3 plasmodium
696	32	59.3	104	2	Q9SCG2_9HIV1	Q9SCg2 human immun	769	32	59.3	129	2	Q4Z5W0_PLABE	Q4z5w0 plasmodium
697	32	59.3	104	2	Q9SCG3_9HIV1	Q9SCg3 human immun	770	32	59.3	130	1	KV5G_MOUSE	P01639 mus musculus
698	32	59.3	104	2	Q9SCG4_9HIV1	Q9SCg4 human immun	771	32	59.3	130	2	Q56JL5_9HIV1	Q56jl5 human immun
699	32	59.3	104	2	Q9SCG5_9HIV1	Q9SCg5 human immun	772	32	59.3	130	2	Q56JL6_9HIV1	Q56jl6 human immun
700	32	59.3	104	2	Q9SCG7_9HIV1	Q9SCg7 human immun	773	32	59.3	130	2	Q56JL7_9HIV1	Q56jl7 human immun
701	32	59.3	104	2	Q9SCG8_9HIV1	Q9SCg8 human immun	774	32	59.3	130	2	Q56JL8_9HIV1	Q56jl8 human immun
702	32	59.3	104	2	Q9SCG9_9HIV1	Q9SCg9 human immun	775	32	59.3	130	2	Q56JL9_9HIV1	Q56jl9 human immun
703	32	59.3	104	2	Q9SCH0_9HIV1	Q9SCH0 human immun	776	32	59.3	130	2	Q56JMO_9HIV1	Q56jmo human immun
704	32	59.3	104	2	Q9SCH1_9HIV1	Q9SCH1 human immun	777	32	59.3	130	2	Q56JN1_9HIV1	Q56jnl1 human immun
705	32	59.3	104	2	Q9SCH2_9HIV1	Q9SCH2 human immun	778	32	59.3	130	2	Q56JN2_9HIV1	Q56jnl2 human immun
706	32	59.3	104	2	Q9SCH4_9HIV1	Q9SCH4 human immun	779	32	59.3	130	2	Q58S05_9HIV1	Q58s05 human immun
707	32	59.3	104	2	Q9SCH5_9HIV1	Q9SCH5 human immun	780	32	59.3	130	2	Q7ZBS3_9HIV1	Q7zbs3 human immun
708	32	59.3	104	2	Q9SCH6_9HIV1	Q9SCH6 human immun	781	32	59.3	130	2	Q7ZSP5_9HIV1	Q7zsp5 human immun
709	32	59.3	104	2	Q9SCH7_9HIV1	Q9SCH7 human immun	782	32	59.3	130	2	Q90QU6_9HIV1	Q90qu6 human immun
710	32	59.3	104	2	Q9SCH8_9HIV1	Q9SCH8 human immun	783	32	59.3	130	2	Q90QW4_9HIV1	Q90qw4 human immun
711	32	59.3	105	2	Q931I0_STAAM	Q931i0 staphylococ	784	32	59.3	130	2	Q9QKV1_9HIV1	Q9qkv1 human immun
712	32	59.3	105	2	Q9SM1_STAAM	Q9sm1 staphylococ	785	32	59.3	130	2	Q9QKV7_9HIV1	Q9qkv7 human immun
713	32	59.3	106	2	Q6TJU2_9HIV1	Q6tjj2 human immun	786	32	59.3	130	2	Q9QKV8_9HIV1	Q9qkv8 human immun
714	32	59.3	106	2	Q6TJU3_9HIV1	Q6tjj3 human immun	787	32	59.3	130	2	Q9QKY4_9HIV1	Q9qky4 human immun
715	32	59.3	108	1	KV07_RABIT	Q6cjj1 human immun	788	32	59.3	130	2	Q9QL27_9HIV1	Q9ql27 human immun
716	32	59.3	111	2	Q4V2B9_BURMA	P01688 cryptotolagus	789	32	59.3	130	2	Q9QL43_9HIV1	Q9ql43 human immun
717	32	59.3	113	2	Q9WK46_9HIV1	Q9wk46 human immun	790	32	59.3	131	2	Q7ZBS1_9HIV1	Q7zbs1 human immun
718	32	59.3	113	2	Q9WK48_9HIV1	Q9wk48 human immun	791	32	59.3	131	2	Q90QR2_9HIV1	Q90qr2 human immun
719	32	59.3	113	2	Q9WK50_9HIV1	Q9wk50 human immun	792	32	59.3	131	2	Q90RS5_9HIV1	Q90rs5 human immun
720	32	59.3	113	2	Q9WK52_9HIV1	Q9wk52 human immun	793	32	59.3	131	2	Q90QU0_9HIV1	Q90qu0 human immun
721	32	59.3	113	2	Q9WK53_9HIV1	Q9wk53 human immun	794	32	59.3	131	2	Q90QU1_9HIV1	Q90qu1 human immun
722	32	59.3	113	2	Q9WK54_9HIV1	Q9wk54 human immun	795	32	59.3	131	2	Q9QKZ1_9HIV1	Q9qkz1 human immun
723	32	59.3	113	2	Q9WK55_9HIV1	Q9wk55 human immun	796	32	59.3	132	2	Q56JN4_9HIV1	Q56jnl4 human immun
724	32	59.3	113	2	Q9WK56_9HIV1	Q9wk56 human immun	797	32	59.3	132	2	Q56JN5_9HIV1	Q56jnl5 human immun
725	32	59.3	113	2	Q9WK57_9HIV1	Q9wk57 human immun	798	32	59.3	132	2	Q56JN6_9HIV1	Q56jnl6 human immun
726	32	59.3	113	2	Q9WK61_9HIV1	Q9wk61 human immun	799	32	59.3	132	2	Q56JN7_9HIV1	Q56jnl7 human immun
727	32	59.3	113	2	Q9WK62_9HIV1	Q9wk62 human immun	800	32	59.3	132	2	Q56JN8_9HIV1	Q56jnl8 human immun
728	32	59.3	113	2	Q9WK63_9HIV1	Q9wk63 human immun	801	32	59.3	132	2	Q56JN9_9HIV1	Q56jnl9 human immun
729	32	59.3	113	2	Q9WK64_9HIV1	Q9wk64 human immun	802	32	59.3	132	2	Q56JP0_9HIV1	Q56jpl0 human immun
730	32	59.3	113	2	Q9WK65_9HIV1	Q9wk65 human immun	803	32	59.3	132	2	Q56JP1_9HIV1	Q56jpl1 human immun
731	32	59.3	113	2	Q9WK66_9HIV1	Q9wk66 human immun	804	32	59.3	132	2	Q56JP2_9HIV1	Q56jpl2 human immun
732	32	59.3	113	2	Q9WK67_9HIV1	Q9wk67 human immun	805	32	59.3	132	2	Q56JP3_9HIV1	Q56jpl3 human immun
733	32	59.3	113	2	Q9WK68_9HIV1	Q9wk68 human immun	806	32	59.3	132	2	Q56JP4_9HIV1	Q56jpl4 human immun
734	32	59.3	113	2	Q9WK69_9HIV1	Q9wk69 human immun	807	32	59.3	132	2	Q7ZSP0_9HIV1	Q7zsp0 human immun
735	32	59.3	113	2	Q9WK70_9HIV1	Q9wk70 human immun	808	32	59.3	132	2	Q7ZSQ3_9HIV1	Q7zsq3 human immun
736	32	59.3	113	2	Q9WK71_9HIV1	Q9wk71 human immun	809	32	59.3	132	2	Q9QKU7_9HIV1	Q9qku7 human immun
737	32	59.3	113	2	Q9WK72_9HIV1	Q9wk72 human immun	810	32	59.3	132	2	Q9QKU8_9HIV1	Q9qku8 human immun
738	32	59.3	113	2	Q9WK73_9HIV1	Q9wk73 human immun	811	32	59.3	132	2	Q9QKU9_9HIV1	Q9qku9 human immun
739	32	59.3	113	2	Q9WK74_9HIV1	Q9wk74 human immun	812	32	59.3	132	2	Q9QKV2_9HIV1	Q9qkv2 human immun
740	32	59.3	113	2	Q9WK75_9HIV1	Q9wk75 human immun	813	32	59.3	132	2	Q9QKV8_9HIV1	Q9qkv8 human immun
741	32	59.3	113	2	Q9WK76_9HIV1	Q9wk76 human immun	814	32	59.3	132	2	Q9QKZ0_9HIV1	Q9qkz0 human immun
742	32	59.3	113	2	Q9WK78_9HIV1	Q9wk78 human immun	815	32	59.3	132	2	Q9QL01_9HIV1	Q9ql01 human immun
743	32	59.3	113	2	Q9WK80_9HIV1	Q9wk80 human immun	816	32	59.3	132	2	Q9QL29_9HIV1	Q9ql29 human immun
744	32	59.3	113	2	Q9WK81_9HIV1	Q9wk81 human immun	817	32	59.3	132	2	Q9QL30_9HIV1	Q9ql30 human immun
745	32	59.3	113	2	Q9WK82_9HIV1	Q9wk82 human immun	818	32	59.3	132	2	Q56JL1_9HIV1	Q56jl1 human immun
746	32	59.3	113	2	Q9WK83_9HIV1	Q9wk83 human immun	819	32	59.3	133	2	Q56JL3_9HIV1	Q56jl3 human immun
747	32	59.3	113	2	Q9WK85_9HIV1	Q9wk85 human immun	820	32	59.3	133	2	Q56JL4_9HIV1	Q56jl4 human immun
748	32	59.3	113	2	Q9WK89_9HIV1	Q9wk89 human immun	821	32	59.3	133	2	Q7ZBS5_9HIV1	Q7zbs5 human immun
749	32	59.3	113	2	Q9WKA0_9HIV1	Q9wka0 human immun	822	32	59.3	133	2	Q7ZBS7_9HIV1	Q7zbs7 human immun
750	32	59.3	115	1	KV31_HUMAN	P04433 homo sapien	823	32	59.3	133	2	Q7ZB65_9HIV1	Q7zbs6 human immun
751	32	59.3	115	2	Q6TIT3_9HIV1	Q6tit3 human immun	824	32	59.3	133	2	Q7ZB69_9HIV1	Q7zbs9 human immun
752	32	59.3	115	2	Q6TIW6_9HIV1	Q6tiw6 human immun	825	32	59.3	133	2	Q7ZB75_9HIV1	Q7zbs7 human immun
753	32	59.3	115	2	Q6TJ16_9HIV1	Q6tj16 human immun	826	32	59.3	133	2	Q7ZSP2_9HIV1	Q7zsp2 human immun
754	32	59.3	115	2	Q6TJ74_9HIV1	Q6tj74 human immun	827	32	59.3	133	2	Q7ZSP6_9HIV1	Q7zsp6 human immun
755	32	59.3	115	2	Q6TJDO_9HIV1	Q6tjdo human immun	828	32	59.3	133	2	Q7ZSQ2_9HIV1	Q7zsq2 human immun
756	32	59.3	117	2	Q6TJ82_9HIV1	Q6tj82 human immun	829	32	59.3	133	2	Q7ZSQ8_9HIV1	Q7zsq8 human immun
757	32	59.3	118	2	Q6TQC4_9HIV1	Q6tqc4 human immun	830	32	59.3	133	2	Q90QS8_9HIV1	Q90qs8 human immun
758	32	59.3	118	2	Q6TJBO_9HIV1	Q6tjbo human immun	831	32	59.3	133	2	Q90QS5_9HIV1	Q90qs5 human immun
759	32	59.3	121	2	Q57485_DRONO	Q57485 dromaelus no	832	32	59.3	133	2	Q90QT6_9HIV1	Q90qt6 human immun
760	32	59.3	121	2	Q6ECP3_9HIV1	Q6ecp3 human immun	833	32	59.3	133	2	Q90QT7_9HIV1	Q90qt7 human immun
761	32	59.3	122	2	Q5A6T7_CANAL	Q5a6t7 candida alb	834	32	59.3	133	2	Q90QU2_9HIV1	Q90qu2 human immun



835	32	59.3	133	2	Q90QU4_9H1V1	Q90QU4	human	immun	908	32	59.3	174	2	Q7SPM7_9H1V1	Q7SPM7	human	immun
836	32	59.3	133	2	Q90QU7_9H1V1	Q90QU7	human	immun	909	32	59.3	174	2	Q7SPM8_9H1V1	Q7SPM8	human	immun
837	32	59.3	133	2	Q90QU9_9H1V1	Q90QU9	human	immun	910	32	59.3	174	2	Q7SPM9_9H1V1	Q7SPM9	human	immun
838	32	59.3	133	2	Q90QV0_9H1V1	Q90QV0	human	immun	911	32	59.3	174	2	Q7SPN0_9H1V1	Q7SPN0	human	immun
839	32	59.3	133	2	Q90QV5_9H1V1	Q90QV5	human	immun	912	32	59.3	174	2	Q7SPN1_9H1V1	Q7SPN1	human	immun
840	32	59.3	133	2	Q90QV6_9H1V1	Q90QV6	human	immun	913	32	59.3	175	1	REG3A_MOUSE	O9037	mus musculus	
841	32	59.3	133	2	Q90QW1_9H1V1	Q90QW1	human	immun	914	32	59.3	175	2	Q794C6_MOUSE	O9037	mus musculus	
842	32	59.3	133	2	Q90QV0_9H1V1	Q90QV0	human	immun	915	32	59.3	178	2	Q4YEJ0_PLABE	Q4YEJ0	plasmodium	
843	32	59.3	133	2	Q90KV3_9H1V1	Q90KV3	human	immun	916	32	59.3	182	2	Q8EBW8_SHEON	Q8EBW8	shewanella	
844	32	59.3	133	2	Q90KV5_9H1V1	Q90KV5	human	immun	917	32	59.3	182	2	Q5SCZ1_RUPLU	Q5SCZ1	huperzia lu	
845	32	59.3	133	2	Q90KV2_9H1V1	Q90KV2	human	immun	918	32	59.3	188	2	Q89ZC6_BACTN	Q89ZC6	bacteroides	
846	32	59.3	133	2	Q90KX3_9H1V1	Q90KX3	human	immun	919	32	59.3	189	2	Q9J6W4_9H1V1	Q9J6W4	human	immun
847	32	59.3	133	2	Q90KX4_9H1V1	Q90KX4	human	immun	920	32	59.3	197	2	Q4YFZ2_PLABE	Q4YFZ2	plasmodium	
848	32	59.3	133	2	Q90KX9_9H1V1	Q90KX9	human	immun	921	32	59.3	201	2	Q3JVP5_NEIMA	Q3JVP5	neisseria m	
849	32	59.3	133	2	Q90KZ2_9H1V1	Q90KZ2	human	immun	922	32	59.3	201	2	Q9KOM0_NEIMB	Q9KOM0	neisseria m	
850	32	59.3	133	2	Q90KZ8_9H1V1	Q90KZ8	human	immun	923	32	59.3	202	2	Q4YSC8_PLABE	Q4YSC8	plasmodium	
851	32	59.3	133	2	Q90KZ9_9H1V1	Q90KZ9	human	immun	924	32	59.3	202	2	Q9IUL6_9H1V1	Q9IUL6	human	immun
852	32	59.3	133	2	Q90L00_9H1V1	Q90L00	human	immun	925	32	59.3	202	2	Q9IULP_9H1V1	Q9IULP	human	immun
853	32	59.3	133	2	Q90L02_9H1V1	Q90L02	human	immun	926	32	59.3	202	2	Q9IUR6_9H1V1	Q9IUR6	human	immun
854	32	59.3	133	2	Q90L03_9H1V1	Q90L03	human	immun	927	32	59.3	203	2	Q5E0W9_VTBF1	Q5E0W9	vibrio floc	
855	32	59.3	133	2	Q90L04_9H1V1	Q90L04	human	immun	928	32	59.3	206	2	Q7ZN55_9H1V1	Q7ZN55	human	immun
856	32	59.3	133	2	Q90L06_9H1V1	Q90L06	human	immun	929	32	59.3	206	2	Q7ZN87_9H1V1	Q7ZN87	human	immun
857	32	59.3	133	2	Q90L07_9H1V1	Q90L07	human	immun	930	32	59.3	206	2	Q7ZN88_9H1V1	Q7ZN88	human	immun
858	32	59.3	133	2	Q90L32_9H1V1	Q90L32	human	immun	931	32	59.3	206	2	Q7ZN92_9H1V1	Q7ZN92	human	immun
859	32	59.3	133	2	Q90L37_9H1V1	Q90L37	human	immun	932	32	59.3	206	2	Q7ZN95_9H1V1	Q7ZN95	human	immun
860	32	59.3	133	2	Q90QV4_9H1V1	Q90QV4	human	immun	933	32	59.3	206	2	Q7ZN97_9H1V1	Q7ZN97	human	immun
861	32	59.3	134	2	Q58S13_9H1V1	Q58S13	human	immun	934	32	59.3	206	2	Q9J6X8_9H1V1	Q9J6X8	human	immun
862	32	59.3	134	2	Q67QC5_9H1V1	Q67QC5	human	immun	935	32	59.3	206	2	Q9J6X9_9H1V1	Q9J6X9	human	immun
863	32	59.3	134	2	Q90Q74_9H1V1	Q90Q74	human	immun	936	32	59.3	207	1	Y896_THETN	Q8RBC6	thermoanaer	
864	32	59.3	136	2	Q58S06_9H1V1	Q58S06	human	immun	937	32	59.3	207	2	Q9DUV7_9H1V1	Q9DUV7	human	immun
865	32	59.3	136	2	Q51K82_9H1V1	Q51K82	human	immun	938	32	59.3	207	2	Q9DUW4_9H1V1	Q9DUW4	human	immun
866	32	59.3	138	2	Q51K81_9H1V1	Q51K81	human	immun	939	32	59.3	207	2	Q9DUX0_9H1V1	Q9DUX0	human	immun
867	32	59.3	138	2	Q51K93_9H1V1	Q51K93	human	immun	940	32	59.3	207	2	Q9DUX2_9H1V1	Q9DUX2	human	immun
868	32	59.3	138	2	Q51K98_9H1V1	Q51K98	human	immun	941	32	59.3	207	2	Q9DUX5_9H1V1	Q9DUX5	human	immun
869	32	59.3	138	2	Q7S1R5_9H1V1	Q7S1R5	human	immun	942	32	59.3	207	2	Q9DUX5_9H1V1	Q9DUX5	human	immun
870	32	59.3	138	2	Q7SKP9_9H1V1	Q7SKP9	human	immun	943	32	59.3	207	2	Q9DUX6_9H1V1	Q9DUX6	human	immun
871	32	59.3	139	2	Q51K87_9H1V1	Q51K87	human	immun	944	32	59.3	207	2	Q9DUZ2_9H1V1	Q9DUZ2	human	immun
872	32	59.3	139	2	Q51K91_9H1V1	Q51K91	human	immun	945	32	59.3	207	2	Q9DV02_9H1V1	Q9DV02	human	immun
873	32	59.3	140	2	Q51K90_9H1V1	Q51K90	human	immun	946	32	59.3	207	2	Q9IU05_9H1V1	Q9IU05	human	immun
874	32	59.3	140	2	Q51K90_9H1V1	Q51K90	human	immun	947	32	59.3	207	2	Q9IUR1_9H1V1	Q9IUR1	human	immun
875	32	59.3	140	2	Q51KCA_9H1V1	Q51KCA	human	immun	948	32	59.3	207	2	Q9J6Y0_9H1V1	Q9J6Y0	human	immun
876	32	59.3	140	2	Q698Z8_9H1V1	Q698Z8	human	immun	949	32	59.3	207	2	Q9Q2J0_9H1V1	Q9Q2J0	human	immun
877	32	59.3	140	2	Q67QC2_9H1V1	Q67QC2	human	immun	950	32	59.3	207	2	Q9Q2K1_9H1V1	Q9Q2K1	human	immun
878	32	59.3	140	2	Q67QC3_9H1V1	Q67QC3	human	immun	951	32	59.3	208	2	Q5W3W9_9H1V1	Q5W3W9	human	immun
879	32	59.3	140	2	Q7SKQ9_9H1V1	Q7SKQ9	human	immun	952	32	59.3	208	2	Q9IUS8_9H1V1	Q9IUS8	human	immun
880	32	59.3	141	2	Q8J78E7_9H1V1	Q8J78E7	human	immun	953	32	59.3	208	2	Q9J6X7_9H1V1	Q9J6X7	human	immun
881	32	59.3	142	2	Q58S03_9H1V1	Q58S03	human	immun	954	32	59.3	209	2	Q7ZN66_9H1V1	Q7ZN66	human	immun
882	32	59.3	142	2	Q8J8F9_9H1V1	Q8J8F9	human	immun	955	32	59.3	209	2	Q9IUK5_9H1V1	Q9IUK5	human	immun
883	32	59.3	143	2	Q51K85_9H1V1	Q51K85	human	immun	956	32	59.3	211	2	Q9IUM5_9H1V1	Q9IUM5	human	immun
884	32	59.3	143	2	Q51KCS_9H1V1	Q51KCS	human	immun	957	32	59.3	211	2	Q9IUP6_9H1V1	Q9IUP6	human	immun
885	32	59.3	144	2	Q58RZ9_9H1V1	Q58RZ9	human	immun	958	32	59.3	212	2	Q5DB91_SCHJA	Q5DB91	schistosoma	
886	32	59.3	145	2	Q58S00_9H1V1	Q58S00	human	immun	959	32	59.3	212	2	Q9J783_9H1V1	Q9J783	human	immun
887	32	59.3	145	2	Q58S22_9H1V1	Q58S22	human	immun	960	32	59.3	213	2	Q5W3X9_9H1V1	Q5W3X9	human	immun
888	32	59.3	146	2	Q9CVFA_MOUSE	Q9CVFA	mus musculus		961	32	59.3	213	2	Q9J6W8_9H1V1	Q9J6W8	human	immun
889	32	59.3	146	2	Q76256_9H1V1	Q76256	human	immun	962	32	59.3	214	2	Q74JW7_LACJO	Q74JW7	lactobacill	
890	32	59.3	146	2	Q76260_9H1V1	Q76260	human	immun	963	32	59.3	214	2	Q6TUY8_YMTV	Q6TUY8	yaba monkey	
891	32	59.3	146	2	Q76261_9H1V1	Q76261	human	immun	964	32	59.3	214	2	Q9DHT8_YLDD	Q9DHT8	yaba-like d	
892	32	59.3	146	2	Q76262_9H1V1	Q76262	human	immun	965	32	59.3	215	2	Q5VG56_9H1V1	Q5VG56	human	immun
893	32	59.3	147	2	Q51KB4_9H1V1	Q51KB4	human	immun	966	32	59.3	216	2	Q4UF99_THEAN	Q4UF99	theileria a	
894	32	59.3	148	2	Q7QJH8_ANOGA	Q7QJH8	anopheles g		967	32	59.3	216	2	Q9RN47_SALTI	Q9RN47	salmonella	
895	32	59.3	148	2	Q58S18_9H1V1	Q58S18	human	immun	968	32	59.3	216	2	Q9IDR2_9H1V1	Q9IDR2	human	immun
896	32	59.3	149	2	Q4YE48_PLABE	Q4YE48	plasmodium		969	32	59.3	217	2	Q9IVR1_9H1V1	Q9IVR1	human	immun
897	32	59.3	149	2	Q58S01_9H1V1	Q58S01	human	immun	970	32	59.3	220	2	Q52PW6_9H1V1	Q52PW6	human	immun
898	32	59.3	151	2	Q4HP61_CAMUP	Q4HP61	campylobact		971	32	59.3	220	2	Q52PX7_9H1V1	Q52PX7	human	immun
899	32	59.3	156	1	RS7_CHRVO	Q7HGE9	chromobacte		972	32	59.3	220	2	Q52PX8_9H1V1	Q52PX8	human	immun
900	32	59.3	156	2	Q9J6Y6_9H1V1	Q9J6Y6	human	immun	973	32	59.3	220	2	Q52PX9_9H1V1	Q52PX9	human	immun
901	32	59.3	158	2	Q9U509_MANSE	Q9U509	manduca sex		974	32	59.3	220	2	Q52PY1_9H1V1	Q52PY1	human	immun
902	32	59.3	161	2	Q4IMV3_GIBZE	Q4IMV3	gibberella		975	32	59.3	220	2	Q52PY2_9H1V1	Q52PY2	human	immun
903	32	59.3	162	2	Q5A3M0_CANAL	Q5A3M0	cardida alb		976	32	59.3	220	2	Q52PY3_9H1V1	Q52PY3	human	immun
904	32	59.3	166	2	O89J36_ASF	O89J36	african ewi		977	32	59.3	220	2	Q52PV7_9H1V1	Q52PV7	human	immun
905	32	59.3	167	2	Q4XT00_PLACH	Q4XT00	plasmodium		978	32	59.3	220	2	Q52PV8_9H1V1	Q52PV8	human	immun
906	32	59.3	168	2	Q4Z700_PLABE	Q4Z700	plasmodium		979	32	59.3	220	2	Q9IDQ1_9H1V1	Q9IDQ1	human	immun
907	32	59.3	174	1	REG3A_RAT	P35231	rattus norv		980	32	59.3	220	2	Q9IUT6_9H1V1	Q9IUT6	human	immun

981 32 59.3 222 2 Q5F8M4 NEIG1  
982 32 59.3 222 2 Q9JTS4 NEIMA  
983 32 59.3 222 2 Q9JYT3 NEISSERIA m  
984 32 59.3 222 2 Q52PW7 H9HIV1  
985 32 59.3 222 2 Q52PW8 H9HIV1  
986 32 59.3 222 2 Q52PW9 H9HIV1  
987 32 59.3 222 2 Q52PX0 H9HIV1  
988 32 59.3 222 2 Q52PX1 H9HIV1  
989 32 59.3 222 2 Q52PX2 H9HIV1  
990 32 59.3 222 2 Q52PX3 H9HIV1  
991 32 59.3 222 2 Q52PX4 H9HIV1  
992 32 59.3 222 2 Q52PX5 H9HIV1  
993 32 59.3 222 2 Q52PX6 H9HIV1  
994 32 59.3 222 2 Q70Q94 H9HIV1  
995 32 59.3 222 2 Q91UY1 H9HIV1  
996 32 59.3 222 2 Q91UY4 H9HIV1  
997 32 59.3 222 2 Q91VR5 H9HIV1  
998 32 59.3 224 2 Q5W400 H9HIV1  
999 32 59.3 225 2 Q7ZN23 H9HIV1  
1000 32 59.3 226 2 Q91DN4 H9HIV1

## ALIGNMENTS

RESULT 1  
ID KV5U MOUSE STANDARD; PRT; 108 AA.  
AC P04946;  
DT 13-AUG-1987 (Rel. 05, Created)  
DT 13-AUG-1987 (Rel. 05, Last sequence update)  
DE 10-MAY-2005 (Rel. 47, Last annotation update)  
DE IG kappa chain V-V region NQ5-89.4.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridea; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=83271467; PubMed=6877353;  
RA Kaartinen M., Griffiths G.M., Markham A.F., Milestein C.;  
RT "mRNA sequences define an unusually restricted IgG response to 2-phenyloxazalone and its early diversification."  
RL Nature 304:320-324 (1983).  
CC -!- FUNCTION: Anti-2-phenyl oxazalone (PROX) Antibody.  
CC -----  
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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CC use as long as its content is in no way modified and this statement is not  
CC removed.  
CC -----  
DR EMBL; K00745; AAA38690.1; -; mRNA.  
DR HSP; P01594; 1JUV5.  
DR SMR; P04946; 1-107.  
DR Ensembl; ENSMUSG00000029991; Mus musculus.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003596; IG\_V.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW Hybridoma; Immunoglobulin domain; Immunoglobulin V region.  
FT REGION 1 23 Framework-1.  
FT REGION 24 34 Complementarity-determining-1.  
FT REGION 35 49 Framework-2.  
FT REGION 50 56 Complementarity-determining-2.  
FT REGION 57 88 Framework-3.  
FT REGION 89 97 Complementarity-determining-3.  
FT REGION 98 107 Framework-4.  
FT DISULFID 23 88 By similarity.  
FT NON TER 108 108  
SQ SEQUENCE 108 AA; 11870 MW; DB3C885920DC6DDD CRC64;

Query Match 100.0%; Score 54; DB 1; Length 108;  
Best Local Similarity 100.0%; Pred. No. 0.039;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SASQDISNYLN 11  
| | | | | | | | | |  
DB 24 SASQDISNYLN 34  
| | | | | | | | | |  
RESULT 2  
Q6LBV5 HUMAN PRELIMINARY; PRT; 50 AA.  
ID Q6LBV5 HUMAN  
AC Q6LBV5  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE DNA rearranged by a t(2;8) translocation leading to Burkitt's lymphoma  
DE in the cell line JI (clone Jip) (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=87259967; PubMed=3110741;  
RA Klobbeck H.G., Combrato G., Zachau H.G.;  
RT "N segment insertion and region directed somatic hypermutation in a  
RT kappa gene of a t(2;8) chromosomal translocation."  
RL Nucleic Acids Res. 15:4877-4888 (1987).  
DR EMBL; X05929; CAE82012.1; -; Genomic\_DNA.  
DR HSP; P01607; 1AR2.  
DR SMR; Q6LBV5; 4-50.  
FT NON TER 1 1  
FT NON TER 50 50  
SQ SEQUENCE 50 AA; 5486 MW; 3A74178720E0DA21 CRC64;  
Query Match 92.6%; Score 50; DB 2; Length 50;  
Best Local Similarity 100.0%; Pred. No. 0.1;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 ASQDISNYLN 11  
| | | | | | | | | |  
DB 28 ASQDISNYLN 37  
| | | | | | | | | |  
RESULT 3  
KV5K MOUSE STANDARD; PRT; 108 AA.  
ID KV5K MOUSE  
AC P01644;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 10-MAY-2005 (Rel. 47, Last annotation update)  
DE IG kappa chain V-V region HP R16.7.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridea; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP PROTEIN SEQUENCE.  
RC STRAIN=AJ/J;  
RX MEDLINE=82150934; PubMed=6801658;  
RA Siegelman M., Capra J.D.;  
RT "Complete amino acid sequence of light chain variable regions derived  
RT from five monoclonal anti-p-azophenylarsenate antibodies differing  
RT with respect to a crossreactive idiotype."  
RL Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683 (1981).  
CC -!- MUSCLEANEUS: Anti-arsenate hybridoma protein.  
CC -----  
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-----  
 DR PIR; A01927; KVSAR.  
 DR HSP; P01594; 1JVS.  
 DR SMR; P01644; 1-108.  
 DR Ensembl; ENSMUSG0000029991; Mus musculus.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003596; IG\_v.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; P550835; IG LIKE; 1.  
 KW Direct protein sequencing; Immunoglobulin domain;  
 KW Immunoglobulin V region.

FT REGION 1 23  
 FT REGION 24 34  
 FT REGION 35 49  
 FT REGION 50 56  
 FT REGION 57 88  
 FT REGION 89 97  
 FT REGION 98 108  
 FT DISULFID 23 88  
 FT NON TER 108 108  
 SQ SEQUENCE 108 AA; 11910 MW; A554642C63E9F597 CRC64;

Query Match 92.6%; Score 50; DB 1; Length 108;  
 Best Local Similarity 100.0%; Pred. No. 0.22;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASQDISNYLN 11  
 |||||  
 Db 25 ASQDISNYLN 34

## RESULT 4

KV5L MOUSE STANDARD; PRT; 108 AA.  
 AC P01645;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 10-MAY-2005 (Rel. 47, Last annotation update)  
 DE Ig kappa chain V-V region HP 93G7.  
 OS Mus musculus (Mouse)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Muridae; Murinae; Mus.  
 OC NCBI\_TaxID=10090;  
 RN [1]  
 RP PROTEIN SEQUENCE.

RC STRAIN=A/J;  
 RX MEDLINE=82150934; PubMed=6801658;  
 RA Siegelman M., Capra J.D.;  
 RT "Complete amino acid sequence of light chain variable regions derived  
 RT from five monoclonal anti-p-azophenylarsenate antibodies differing  
 RT with respect to a crossreactive idiotype."  
 RL Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).  
 CC -!- MISCELLANEOUS: Anti-arsenate hybridoma protein.

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 CC removed.

CC PDB; 1A14; X-ray; L=5-102.  
 DR SMR; P01645; 1-108.  
 DR Ensembl; ENSMUSG0000029991; Mus musculus.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003596; IG\_v.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; P550835; IG LIKE; 1.  
 KW 3D-structure; Direct protein sequencing; Immunoglobulin domain;  
 KW Immunoglobulin V region.

FT REGION 1 23 Framework-1.

FT REGION 24 34  
 FT REGION 35 49  
 FT REGION 50 56  
 FT REGION 57 88  
 FT REGION 89 97  
 FT REGION 98 108  
 FT DISULFID 23 88  
 FT NON TER 108 108  
 SQ SEQUENCE 108 AA; 11954 MW; 22F4642C63E9F58E CRC64;

Query Match 92.6%; Score 50; DB 1; Length 108;  
 Best Local Similarity 100.0%; Pred. No. 0.22;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASQDISNYLN 11  
 |||||  
 Db 25 ASQDISNYLN 34

## RESULT 5

KV5M MOUSE STANDARD; PRT; 108 AA.  
 AC P01646;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 10-MAY-2005 (Rel. 47, Last annotation update)  
 DE Ig kappa chain V-V region HP 123B6.  
 OS Mus musculus (Mouse)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Muridae; Murinae; Mus.  
 OC NCBI\_TaxID=10090;  
 RN [1]  
 RP PROTEIN SEQUENCE.

RC STRAIN=A/J;  
 RX MEDLINE=82150934; PubMed=6801658;  
 RA Siegelman M., Capra J.D.;

RT "Complete amino acid sequence of light chain variable regions derived  
 RT from five monoclonal anti-p-azophenylarsenate antibodies differing  
 RT with respect to a crossreactive idiotype."  
 RL Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).  
 CC -!- MISCELLANEOUS: Anti-arsenate hybridoma protein.

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 CC removed.

CC HSP; P01594; 1JVS.  
 DR Ensembl; ENSMUSG0000029991; Mus musculus.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003596; IG\_v.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; P550835; IG LIKE; 1.  
 KW Direct protein sequencing; Immunoglobulin domain;  
 KW Immunoglobulin V region.

FT REGION 1 23 Framework-1.  
 FT REGION 24 34  
 FT REGION 35 49  
 FT REGION 50 56  
 FT REGION 57 88  
 FT REGION 89 97  
 FT REGION 98 108  
 FT DISULFID 23 88  
 FT NON TER 108 108  
 SQ SEQUENCE 108 AA; 11989 MW; 4C98599C08EBA09A CRC64;

Query Match 92.6%; Score 50; DB 1; Length 108;  
 Best Local Similarity 100.0%; Pred. No. 0.22;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASQDISNYLN 11

```
Db          |||||
25 ASQDISNYLN 34

RESULT 6
KV5N MOUSE
ID_KV5N_MOUSE STANDARD; PRT; 108 AA.
AC P01647;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-V region HP 124E1.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP PROTEIN SEQUENCE.
RC STRAIN=A/J;
RX MEDLINE=82150934; PubMed=6801658;
RA Siegelman M., Capra J.D.;
RT "Complete amino acid sequence of light chain variable regions derived
from five monoclonal anti-p-azophenylarsenate antibodies differing
with respect to a crossreactive idiotype."
RL Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).
CC -!- MISCELLANEOUS: Anti-arsenate hybridoma protein.
-----
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use as long as its content is in no way modified and this statement is not
removed.
-----
CC HSSP; P01594; 1JUV5.
DR SMR; P01648; 1-108.
DR Ensembl; ENSMUSG00000029991; Mus musculus.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 1_v.
DR PROSITE; PS0835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
FT REGION 1 23
FT REGION 24 34
FT REGION 35 49
FT REGION 50 56
FT REGION 57 88
FT REGION 89 97
FT REGION 98 108
FT DISULFID 23 88
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11961 MW; 39971BC653EFBFA2 CRC64;

Query Match 87.0%; Score 47; DB 1; Length 108;
Best Local Similarity 90.0%; Pred. No. 0.83;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ASQDISNYLN 11
Db 25 ASQDISNYLN 34

RESULT 8
KV1B_HUMAN
ID_KV1B_HUMAN STANDARD; PRT; 108 AA.
AC P01594;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-I region AU.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=72189444; PubMed=5028201;
RA Schiechl H., Hilschmann N.;
RT "Rule of antibody structure. The primary structure of a monoclonal
immunoglobulin L-chain of the kappa-type, subgroup I (Bence-Jones
protein Au).";
RL Hoppe-Seyler's Z. Physiol. Chem. 353:345-370(1972).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RX MEDLINE=77022433; PubMed=1234024;

Query Match 87.0%; Score 47; DB 1; Length 108;
Best Local Similarity 90.0%; Pred. No. 0.83;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ASQDISNYLN 11
Db 25 ASQDISNYLN 34

RESULT 7
KV5O MOUSE
ID_KV5O_MOUSE STANDARD; PRT; 108 AA.
AC P01648;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-V region HP 91A3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

RA Fehhammer H., Schiffer M., Epp O., Colman P.M., Lattman E.E.,  
 RA Schwager P., Steigemann W., Schramm H.J.;  
 RT "The structure determination of the variable portion of the Bence-  
 RT Jones protein Au.";  
 RL Biophys. Struct. Mech. 1:139-146(1975).  
 CC -1- MISCELLANEOUS: The structure of the V region was determined by  
 CC molecular replacement methods using the known structure of the V  
 CC region of the kappa chain REI.  
 CC -1- MISCELLANEOUS: The C region of this chain has the INV (3) marker.  
 CC -1- MISCELLANEOUS: This is a Bence-Jones protein.  
 CC -----  
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 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC -----  
 DR PIR; A91653; KIHUAU.  
 DR PDB; 1JVS; X-ray; A=1-107.  
 DR Ensembl; ENSG00000173782; Homo sapiens. NAS.  
 DR GO; GO:0005576; C:extracellular region; NAS.  
 DR GO; GO:0003823; F:antigen binding; NAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003596; IG\_v.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS00835; IG\_LIKE; 1.  
 DR PROSITE; PS00835; IG\_LIKE; 1.  
 DR 3D-structure; Bence-Jones protein; Direct protein sequencing;  
 KW Immunoglobulin domain; Immunoglobulin V region.  
 FT REGION 1 23  
 FT FRAMEWORK-1.  
 FT REGION 24 34  
 FT FRAMEWORK-2.  
 FT REGION 35 49  
 FT FRAMEWORK-3.  
 FT REGION 50 56  
 FT FRAMEWORK-4.  
 FT REGION 57 88  
 FT FRAMEWORK-5.  
 FT REGION 89 97  
 FT FRAMEWORK-6.  
 FT REGION 98 107  
 FT FRAMEWORK-7.  
 FT DISULFID 23 88  
 FT NON\_TER 108 108  
 FT STRAND 4 5  
 FT STRAND 10 13  
 FT TURN 15 16  
 FT STRAND 19 25  
 FT TURN 20 21  
 FT STRAND 30 31  
 FT STRAND 33 38  
 FT TURN 40 41  
 FT STRAND 44 49  
 FT TURN 50 52  
 FT STRAND 53 54  
 FT TURN 56 57  
 FT TURN 60 61  
 FT STRAND 62 67  
 FT TURN 68 69  
 FT STRAND 70 75  
 FT TURN 80 82  
 FT STRAND 85 90  
 FT TURN 97 98  
 FT STRAND 102 106  
 SQ SEQUENCE 108 AA; E8011187E6F6FB9 CRC64;  
 Query Match 83.3%; Score 45; DB 1; Length 108;  
 Best Local Similarity 90.0%; Pred. No. 2; Mismatches 0; Indels 0; Gaps 0;  
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 ASQDISNYLN 11  
 DB 25 ASQDISNYLN 34  
 RESULT 9  
 Q9UL81 HUMAN  
 ID Q9UL81 HUMAN PRELIMINARY; PRT; 107 AA.  
 AC Q9UL81;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Myosin-reactive immunoglobulin light chain variable region  
 DE (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;  
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,  
 RA Young D.C.;  
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
 RT fetus.";  
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
 DR EMBL; AF035033; AAD56269.1; -; mRNA.  
 DR HSP; P01607; 1BWW.  
 DR SMR; Q9UL81; 1-107.  
 DR Ensembl; ENSG00000163245; Homo sapiens.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003596; IG\_v.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS00835; IG\_LIKE; 1.  
 FT NON\_TER 1 107  
 FT NON\_TER 107 107  
 SQ SEQUENCE 107 AA; 11501 MW; 070549FDE0754748 CRC64;  
 Query Match 81.5%; Score 44; DB 2; Length 107;  
 Best Local Similarity 90.0%; Pred. No. 3;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 ASQDISNYLN 11  
 DB 25 ASQDISNYLN 34  
 RESULT 10  
 KVLY HUMAN  
 ID KVLY HUMAN STANDARD; PRT; 108 AA.  
 AC P80362;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 10-MAY-2005 (Rel. 47, Last annotation update)  
 DE Ig kappa chain V-I region WAT.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP PROTEIN SEQUENCE, AND X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).  
 RX MEDLINE=95086080; PubMed=7993911;  
 RA Huang D.-B., Chang C.-H., Ainsworth C., Bruenger A.T., Eulitz M.,  
 RA Solomon A., Stevens F.J., Schiffer M.;  
 RT "Comparison of crystal structures of two homologous proteins:  
 RT structural origin of altered domain interactions in immunoglobulin  
 RT light-chain dimers.";  
 RL Biochemistry 33:14848-14857(1994).  
 RN [2]  
 RP PROTEIN SEQUENCE OF 1-35.  
 RX MEDLINE=81267384; PubMed=6167731;  
 RA Stevens F.J., Westholm F.A., Panagiotopoulos N., Schiffer M.,  
 RA Popp R.A., Solomon A.;  
 RT "Characterization and preliminary crystallographic data on the VL-  
 RT related fragment of the human kappa Bence Jones protein Wat.";  
 RL J. Mol. Biol. 147:185-193(1981).  
 CC -1- MISCELLANEOUS: This is a Bence-Jones protein.  
 CC -----  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its



RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE-Skeletal Muscle;  
 RA Strausberg R.;  
 RL Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; BC005332; AA005332.1; -; mRNA.  
 DR HSSP; P01834; 1HEZ.  
 DR Ensemble; ENSG00000163245; Homo sapiens.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig\_C1.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_V.  
 DR Pfam; PF07654; C1-set; I.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG LIKE; 2.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN 1.  
 KW Hypothetical protein; Immunoglobulin domain.  
 SQ SEQUENCE 236 AA; 25702 MW; 7FBFE4ED23084BC6 CRC64;  
 Query Match 81.5%; Score 44; DB 2; Length 236;  
 Best Local Similarity 100.0%; Pred. No. 7;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 ASQDISNYL 10  
 DB 47 ASQDISNYL 55  
 RESULT 13  
 KVIA HUMAN STANDARD; PRT; 108 AA.  
 ID KVIA HUMAN STANDARD; PRT; 108 AA.  
 AC P01593;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 10-MAY-2005 (Rel. 47, Last annotation update)  
 DE Ig kappa chain V-I region AG.  
 OS Homo sapiens (Human)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP PROTEIN SEQUENCE.  
 RX MEDLINE=69234734; PubMed=4893682;  
 RA Titani K., Shinoda T., Putnam F.W.;  
 RT "The amino acid sequence of a kappa type Bence-Jones protein. 3. The  
 complete sequence and the location of the disulfide bridges.";  
 RL J. Biol. Chem. 244:3550-3560 (1969).  
 CC -!- MISCELLANEOUS: The C region of this chain has the INV (3) marker.  
 CC -!- MISCELLANEOUS: This is a Bence-Jones protein.  
 CC -----  
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 between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 the European Bioinformatics Institute. There are no restrictions on its  
 use as long as its content is in no way modified and this statement is not  
 removed.  
 CC -----  
 DR PIR; A01861; KIHUAG.  
 DR HSSP; P01607; 1BWV.  
 DR SMR; P01593; 1-108.  
 DR Ensemble; ENSG00000173782; Homo sapiens.  
 DR GO; GO:0005576; C:extracellular region; NAS.  
 DR GO; GO:0003823; F:antigen binding; NAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003596; IGV.  
 DR SMART; SM00406; IGV; 1.

DR PROSITE; PS50835; IG LIKE; 1.  
 KW Bence-Jones protein; Direct protein sequencing; Immunoglobulin domain;  
 KW Immunoglobulin V region.  
 FT REGION 1 23 Framework-1.  
 FT REGION 24 34 Complementarity-determining-1.  
 FT REGION 35 49 Framework-2.  
 FT REGION 50 56 Complementarity-determining-2.  
 FT REGION 57 88 Framework-3.  
 FT REGION 89 97 Complementarity-determining-3.  
 FT REGION 98 107 Framework-4.  
 FT DISULFID 23 88  
 FT NON\_TER 108 108  
 SQ SEQUENCE 108 AA; 11992 MW; E3B3B246C18FOC4F CRC64;  
 Query Match 77.8%; Score 42; DB 1; Length 108;  
 Best Local Similarity 80.0%; Pred. No. 7.3;  
 Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 ASQDISNYL 11  
 DB 25 ASQDIINHYLN 34  
 RESULT 14  
 Q96PF6 HUMAN  
 ID Q96PF6 HUMAN PRELIMINARY; PRT; 116 AA.  
 AC Q96PF6;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Kappa 1 light chain variable region (Fragment).  
 GN Name=SDNK1;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=21361171; PubMed=11468171; DOI=10.1182/blood.V98.3.714;  
 RA Comenzo R.L., Zhang Y., Martinez C., Osman K., Herrera G.A.;  
 RT "The tropism of organ involvement in primary systemic amyloidosis:  
 contributions of Ig V(L) germ line gene use and clonal plasma cell  
 burden.";  
 RL Blood 98:714-720 (2001).  
 DR EMBL; AF361758; AAK51465.1; -; Genomic\_DNA.  
 DR HSSP; P80362; 1WTL.  
 DR SMR; Q96PF6; 1-115.  
 DR Ensemble; ENSG00000163245; Homo sapiens.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003596; IGV.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG LIKE; 1.  
 FT NON\_TER 1 116  
 FT NON\_TER 116 116  
 SQ SEQUENCE 116 AA; 12735 MW; E796FC2217BFCE57 CRC64;  
 Query Match 77.8%; Score 42; DB 2; Length 116;  
 Best Local Similarity 80.0%; Pred. No. 7.9;  
 Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 ASQDISNYL 11  
 DB 25 ASQDIANHLN 34  
 RESULT 15  
 Q6GMX0 HUMAN  
 ID Q6GMX0 HUMAN PRELIMINARY; PRT; 236 AA.  
 AC Q6GMX0;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

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DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Splicein;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Splicein;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC073775; AAH73775.1; -; mRNA.
DR SMR; QGGMX0; 23-236.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG.c1.
DR InterPro; IPR003006; IG.MHC.
DR InterPro; IPR003596; IG.v.
DR Pfam; PF07654; CI-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 2.
DR PROSITE; PS00290; IG.MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25807 MW; 864EA08C7E92BF8F CRC64;

Query Match 77.8%; Score 42; DB 2; Length 236;
Best Local Similarity 80.0%; Pred. No. 17;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 2 ASQDISNYLN 11
DB 47 ASQINNNYLN 56

RESULT 16
KV5J MOUSE STANDARD; PRT; 108 AA.
AC P01643;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-v region MOPC 173.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.

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OX NCBI_TaxID=10090;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=76091934; PubMed=812696;
RA Schiff C., Fougereau M.;
RT "Determination of the primary structure of a mouse IGG2a
RL immunoglobulin. Amino-acid sequence of the light chain.";
RL Eur. J. Biochem. 59:525-537(1975).
CC -!- MISCELLANEOUS: This chain was isolated from a myeloma protein.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
DR PIR; A01926; KVM573.
DR HSSP; P01594; 1JY5.
DR Ensembl; ENSMUSG0000058965; Mus musculus.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG.v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 1.
KW Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
FT REGION 1 23
FT REGION 24 34
FT REGION 35 49
FT REGION 50 56
FT REGION 57 88
FT REGION 89 97
FT REGION 98 108
FT DISULFID 23 88
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11819 MW; 2AD29D92A72AA0A3 CRC64;

Query Match 75.9%; Score 41; DB 1; Length 108;
Best Local Similarity 72.7%; Pred. No. 11;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 SASQDISNYLN 11
DB 24 SASQSIGNLYB 34

RESULT 17
O7PDL4 PLAYO PRELIMINARY; PRT; 859 AA.
AC O7PDL4;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Erythrocyte membrane protein PFEMP3.
GN Name=PY06116;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=73239;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=17XNL;
RX MEDLINE=22255706; PubMed=12368865; DOI=10.1038/nature01059;
RA Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Pertea M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA Shallom S.J., van Aken S.E., Riedmiller S.B., Feldblum T.V.,
RA Cho J.K., Quackenbush J., Sedegah M., Shoabi A., Cummings L.M.,
RA Florens L., Yates J.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.J.;
RT "Genome sequence and comparative analysis of the model rodent malaria
RT parasite Plasmodium yoelii yoelii.";

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RL Nature 419:512-519(2002).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBS whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL: AABL01002034; EAA18272.1; -; Genomic_DNA.
DR InterPro: IPR000276; GPCR Rhodopsin.
DR PROSITE: PS00237; G PROTEIN RECP.F1.1; UNKNOWN 1.
SQ SEQUENCE 859 AA; 96311 MW; 1C35C377A8DB8064 CRC64;

Query Match 75.9%; Score 41; DB 2; Length 859;
Best Local Similarity 63.6%; Pred. No. 1e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 SASQDISNYLN 11
DB 161 SAPSDVSNNYN 171
|||:|:|:|:|

RESULT 18
Q5ZHNA CHICK
ID Q5ZHNA4_CHICK PRELIMINARY; PRT; 357 AA.
AC Q5ZHNA4;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein.
GN ORFNames=RCUMB04_35C24;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CB; TISSUE=Bursa;
RA Caldwell R.B., Kierzek A.M., Atakawa H., Bezzubov Y., Zaim J.,
RA Fiedler P., Kurter S., Blagodatski A., Kostovska D., Koter M.,
RA Flachy J., Carninci P., Hayashizaki Y., Buerstedde J.M.;
RT "Full-length cDNAs from chicken bursal lymphocytes to facilitate
RT genefunction analysis.";
RL Genome Biol. 6:R6-R6(2005).
DR EMBL: AJ721100; CAG32759.1; -; mRNA.
DR GO: GO:0016020; C.membrane; IEA.
DR GO: GO:0005524; F.ATP binding; IEA.
DR GO: GO:0004550; F.nucleoside-diphosphate kinase activity; IEA.
DR GO: GO:0006241; P.CTP biosynthesis; IEA.
DR GO: GO:0006183; P.GTP biosynthesis; IEA.
DR GO: GO:0006228; P.UTP biosynthesis; IEA.
DR InterPro: IPR006599; CARP.
DR InterPro: IPR001584; NDK.
DR SMART: SM00673; CARP; 2.
KW Hypothetical protein.
SQ SEQUENCE 357 AA; 39723 MW; 0EC08E3C9E1CAF66 CRC64;

Query Match 74.1%; Score 40; DB 2; Length 357;
Best Local Similarity 63.6%; Pred. No. 62;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 SASQDISNYLN 11
DB 339 SASQDVDFNYN 349
|||:|:|:|:|

RESULT 19
Q6LZW4 METMP
ID Q6LZW4_METMP PRELIMINARY; PRT; 583 AA.
AC Q6LZW4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Formylmethanofuran dehydrogenase, subunit A (EC 1.2.99.5).
GN Name=fmdA; Ordered locus Names=MMP0509;
OS Methanococcus maripaludis.

OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC Methanococcaceae; Methanococcus.
OX NCBI_TaxID=39152;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX STRAIN=S2 / LL;
RX PubMed=15466049; DOI=10.1128/JB.186.20.6956-6969.2004;
RA Hendrickson E.L., Kaul R., Zhou Y., Boyse D., Chapman P., Chung J.,
RA Conway de Macario E., Dodsworth J.A., Gillett W., Graham D.E.,
RA Hackett M., Haydock A.K., Kang A., Land M.L., Levy R., Lie T.J.,
RA Major T.A., Moore B.C., Porat I., Palmeiri A., Rouse G.,
RA Saenphimmachak C., Soell D., Van Dien S., Wang T., Whitman W.B.,
RA Xia Q., Zhang Y., Larimer F.W., Olson M.V., Leigh J.A.;
RT "Complete genome sequence of the genetically tractable
RT hydrogenotrophic methanogen Methanococcus maripaludis.";
RL J. Bacteriol. 186:6956-6969(2004).
DR EMBL: BX957220; CAF30065.1; -; Genomic_DNA.
DR GO: GO:0018493; F.formylmethanofuran dehydrogenase activity; IEA.
DR GO: GO:0016787; F.hydrolase activity; IEA.
DR GO: GO:0016491; F.oxidoreductase activity; IEA.
DR InterPro: IPR012027; FwDA.
DR PIRSF: PIRSF006453; FwDA; 1.
KW Complete proteome; Oxidoreductase.
SQ SEQUENCE 583 AA; 64594 MW; 76CFF31FF5DA0263 CRC64;

Query Match 74.1%; Score 40; DB 2; Length 583;
Best Local Similarity 63.6%; Pred. No. 1e+02;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 SASQDISNYLN 11
DB 305 SKAEDISNYN 315
|||:|:|:|:|

RESULT 20
Q8ILX3 PLAF7
ID Q8ILX3_PLAF7 PRELIMINARY; PRT; 956 AA.
AC Q8ILX3;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
GN ORFNames=PF14_0120;
OS Plasmodium falciparum (isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=36329;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22255705; PubMed=12368864; DOI=10.1038/nature01097;
RA Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,
RA Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.,
RA Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,
RA Chan M.-S., Nene V., Shallow S.J., Suh B., Peterson J., Angiuoli S.,
RA Pertea M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B.,
RA Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,
RA McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C.,
RA Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
RA Fraser C.M., Barrell B.G.;
RT "Genome sequence of the human malaria parasite Plasmodium
RT falciparum.";
RL Nature 419:498-511(2002).
DR EMBL: AE014817; AAN36732.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 956 AA; 112773 MW; D32D85CA78D40D58 CRC64;

Query Match 74.1%; Score 40; DB 2; Length 956;
Best Local Similarity 63.6%; Pred. No. 1.7e+02;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 SASQDISNYLN 11
DB 339 ASSTDISNYN 349
|||:|:|:|:|

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RESULT 21
Q7RDE1 PLAYO PRELIMINARY; PRT; 1116 AA.
AC Q7RDE1;
DT 01-MAR-2004 (TReMBLrel. 26, Created)
DT 01-MAR-2004 (TReMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Hypothetical protein.
GN Name=PY05481;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=73239;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=17XNL;
RX MEDLINE=22255706; PubMed=12368865; DOI=10.1038/nature01099;
RA Carlton J.M., Anguoli S.V., Suh B.B., Koij T.W., Perteu M.,
RA Silva J.C., Emolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.B.,
RA Shallow S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
RA Cho J.K., Quackenbush J., Sedegah M., Shoab A., Cummings L.M.,
RA Florens L., Yates J.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.J.;
RA "Genome sequence and comparative analysis of the model rodent malaria
RT parasite Plasmodium yoelii yoelii.";
RL Nature 419:512-519(2002).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AABL01001745; EAA17511.1; -; Genomic_DNA.
DR GO; GO:0005488; F:binding; IEA.
DR GO; GO:0007076; P:mitotic chromosome condensation; IEA.
DR InterPro; IPR001989; ARM-like.
DR InterPro; IPR000357; HEAT.
DR Pfam; PF02985; HEAT; 2.
KW Hypothetical protein.
SQ SEQUENCE 1116 AA; 132831 MW; E24DA27C89B70495 CRC64;

Query Match 74.1%; Score 40; DB 2; Length 1116;
Best Local Similarity 63.6%; Pred. No. 26+0;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 SASQDISVNLN 11
:|:|:|:|
DB 339 NAKEDIDNVLN 349

RESULT 22
Q7KTP3 DROME PRELIMINARY; PRT; 7500 AA.
AC Q7KTP3;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE CG33549-PC, isoform C.
GN Name=Mp-100; ORFNames=CG33549;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Vandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

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Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
ABRIL J.F., Agbayani A., An H.-J., Andrews-Pfankoch C., Baldwin D.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
Burtis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
Durbini K.J., Evangelista C.C., Ferraz C., Ferrera S., Fleischmann W.,
Foster K., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
Glodek A., Gong P., Gorrell J.H., Gu Z., Guan P., Harris M.,
Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwan C.,
Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai X.,
Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
Palazzo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
Williams S.M., Wodgale T., Worley K.C., Wu D., Yang S., Yao Q.A.,
Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
"Finishing a whole-genome shotgun: release 3 of the Drosophila
melanogaster euchromatic genome sequence.";
Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
[3]
NUCLEOTIDE SEQUENCE.
MEDLINE=22426070; PubMed=12537573;
RA Kaminer J.S., Bergman C.M., Krommiller B., Carlson J.W., Svirskas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:
a genomics perspective.";
Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).
[4]
NUCLEOTIDE SEQUENCE.
MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochownik S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bertencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
systematic review.";
Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
[5]
NUCLEOTIDE SEQUENCE.
Berkeley Drosophila Genome Project;
RA Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
RA Hoskins R., Stapleton M., Pacleb J., Park S., Svirskas R., Smith E.,
RA Yu C., Rubin G.;

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RT "Drosophila melanogaster release 4 sequence.";   
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.   
 RN [6]   
 RP NUCLEOTIDE SEQUENCE.   
 RG FlyBase;   
 RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.   
 DR EMBL: AE003608; AAS64640.1; -: Genomic DNA.   
 DR Ensembl: CG18251; Drosophila melanogaster.   
 DR InterPro: IPR002017; Spectrin.   
 DR Pfam: PF00435; Spectrin; 34.   
 DR SMART: SM00150; SPEC; 44.   
 SQ SEQUENCE 7500 AA; 861746 MW; 44477BA9FC38667B CRC64;

Query Match 74.1%; Score 40; DB 2; Length 7500;   
 Best Local Similarity 72.7%; Pred. No. 1.5e+03;   
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 SASQDISNYLN 11   
 Db 6615 SUSQDIESYLN 6625

## RESULT 23

QVMT8 DROME   
 ID QVMT8\_DROME PRELIMINARY; PRT; 7735 AA.   
 AC QVMT8;   
 DT 01-MAY-2000 (TREMBLrel. 13, Created)   
 DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)   
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)   
 DE CG33549-PB isoform B.   
 GN Name=Mop-300; ORFNames=CG33549;   
 OS Drosophila melanogaster (Fruit fly).   
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;   
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;   
 OC Ephydroidea; Drosophilidae; Drosophila.   
 OX NCBI\_TaxID=7227;   
 RN [1]   
 RP NUCLEOTIDE SEQUENCE.   
 RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;   
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,   
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,   
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,   
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,   
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,   
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,   
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,   
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,   
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,   
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,   
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,   
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,   
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,   
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,   
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,   
 RA Folsler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,   
 RA Glöck A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,   
 RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,   
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,   
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,   
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,   
 RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,   
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,   
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,   
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,   
 RA Nelson D.R., Nelson K.A., Nixon K., Nusse D.R., Pacle J.M.,   
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,   
 RA Reiner K.C., Remington K., Saunders R.D.C., Scheeler F., Shen H.,   
 RA Shue B.C., Siden-Kianos I., Simpson M., Skupski M.P., Smith T.,   
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,   
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,   
 RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,   
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,   
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,

RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Smith H.O.,   
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;   
 RT "The genome sequence of Drosophila melanogaster.";   
 RL Science 287:2185-2195(2000).   
 RN [2]   
 RP NUCLEOTIDE SEQUENCE.   
 RX MEDLINE=22426065; PubMed=12537568;   
 RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,   
 RA Patel S., Adams M., Champe M., Dugan S.P., Friese E., Hodgson A.,   
 RA George R.A., Hoskins R.A., Lavery T., Muzny D.M., Nelson C.R.,   
 RA Pacle J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,   
 RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,   
 RA Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;   
 RT "Finishing a whole-genome shotgun: release 3 of the Drosophila   
 melanogaster euchromatic genome sequence.";   
 RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).   
 RN [3]   
 RP NUCLEOTIDE SEQUENCE.   
 RX MEDLINE=22426070; PubMed=12537573;   
 RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Svirskas R.,   
 RA Patel S., Friese E., Wheeler D.A., Lewis S.E., Rubin G.M.,   
 RA Ashburner M., Celniker S.E.;   
 RT "The transposable elements of the Drosophila melanogaster euchromatin:   
 a genomics perspective.";   
 RL Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).   
 RN [4]   
 RP NUCLEOTIDE SEQUENCE.   
 RX MEDLINE=22426069; PubMed=12537572;   
 RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,   
 RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.E.,   
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,   
 RA Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,   
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,   
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,   
 RA Lewis S.E.;   
 RT "Annotation of the Drosophila melanogaster euchromatic genome: a   
 systematic review.";   
 RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).   
 RN [5]   
 RP NUCLEOTIDE SEQUENCE.   
 RG Berkeley Drosophila Genome Project;   
 RA Celniker S., Carlson J., Wan K., Pfeiffer B., Friese E., George R.,   
 RA Hoskins R., Stapleton M., Pacle J., Park S., Svirskas R., Smith E.,   
 RA Yu C., Rubin G.;   
 RT "Drosophila melanogaster release 4 sequence.";   
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.   
 RN [6]   
 RP NUCLEOTIDE SEQUENCE.   
 RG FlyBase;   
 RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.   
 CC -I- INTERACTION:   
 CC Q9V8X3:CG15124; NbExp=1; IntAct=EBI-134218, EBI-173665;   
 DR EMBL: AE003608; AAF52223.3; -: Genomic DNA.   
 DR HSPF: Q15149; 1MB8.   
 DR InAct: Q9VMT8; -.   
 DR Ensembl: CG18251; Drosophila melanogaster.   
 DR FlyBase: FBgn0010070; CG18251.   
 DR FlyBase: FBgn0010070; Map-300.   
 DR GO: GO:0005856; Cytoskeleton; IEA.   
 DR GO: GO:0003779; F-actin binding; IEA.   
 DR InterPro: IPR001589; Actbind\_actnln.   
 DR InterPro: IPR001715; Calponin-like.   
 DR InterPro: IPR002017; Spectrin.   
 DR Pfam: PF00307; CH; 2.   
 DR Pfam: PF00435; Spectrin; 34.   
 DR SMART: SM00033; CH; 2.   
 DR SMART: SM00150; SPEC; 44.   
 DR PROSITE: PS00020; ACTININ\_2; 1.   
 DR PROSITE: PS50021; CH; 2.   
 SQ SEQUENCE 7735 AA; 887874 MW; D3A2D5980B7C9D23 CRC64;

Query Match 74.1%; Score 40; DB 2; Length 7735;   
 Best Local Similarity 72.7%; Pred. NO. 1.6e+03;

Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 SASQDISNYLN 11  
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 Db 6850 SLSQDISNYLN 6860

RESULT 24  
 Q96SA9 HUMAN  
 ID Q96SA9 HUMAN PRELIMINARY; PRT; 107 AA.  
 AC Q96SA9;  
 DT 01-DEC-2001 (TRENBLrel. 19, Created)  
 DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)  
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)  
 DE Anti-streptococcal/anti-myoisin immunoglobulin kappa light chain  
 DE variable region (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=98375893; PubMed=9712075;  
 RA "Molecular analysis of polyreactive monoclonal antibodies from  
 RT rheumatic arthritis: human anti-N-acetylglucosamine/anti-myoisin  
 RT antibody V region genes.";  
 RL J. Immunol. 161:2020-2031(1998).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RX PubMed=1516616;  
 RA Victor K.D., Pascual V., Williams C.L., Lennon V.A., Capra J.D.;  
 RT "Human monoclonal striational autoantibodies isolated from thymic B  
 RT lymphocytes of patients with myasthenia gravis use VH and VL gene  
 RT segments associated with the autoimmune repertoire.";  
 RL Eur. J. Immunol. 22:2231-2236(1992).  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE.  
 RX PubMed=1660528;  
 RA Manheimer-Lory A., Katz J.B., Pillinger M., Grossein C., Smith A.,  
 RA Diamond B.;  
 RT "Molecular characteristics of antibodies bearing an anti-DNA-  
 RT associated idiotype.";  
 RL J. Exp. Med. 174:1639-1652(1991).  
 RN [5]  
 RP NUCLEOTIDE SEQUENCE.  
 RX PubMed=1903706;  
 RA Blaison G., Kuntz J.L., Pasquali J.L.;  
 RT "Molecular analysis of V kappa III variable regions of polyclonal  
 RT rheumatoid factors during rheumatoid arthritis.";  
 RL Eur. J. Immunol. 21:1221-1227(1991).  
 DR EMBL; U96396; AA68785.1; -; mRNA.  
 DR PIR; B49047; B49047.  
 DR PIR; PH0867; PH0867.  
 DR PIR; S16840; S16840.  
 DR PIR; S31977; S31977.  
 DR PIR; S34083; S34083.  
 DR PIR; S34086; S34086.  
 DR HSSP; P01607; 1BW.  
 DR SMR; Q96SA9; 1-107.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003596; Ig\_v.  
 DR SMART; SM00406; IGV; 1  
 DR PROSITE; PS50835; IG\_LIKE; 1.

FT NON\_TER 1 1  
 FT NON\_TER 107 107  
 SQ SEQUENCE 107 AA; 11520 MW; 4BB43E9C5B577F16 CRC64;

Query Match 72.2%; Score 39; DB 2; Length 107;  
 Best Local Similarity 80.0%; Pred. No. 27;  
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 ASQDISNYLN 11  
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 Db 25 ASQDISNYLN 34

RESULT 25  
 Q9UL77 HUMAN  
 ID Q9UL77 HUMAN PRELIMINARY; PRT; 108 AA.  
 AC Q9UL77;  
 DT 01-MAY-2000 (TRENBLrel. 13, Created)  
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)  
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)  
 DE Myosin-reactive immunoglobulin light chain variable region  
 DE (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;  
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,  
 RA Young D.C.;  
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
 RT fetus.";  
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RX PubMed=1516616;  
 RA Victor K.D., Pascual V., Williams C.L., Lennon V.A., Capra J.D.;  
 RT "Human monoclonal striational autoantibodies isolated from thymic B  
 RT lymphocytes of patients with myasthenia gravis use VH and VL gene  
 RT segments associated with the autoimmune repertoire.";  
 RL Eur. J. Immunol. 22:2231-2236(1992).  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE.  
 RX PubMed=8436174;  
 RA Wagner S.D., Luzzatto L.;  
 RT "V kappa gene segments rearranged in chronic lymphocytic leukemia are  
 RT distributed over a large portion of the V kappa locus and do not show  
 RT somatic mutation.";  
 RL Eur. J. Immunol. 23:391-397(1993).  
 DR EMBL; AF035037; AAD56273.1; -; mRNA.  
 DR PIR; B49047; B49047.  
 DR PIR; S34083; S34083.  
 DR HSSP; P01607; 1BW.  
 DR SMR; Q9UL77; 1-108.  
 DR Ensemble; ENSG00000163245; Homo sapiens.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003596; Ig\_v.  
 DR SMART; SM00406; IGV; 1  
 DR PROSITE; PS50835; IG\_LIKE; 1.

FT NON\_TER 1 1  
 FT NON\_TER 108 108  
 SQ SEQUENCE 108 AA; 11738 MW; C06681716C4D16F3 CRC64;

Query Match 72.2%; Score 39; DB 2; Length 108;  
 Best Local Similarity 80.0%; Pred. No. 27;  
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 ASQDISNYLN 11  
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 Db 25 ASQDISNYLN 34

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RESULT 26
KV5H MOUSE
ID KV5H MOUSE STANDARD; PRT; 117 AA.
AC P01641;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-V region MOPC 173B precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=81064681; PubMed=6777049; DOI=10.1016/0092-8674(80)90442-0;
RA Max E.E., Seidman J.G., Miller H., Leder P.;
RT "Variation in the crossover point of kappa immunoglobulin gene V-J
recombination: evidence from a cryptic gene.";
RL Cell 21:793-799(1980).
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; K00880; AAA39031.1; -; Genomic_DNA.
DR PIR; A01924; KVM53B.
DR HSSP; P01607; LBWV.
DR SMR; P01641; 23-117.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin domain; Immunoglobulin V region; Signal.
FT SIGNAL 1 22
FT CHAIN 23 117 Ig kappa chain V-V region MOPC 173B.
FT REGION 23 45 Framework-1.
FT REGION 46 56 Complementarity-determining-1.
FT REGION 57 71 Framework-2.
FT REGION 72 78 Complementarity-determining-2.
FT REGION 79 110 Framework-3.
FT REGION 111 >117 Complementarity-determining-3.
FT DISULFID 45 110 By similarity.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12955 MW; 24B3D4B9AC2E4D6C CRC64;

Query Match 72.2%; Score 39; DB 1; Length 117;
Best Local Similarity 80.0%; Pred. No. 29;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 ASQDISNYLN 11
DB 47 ASQDIHGYLN 56

RESULT 27
Q56917 HUMAN
ID Q56917 HUMAN PRELIMINARY; PRT; 189 AA.
AC Q56917;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.

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RC TISSUE=Glandular pool- thyroid;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altshuler S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Maman A.C., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Glandular pool- thyroid;
RG NIH MGC Project;
RL Submitted (APR-2005) to the EMBL/GenBank/DBSJ databases.
DR EMBL; BC092455; AAH92455.1; -; mRNA.
DR SMR; Q56917; 23-186.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 2.
KW Hypothetical protein; Immunoglobulin domain.
SQ SEQUENCE 189 AA; 20668 MW; CFFD14A19F6B3622 CRC64;

Query Match 72.2%; Score 39; DB 2; Length 189;
Best Local Similarity 80.0%; Pred. No. 49;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 ASQDISNYLN 11
DB 47 ASQDIRKYL 56

RESULT 28
Q4XR33 PLACH
ID Q4XR33 PLACH PRELIMINARY; PRT; 204 AA.
AC Q4XR33;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein (Fragment).
GN ORFNames=PC000134.04.0;
OS Plasmodium chabaudi.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5825;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hall N., Karras M., Raine J.D., Carlton J.M., Kool J.T.W.A.,
RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
RA Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;
RT "A comprehensive survey of the Plasmodium life cycle by genomic,
transcriptomic, and proteomic analyses.";
RL Science 307:82-86(2005).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBSJ whole genome shotgun (WGS) entry which is
CC preliminary data.

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DR EMBL: CAJ01003825; CAH80629.1; -; Genomic_DNA.
KW Hypothetical protein.
FT NON_TER 1
FT NON_TER 204
SQ SEQUENCE 204 AA; 24305 MW; 4EBD665B2528D9E4 CRC64;

Query Match 72.2%; Score 39; DB 2; Length 204;
Best Local Similarity 70.0%; Pred. No. 53;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 ASQDISNYLN 11
| : : : : :
DB 45 AKEDIDNYLN 54

RESULT 29
ID Q9X556 ENTFC PRELIMINARY; PRT; 225 AA.
AC Q9X556
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Cysteine aminopeptidase (Fragment).
GN Name=pepC;
OS Enterococcus faecium (Streptococcus faecium).
OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
OX NCBI_TaxID=1352;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BFE 900;
RX MEDLINE=99240446; PubMed=10224016;
RA Franz C.M.A.P., Worobo R.W., Quadri L.E.N., Schillinger U.,
RA Holzapfel W.H., Vederas J.C., Stiles M.E.;
RT "Atypical genetic locus associated with constitutive production of
RT enterocin B by Enterococcus faecium BFE 900.";
RL Appl. Environ. Microbiol. 65:2170-2178(1999).
DR EMBL: AF121254; RAD28219.1; -; Genomic_DNA.
DR HSSP: Q01532; 3GCB.
DR MEROPS; C01.086; -.
DR GO; GO:0004177; F:aminopeptidase activity; IEA.
DR GO; GO:0004197; F:cysteine-type endopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR004134; Peptidase ClB.
DR PANTHER; PTHR10363; Peptidase ClB; 1.
DR Pfam; PF03051; Pept Cl-like; 1.
DR PROSITE; PS00139; THIOI_PROTEASE_CYS; UNKNOWN_1.
KW Aminopeptidase.
FT NON_TER 225
SQ SEQUENCE 225 AA; 25625 MW; 194451D51DF51C56 CRC64;

Query Match 72.2%; Score 39; DB 2; Length 225;
Best Local Similarity 63.6%; Pred. No. 59;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 SASQDISNYLN 11
| : : : : :
DB 166 SNSRDLNNYLN 176

RESULT 30
Q838Y1 ENTFA PRELIMINARY; PRT; 461 AA.
AC Q838Y1
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Aminopeptidase C.
GN Name=pepC; OrderedLocusNames=EF0302;
OS Enterococcus faecalis (Streptococcus faecalis).
OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
OX NCBI_TaxID=1351;
RN [1]

RP NUCLEOTIDE SEQUENCE.
RC STRAIN=V583 / ATCC 700802;
RX MEDLINE=22550857; PubMed=12663927; DOI=10.1126/science.1080613;
RA Paulsen I.T., Banerjee L., Myers G.S.A., Nelson K.E., Seshadri R.,
RA Read T.D., Fouts D.B., Eisen J.A., Gill S.R., Heidelberg J.F.,
RA Tetelin H., Dodson R.J., Umayam L.A., Brinkac L.M., Beanan M.J.,
RA Daugherty S.C., DeBoy R.T., Durkin S.A., Kolonay J.F., Madupu R.,
RA Nelson W.C., Vamathevan J.J., Tran B., Upton J., Hansen T., Shetty J.,
RA Khouri H.M., Utterback T.R., Radune D., Ketchum K.A., Dougherty B.A.,
RA Fraser C.M.;
RT "Role of mobile DNA in the evolution of vancomycin-resistant
RT Enterococcus faecalis.";
RL Science 299:2071-2074(2003).
DR EMBL: AE016947; AA080165.1; -; Genomic_DNA.
DR HSSP: Q13867; 1CB5.
DR MEROPS; C01.086; -.
DR TIGR; EF0302; -.
DR GO; GO:0004177; F:aminopeptidase activity; IEA.
DR GO; GO:0004197; F:cysteine-type endopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR004134; Peptidase ClB.
DR PANTHER; PTHR10363; Peptidase ClB; 1.
DR Pfam; PF03051; Pept Cl-like; 1.
DR PIRSF; PIRSF005700; pepC; 1.
DR PROSITE; PS00139; THIOI_PROTEASE_CYS; 1.
DR PROSITE; PS00639; THIOI_PROTEASE_HIS; UNKNOWN_1.
KW Aminopeptidase; Complete proteome.
SQ SEQUENCE 461 AA; 52197 MW; 0B7FA885E60EE008 CRC64;

Query Match 72.2%; Score 39; DB 2; Length 461;
Best Local Similarity 63.6%; Pred. No. 1.2e+02;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 SASQDISNYLN 11
| : : : : :
DB 166 SNSRDLNNYLN 176

RESULT 31
Q9HI92 THEAC PRELIMINARY; PRT; 506 AA.
AC Q9HI92
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein Tal450.
GN OrderedLocusNames=Tal450;
OS Thermoplasma acidophilum.
OC Archaea; Euryarchaeota; Thermoplasmata; Thermoplasmatales;
OC Thermoplasmataceae; Thermoplasma.
OX NCBI_TaxID=2303;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=DSM 1728;
RX MEDLINE=20479972; PubMed=11029001; DOI=10.1038/35035069;
RA Ruepp A., Graml W., Santos-Martinez M.-L., Koretke K.K., Volker C.,
RA Mewes H.-W., Frishman D., Stocker S., Lupas A.N., Baumeister W.;
RT "The genome sequence of the thermoacidophilic scavenger Thermoplasma
RT acidophilum.";
RL Nature 407:508-513(2000).
DR EMBL: AL445067; CAC12570.1; -; Genomic_DNA.
DR GO; GO:00016874; P:ligase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR000873; AMP-bind.
DR Pfam; PF0501; AMP-binding; 3.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 506 AA; 55694 MW; 88DED97D384EC915 CRC64;

Query Match 72.2%; Score 39; DB 2; Length 506;
Best Local Similarity 80.0%; Pred. No. 1.4e+02;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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QY 1 SASQDISNYLN 10  
|:|||||  
Db 202 SSQDISNYLN 211

RESULT 32  
QSEAT3\_XENLA PRELIMINARY; PRT; 525 AA.  
AC QSEAT3;  
DT 10-MAY-2005 (TrEMBLrel. 30, Created)  
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)  
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)  
DE Hypothetical protein (Fragment)  
OS Xenopus laevis (African clawed frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;  
OC Xenopodinae; Xenopus; Xenopus.  
OX NCBI\_TaxID=8355;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=lung;  
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;  
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,  
RA Richardson P.,  
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus  
RT initiative";  
RL Dev. Dyn. 225:384-391(2002).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=lung;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=lung;  
RA Klein S., Gerhard D.S.;  
RL Submitted (FEB-2005) to the EMBL/GenBank/DBSJ databases.  
DR EMBL; BC090251; AAH90251.1; -; mRNA.  
DR GO; GO:0005737; C:cytoplasm; IEA.  
DR GO; GO:0006817; P:phosphate transport; IEA.  
DR InterPro; IPR001073; Clq.  
DR InterPro; IPR008160; Collagen.  
DR Pfam; PF00386; Clq; 1.  
DR Pfam; PF01391; Collagen; 1.  
DR PRINTS; PR00007; COMPLEMENTC1Q.  
DR SMART; SM00110; Clq; 1.  
KW Collagen; Hypothetical protein.  
FT NON\_TER 1  
SQ SEQUENCE 525 AA; 56950 MW; B8EFDD698A58E3A2 CRC64;

Query Match 72.2%; Score 39; DB 2; Length 525;  
Best Local Similarity 72.7%; Pred. No. 1.4e+02;  
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 SASQDISNYLN 11  
|:|||||  
Db 42 SASRDISHYQN 52

RESULT 33  
QSLFH3\_BACFN PRELIMINARY; PRT; 581 AA.  
AC QSLFH3;  
DT 01-FEB-2005 (TrEMBLrel. 29, Created)  
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)  
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)  
DE Putative phosphoglucomutase.  
GN OrderedLocustNames=BF1409;  
OS Bacteroides fragilis (strain ATCC 25285 / NCTC 9343).  
OC Bacteria; Bacteroidetes; Bacteroidetes (class); Bacteroidales;  
OC Bacteroidaceae; Bacteroides.  
OX NCBI\_TaxID=272559;  
RN [1]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
RX PubMed=15746427; DOI=10.1126/science.1107008;  
RA Cerdeno-Tarraga A.-M., Patrick S., Crossman L.C., Blakely G.,  
RA Abratt V., Lennard N., Poxton I., Duerden B., Harris B., Quail M.A.,  
RA Barron A., Clark L., Corton C., Doggett J., Holden M.T.G., Larke N.,  
RA Line A., Lord A., Norbertczak H., Ormond D., Price C.,  
RA Rabinowitz E., Woodward J., Barrell B.G., Parkhill J.;  
RT "Extensive DNA inversions in the B. fragilis genome control variable  
RT gene expression";  
RL Science 307:1463-1465(2005).  
DR EMBL; CR626927; CAH07121.1; -; Genomic\_DNA.  
DR InterPro; IPR005841; PG/PMM mutase.  
DR InterPro; IPR005844; PG\_PMM\_ABAIL.  
DR InterPro; IPR005845; PG\_PMM\_ABAIL.  
DR InterPro; IPR005846; PG\_PMM\_ABAIL.  
DR Pfam; PF02878; PGM\_PMM\_I; 1.  
DR Pfam; PF02879; PGM\_PMM\_II; 1.  
DR Pfam; PF02880; PGM\_PMM\_III; 1.  
DR PRINTS; PR00509; PGMPMM.  
DR PROSITE; PS00710; PGM\_PMM; 1.  
KW Complete proteome.  
SQ SEQUENCE 581 AA; 64637 MW; BBE99078C76B7CE CRC64;

Query Match 72.2%; Score 39; DB 2; Length 581;  
Best Local Similarity 63.6%; Pred. No. 1.6e+02;  
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 SASQDISNYLN 11  
|:|||||  
Db 75 AATQGLSNYLN 85

RESULT 34  
Q64W97\_BACFR PRELIMINARY; PRT; 581 AA.  
AC Q64W97;  
DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
DE Phosphoglucomutase phosphomannomutase.  
GN OrderedLocustNames=BF1478;  
OS Bacteroides fragilis.  
OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;  
OC Bacteroidaceae; Bacteroides.  
OX NCBI\_TaxID=817;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=YCH46;  
RX PubMed=15466707; DOI=10.1073/pnas.0404172101;  
RA Kuwahara T., Yamashita A., Hirakawa H., Nakayama H., Okada N.,  
RA Kuwaha S., Hattori M., Hayashi T., Ohnishi Y.;  
RT "Genomic analysis of Bacteroides fragilis reveals extensive DNA  
RT inversions regulating cell surface adaptation";  
RL Proc. Natl. Acad. Sci. U.S.A. 101:14919-14924(2004).

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DR EMBL; AP006841; BAD48229.1; -; Genomic DNA.
DR GO; GO:0016869; F:intramolecular transferase activity, phosph. . .; IEA.
DR GO; GO:0016853; F:isomerase activity; IEA.
DR GO; GO:0000287; F:magnesium ion binding; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR005841; PG/PMM mutase.
DR InterPro; IPR005844; PG_PMM_ABAI.
DR InterPro; IPR005845; PG_PMM_ABAIL.
DR InterPro; IPR005846; PG_PMM_ABAILI.
DR Pfam; PF02878; PGM_PMM_II; 1.
DR Pfam; PF02879; PGM_PMM_II; 1.
DR Pfam; PF02880; PGM_PMM_III; 1.
DR PRINTS; PR00509; PGM_PMM.
DR PROSITE; PS00710; PGM_PMM; 1.
KW Complete proteome.
SQ SEQUENCE 581 AA; 64647 MW; BC3B4078FC75B4CE CRC64;

Query Match 72.2%; Score 39; DB 2; Length 581;
Best Local Similarity 63.6%; Pred. No. 1.6e+02;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SASQDISNYLN 11
:|:|:|:|:|
Db 75 AATQGLSNYLN 85

RESULT 35
Q8EV69 MYCPE PRELIMINARY; PRT; 1093 AA.
AC Q8EV69
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein MYPE6990.
GN OrderedLocustNames=MYPE6990;
OS Mycoplasma penetrans.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=28227;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=HF-2;
RX MEDLINE=22354719; PubMed=12466555; DOI=10.1093/nar/gkf667;
RA Sasaki Y., Ishikawa J., Yanashita A., Oshima K., Kenri T., Furuya K.,
RA Yoshino C., Horino A., Shiba T., Sasaki T., Hattori M.;
RT "The complete genomic sequence of Mycoplasma penetrans, an
RT intracellular bacterial pathogen in humans.";
RL Nucleic Acids Res. 30:5293-5300(2002).
DR EMBL; BA000026; BAC44491.1; -; Genomic DNA.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 1093 AA; 119056 MW; 3F2373983DC1CF79 CRC64;

Query Match 72.2%; Score 39; DB 2; Length 1093;
Best Local Similarity 54.5%; Pred. No. 3.1e+02;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SASQDISNYLN 11
:|:|:|:|:|
Db 640 SSEDVSQYIN 650

RESULT 36
Q7PDL3 PLAYO PRELIMINARY; PRT; 1665 AA.
AC Q7PDL3
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Erythrocyte membrane protein PFEMP3.
GN Name=pf06125;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=73239;
RN [1]
```

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RP NUCLEOTIDE SEQUENCE.
RC STRAIN=17XNL;
RX MEDLINE=22255706; PubMed=12368865; DOI=10.1038/nature01099;
RA Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Pertea M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bigwell S.L.,
RA Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
RA Cho J.K., Quackenbush J., Sedegah M., Shoaihi A., Cummings L.M.,
RA Florens L., Yates J.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA Salzberg S.L., Venter J.C., Praser C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.J.;
RT "Genome sequence and comparative analysis of the model rodent malaria
RT parasite Plasmodium yoelii yoelii.";
RL Nature 419:512-519(2002).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AABL01002038; EAA18281.1; -; Genomic DNA.
SQ SEQUENCE 1665 AA; 191206 MW; 03BB304FF802057C CRC64;

Query Match 72.2%; Score 39; DB 2; Length 1665;
Best Local Similarity 70.0%; Pred. No. 4.8e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 ASQDISNYLN 11
:|:|:|:|:|
Db 305 SEQDIENYLN 314

RESULT 37
Q8YXN0 ANASP PRELIMINARY; PRT; 67 AA.
AC Q8YXN0
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Asr1182 protein.
GN OrderedLocustNames=asr1182;
OS Anabaena sp. (strain PCC 7120).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
OX NCBI_TaxID=103690;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21595285; PubMed=11759840;
RA Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
RA Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yanada M.,
RA Yasuda M., Tabata S.;
RT "Complete genomic sequence of the filamentous nitrogen-fixing
RT cyanobacterium Anabaena sp. strain PCC 7120.";
RL DNA Res. 8:205-213(2001).
DR EMBL; BA000019; BAB731139.1; -; Genomic DNA.
DR PIR; AC1954; AC1954.
KW Complete proteome.
SQ SEQUENCE 67 AA; 7732 MW; 441503AD12252766 CRC64;

Query Match 70.4%; Score 38; DB 2; Length 67;
Best Local Similarity 77.8%; Pred. No. 25;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ASQDISNYLN 10
:|:|:|:|:|
Db 7 ASRDLSNYL 15

RESULT 38
KV10 HUMAN STANDARD; PRT; 108 AA.
ID KV10 HUMAN
AC P01607;
DT 21-JUL-1986 (Rel. 01, Created)
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DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 10-MAY-2005 (Rel. 47, Last annotation update)  
 DE Ig kappa chain V-I region Rei.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]\_TaxID=9606;  
 RP PROTEIN SEQUENCE.  
 RX MEDLINE=76023758; PubMed=809329;  
 RA Palm W., Hilschmann N.;  
 RT "The primary structure of a crystalline monoclonal immunoglobulin  
 kappa-type L-chain, subgroup I (Bence-Jones protein Rei); isolation  
 and characterization of the tryptic peptides; the complete amino acid  
 sequence of the protein; a contribution to the elucidation of the  
 three-dimensional structure of antibodies, in particular their  
 combining site.";  
 RT Hoppe-Seyler's Z. Physiol. Chem. 356:167-191(1975).  
 RL [2]  
 RN X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).  
 RX MEDLINE=76039968; PubMed=1192131;  
 RA Epp O., Lattman E.E., Schiffer M., Huber R., Palm W.;  
 RT "The molecular structure of a dimer composed of the variable portions  
 of the Bence-Jones protein REI refined at 2.0-A resolution.";  
 RL Biochemistry 14:4943-4952(1975).  
 CC -!- MISCELLANEOUS: The C region of this chain has the INV (1,2)  
 marker.  
 CC -!- MISCELLANEOUS: This is a Bence-Jones protein.  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 the European Bioinformatics Institute. There are no restrictions on its  
 use as long as its content is in no way modified and this statement is not  
 removed.  
 CC PIR; A91663; KIHURE.  
 DR PDB; 1AR2; X-ray; @=1-107.  
 DR PDB; 1BWW; X-ray; A/B=1-107.  
 DR PDB; 1REI; X-ray; A/B=1-107.  
 DR GO; GO:0005576; C:extracellular region; NAS.  
 DR GO; GO:0003823; P:antigen binding; NAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR007110; IG-like.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG LIKE; 1.  
 KW 3D-structure; Bence-Jones protein; Direct protein sequencing;  
 KW Immunoglobulin domain; Immunoglobulin V region.  
 FT REGION 1 23 Framework-1.  
 FT REGION 24 34 Complementarity-determining-1.  
 FT REGION 35 49 Framework-2.  
 FT REGION 50 56 Complementarity-determining-2.  
 FT REGION 57 88 Framework-3.  
 FT REGION 89 97 Complementarity-determining-3.  
 FT REGION 98 107 Framework-4.  
 FT DISULFID 23 88  
 FT NON TER 108 108  
 FT STRAND 4 7  
 FT TURN 10 13  
 FT TURN 15 16  
 FT TURN 19 25  
 FT TURN 30 31  
 FT STRAND 33 38  
 FT TURN 40 41  
 FT STRAND 45 49  
 FT TURN 50 52  
 FT STRAND 53 54  
 FT TURN 56 57  
 FT TURN 60 61  
 FT STRAND 62 67  
 FT TURN 68 69  
 FT STRAND 70 75

FT HELIX 80 82  
 FT STRAND 84 90  
 FT STRAND 97 98  
 FT STRAND 102 106  
 SQ SEQUENCE 108 AA; 11902 MW; 9E8143E1188BCE2A CRC64;  
 Query Match 70.4%; Score 38; DB 1; Length 108;  
 Best Local Similarity 80.0%; Pred. No. 42;  
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 2 ASQDISNYLN 11  
 Db 25 ASQDIKYLN 34  
 RESULT 39  
 Q54P35 D1CDI PRELIMINARY; PRT; 300 AA.  
 AC Q54P35;  
 DT 13-SEP-2005 (TRENBLrel. 31, Created)  
 DT 13-SEP-2005 (TRENBLrel. 31, Last sequence update)  
 DT 13-SEP-2005 (TRENBLrel. 31, Last annotation update)  
 DE Hypothetical protein.  
 GN ORFNames=DD0186211.  
 OS Dictyostelium discoideum (Slime mold).  
 OC Eukaryota; Mycetozoa; Dictyostellida; Dictyostelium.  
 OX NCBI\_TaxID=44689;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=AX4;  
 RA Eichinger L., Pachebat J.A., Gloeckner G., Rajandream M.-A.,  
 RA Sugand R., Berriman M., Song J., Olsen R., Szafranski K., Xu Q.,  
 RA Tungal B., Kummerfeld S., Madera M., Konfortov B.A., Rivero F.,  
 RA Bankier A.T., Lehmann R., Hamlin N., Davies R., Gaudet P., Fey P.,  
 RA Pilcher K., Chen G., Saunders D., Sodergren E., Davis P.,  
 RA Kerhornou A., Nie X., Hall N., Anjard C., Hemphill L., Bason N.,  
 RA Faltrother P., Desany B., Just E., Morio T., Rost R., Churcher C.,  
 RA Cooper J., Haydock S., van Driessche N., Cronin A., Goodhead I.,  
 RA Muzny D., Mourier T., Pain A., Lu M., Harper D., Lindsay R.,  
 RA Hauser H., James K., Quiles M., Mohan M.B., Saito T., Buchrieser C.,  
 RA Wadrop A., Felder M., Thangavelu M., Johnson D., Knights A.,  
 RA Loulseg H., Mungall K., Oliver K., Price C., Quail M.A., Sanders M.,  
 RA Urushihara H., Hernandez J., Rabinowitsch E., Steffen D., Sanders M.,  
 RA Ma J., Kohara Y., Sharp S., Simmonds M., Spiegler S., Tivey A.,  
 RA Sugano S., White B., Walker D., Woodward J., Winckler T., Tanaka Y.,  
 RA Shaulsky G., Schleicher M., Weinstock G., Rosenthal A., Cox E.C.,  
 RA Chisholm R.L., Gibbs R., Loomis W.F., Platzer M., Kay R.R.,  
 RA Williams J., Dear P.H., Noegel A.A., Barrell B., Kuspa A.,  
 RT "The genome of the social amoeba Dictyostelium discoideum.";  
 RL Nature 0:0(2005).  
 CC -!- CAUTION: The sequence shown here is derived from an  
 EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 preliminary data.  
 CC EMBL; AAF101000114; EAL65060.1; -; Genomic\_DNA.  
 DR Hypothetical protein.  
 KW Hypothetical protein.  
 SQ SEQUENCE 300 AA; 35421 MW; 07B4509F70290B64 CRC64;  
 Query Match 70.4%; Score 38; DB 2; Length 300;  
 Best Local Similarity 87.5%; Pred. No. 1.2e+02;  
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 QDISNYLN 11  
 Db 134 KDISNYLN 141  
 RESULT 40  
 Q7V117\_PROMP  
 ID Q7V117\_PROMP PRELIMINARY; PRT; 433 AA.  
 AC Q7V117;  
 DT 01-OCT-2003 (TRENBLrel. 25, Created)  
 DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)  
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)



DE Putative glucose 6-phosphate dehydrogenase effector OpcA.  
GN OrderedLocustNames=PM1073;  
OS Prochlorococcus marinus subsp. pastoris (strain CCMF 1378 / MED4).  
OC Bacteria; Cyanobacteria; Prochlorales; Prochlorococcaceae;  
OC Prochlorococcus.  
OX NCBI\_TaxID=59919;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=22825698; PubMed=12917642; DOI=10.1038/nature01947;  
RA Rocap G., Larimer F.W., Lamerdin J.E., Malfatti S., Chain P.,  
RA Ahlgren N.A., Arellano A., Coleman M., Hauser L., Hess W.R.,  
RA Johnson Z.I., Land M.L., Lindell D., Post A.F., Regala W., Shah M.,  
RA Shaw S.L., Steglich C., Sullivan M.B., Ting C.S., Tolonen A.,  
RA Webb E.L., Zinser E.R., Chisholm S.W.;  
RT "Genome divergence in two Prochlorococcus ecotypes reflects oceanic  
RT niche differentiation."  
RL Nature 424:1042-1047(2003).  
DR EMBL: BX572092; CAE19532.1; -; Genomic\_DNA.  
KW Complete proteome.  
SQ SEQUENCE 433 AA; 48556 MW; 8ADAI3F3964D2F5E CRC64;  
Query Match 70.4%; Score 38; DB 2; Length 433;  
Best Local Similarity 87.5%; Pred. No. 1.8e+02;  
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 4 QDISNYLN 11  
|:|||||  
DB 16 QDISNYLN 23  
RESULT 41  
QY Q7N5S4 PHOLL PRELIMINARY; PRT; 443 AA.  
AC Q7N5S4;  
DT 01-MAR-2004 (TrEMBLrel. 26, Created)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Similar to nitrotriacetate monooxygenase component A.  
GN OrderedLocustNames=plu1866;  
OS Photorhabdus luminescens (subsp. laumondii).  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Photorhabdus.  
OX NCBI\_TaxID=141679;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX STRAIN=TT01;  
RX MEDLINE=22957627; PubMed=14528314; DOI=10.1038/nbt886;  
RA Duchaud E., Rusniok C., Frangeul L., Buchrieser C., Givaudan A.,  
RA Taourit S., Bocs S., Boursaux-Eude C., Chandler M., Charles J.-F.,  
RA Dassa E., Derose R., Derzelle S., Freysinet G., Gaudriault S.,  
RA Medigue C., Lanois A., Powell K., Sigulier P., Vincent R., Wingate V.,  
RA Zouine M., Glaser P., Boemare N., Danchin A., Kunst F.;  
RT "The genome sequence of the entomopathogenic bacterium Photorhabdus  
RT luminescens."  
RL Nat. Biotechnol. 21:1307-1313(2003).  
DR EMBL: BX571865; CAE14159.1; -; Genomic\_DNA.  
DR PhotocList; plu1866; -.  
DR GO:GO:0004497; F:monooxygenase activity; IEA.  
DR InterPro: IPR011251; Luciferase like.  
KW Complete proteome; Monooxygenase.  
SQ SEQUENCE 443 AA; 49686 MW; 3D62F53C73020D72 CRC64;  
Query Match 70.4%; Score 38; DB 2; Length 443;  
Best Local Similarity 70.0%; Pred. No. 1.8e+02;  
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
QY 2 ASQDISNYLN 11  
|:||||:|  
DB 34 AAQDIGHYLN 43  
RESULT 42  
QY Q4N4X6 THEPA PRELIMINARY; PRT; 476 AA.  
AC Q4N4X6;  
DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
DE Hypothetical protein.  
GN ORFNames=TP02\_0514;  
OS Theileria parva.  
OC Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Theileriidae;  
OC Theileria.  
OX NCBI\_TaxID=5875;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX STRAIN=Muguga;  
RA Gardner M.J., Bishop R., Shah T., de Villiers E.P., Carlton J.M.,  
RA Hall N., Ren Q., Paulsen I.T., Pain A., Berriman M., Wilson R.J.M.,  
RA Sato S., Ralph S.A., Mann D.J., Xiong Z., Shallom S.J., Weidman J.,  
RA Jiang L., Lynn J., Weaver B., Shoaibi A., Wasawo D., Crabtree J.,  
RA Wortman J.R., Haas B., Angiuoli S.V., Creasy T.H., Lu C., Suh B.,  
RA Silva J.C., Utterback T.R., Feldblyum T.V., Pertea M., Allen J.,  
RA Taracha E.L.N., Salzberg S.L., White O.R., Fitzhugh H.A., Morzaria S.,  
RA Venter J.C., Fraser C.M., Nene V.;  
RT "Genome sequence of Theileria parva, a bovine pathogen that transforms  
RT lymphocytes."  
RL Science 309:134-137(2005).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RX STRAIN=Muguga;  
RA Gardner M., Bishop R., Shah T., de Villiers E., Carlton J.M., Hall N.,  
RA Ren Q., Paulsen I.T., Pain A., Berriman M., Wilson R.J.M., Sato S.,  
RA Ralph S.A., Mann D.J., Xiong Z., Shallom S.J., Weidman J., Jiang L.,  
RA Lynn J., Weaver B., Shoaibi A., Wasawo D., Crabtree J., Wortman J.R.,  
RA Haas B., Angiuoli S., Creasy T.H., Lu C., Suh B., Silva J.C.,  
RA Utterback T., Feldblyum T., Pertea M., Allen J., Taracha E.L.,  
RA Salzberg S.L., White O., Fitzhugh H.A., Morzaria S., Venter J.C.,  
RA Fraser C.M., Nene V.;  
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.  
CC -!- CAUTION: The sequence shown here is derived from an  
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
CC preliminary data.  
DR EMBL: AAGK01000002; EAN32797.1; -; Genomic\_DNA.  
KW Hypothetical protein.  
SQ SEQUENCE 476 AA; 54534 MW; 83095EFFCFDC3096 CRC64;  
Query Match 70.4%; Score 38; DB 2; Length 476;  
Best Local Similarity 77.8%; Pred. No. 2e+02;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 3 SODISNYLN 11  
|:|||||  
DB 245 SDDISNYVN 253  
RESULT 43  
QY Q4UEL8 THEAN PRELIMINARY; PRT; 483 AA.  
AC Q4UEL8;  
DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
DE Molecular chaperone, putative.  
GN ORFNames=TA13600;  
OS Theileria annulata.  
OC Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Theileriidae;  
OC Theileria.  
OX NCBI\_TaxID=5874;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX STRAIN=Ankara isolate clone C9;  
RA Pain A., Renaud H., Murphy L., Harris D.A., Quail M.A., Berriman M.,  
RA Hall N., Barrell B.G.;  
RT "The chromosome 2 sequence of Theileria annulata."  
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.



DR EMBL; CR940348; CAI74471.1; -; Genomic\_DNA.

DR InterPro; IPR001623; DnaJ\_N.

DR InterPro; IPR003095; Hsp\_DnaJ.

DR Pfam; PF00226; DnaJ; 1.

DR PRINTS; PR00625; DnaJPROTEIN.

DR SMART; SM00271; DnaJ; 1.

DR PROSITE; PS00076; DnaJ\_2; 1.

KW Chaperone.

SQ SEQUENCE 483 AA; 55230 MW; 22724C292FF09D22 CRC64;

Query Match 70.4%; Score 38; DB 2; Length 483;

Best Local Similarity 77.8%; Pred. No. 2e+02;

Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 SQDISNYLN 11

| : : : : |

Db 252 SDDISNYVN 260

RESULT 44

Q6NIA8\_CORDI

ID Q6NIA8\_CORDI PRELIMINARY; PRT; 581 AA.

AC Q6NIA8;

DT 05-JUL-2004 (TrEMBLrel. 27, Created)

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

DE Glycine betaine transporter.

GN Name=betP; OrderedLocustNames=DIP0869;

OS Corynebacterium diphtheriae.

OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;

OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.

OX NCBI\_TaxID=1717;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=Biotype Gravis / NCTC 13129;

RX MEDLINE=22965443; PubMed=14602910; DOI=10.1093/nar/gkg874;

RA Cerdano-Tarraga A.-M., Efratiou A., Dover L.G., Holden M.T.G.,

RA Pallen M.J., Bentley S.D., Besra G.S., Churcher C.M., James K.D.,

RA De Zoyesa A., Chillingworth T., Cronin A., Dowd L., Feltwell T.,

RA Hamlin N., Holroyd S., Jagels K., Moule S., Quail M.A.,

RA Rabinowitz E., Rutherford K.M., Thomson N.R., Unwin L.,

RA Whitehead S., Barrell B.G., Parkhill J.;

RA "The complete genome sequence and analysis of Corynebacterium

RT diphtheriae NCTC13129.";

RL Nucleic Acids Res. 31:6516-6523 (2003).

DR EMBL; BX248356; CAE49386.1; -; Genomic\_DNA.

DR GO; GO:0016020; C:membrane; IEA.

DR GO; GO:0005215; F:transporter activity; IEA.

DR GO; GO:0008810; P:transport; IEA.

DR InterPro; IPR000060; BCCT\_transporter.

DR Pfam; PF02028; BCCT; 1.

DR ProbDom; PD010111; BCCT\_transporter; 1.

DR TIGRFAMs; TIGR00842; bcct; 1.

DR PROSITE; PS01303; BCCT; 1.

Complete proteome.

SQ SEQUENCE 581 AA; 62840 MW; B698306033308AD1 CRC64;

Query Match 70.4%; Score 38; DB 2; Length 581;

Best Local Similarity 70.0%; Pred. No. 2.5e+02;

Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 ASQDISNYLN 11

| : : : : |

Db 131 ASEPLSNYLN 140

RESULT 45

Q4WSZ8\_ASFPF

ID Q4WSZ8\_ASFPF PRELIMINARY; PRT; 693 AA.

AC Q4WSZ8;

DT 13-SEP-2005 (TrEMBLrel. 31, Created)

DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)

DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)

DE G-patch domain protein, putative.

GN ORFNames=Afu1g1070;

OS Aspergillus fumigatus Af293.

OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;

OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.

RN NCBI\_TaxID=330879;

QY [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=Af293;

RA Nierman W., Pain A., Anderson M.J., Wortman J., Kim H. Stanley.,

RA Artzy-Baron J., Berriman M., Abe K., Archer D.B., Bermejo C., Bennett J.,

RA Bowyer P., Chen D., Collins M., Coulson R., Davies R., Dyer P.S.,

RA Farman M., Fedorova N., Fedorova N., Feldblyum T.V., Fischer R.,

RA Foster M., Fraser A., Garcia J.L., Garcia M.J., Goble A.,

RA Goldman G.H., Goni K., Griffith-Jones S., Gwilliam R., Haas B.,

RA Haas H., Harris D., Horiuchi H., Huang J., Humphrey S., Jimenez J.,

RA Keller N., Khouri H., Kitamoto K., Kobayashi T., Kulkarni R.,

RA Kumagai T., Lafton A., Latge J.-P., Li W., Lord A., Lu C.,

RA Majoros W.H., May G.S., Miller B.L., Mohamoud Y., Molina M., Monod M.,

RA Mouyna I., Mulligan S., Murphy L., O'Neil S., Paulsen I.,

RA Penava M.A., Perte M., Price C., Pritchard B.L., Quail M.A.,

RA Rabinowitsch E., Rawlins N., Rajandream M.-A., Reichard U.,

RA Renauld H., Robson G.D., Rodriguez de Cordoba S., Rodriguez-Pena J.M.,

RA Renning C.M., Rutter S., Salzberg S.L., Sanchez M.,

RA Sanchez-Ferrero J.C., Saunders D., Seeger K., Squares R., Squares S.,

RA Takeuchi M., Tekala F., Turner G., Vazquez de Aldana C.R., Weidman J.,

RA White O., Woodward J., Yu J.-H., Barrell B., Fraser C., Galagan J.E., Asai K.,

RA "Genomic sequence of the pathogenic and allergenic filamentous fungus

RT Aspergillus fumigatus.";

RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.

CC -!- CAUTION: The sequence shown here is derived from an

CC preliminary data.

CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is

SQ SEQUENCE 693 AA; 75690 MW; 66E9BDA7A6CED8F7 CRC64;

Query Match 70.4%; Score 38; DB 2; Length 693;

Best Local Similarity 54.5%; Pred. No. 3e+02;

Matches 6; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASQDISNYLN 11

| : : : : |

Db 345 SAARDVSNYVS 355

RESULT 46

Q7S4J7\_NEUCR

ID Q7S4J7\_NEUCR PRELIMINARY; PRT; 803 AA.

AC Q7S4J7;

DT 01-MAR-2004 (TrEMBLrel. 26, Created)

DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE Predicted protein.

GN Name=NCU08134.1;

OS Neurospora crassa.

OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.

OX NCBI\_TaxID=5141;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=OR74A;

RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,

RA Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehm B.,

RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,

RA Qui D., Iankiev P., Pedersen D., Nelson M., Washburne M.,

RA Selitrennikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,

RA Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,

RA Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,

RA Kamal M., Kamysseles M., Mauceli E., Blellet C., Rudd S.,

RA Krystofova S., Rasmussen C., Metznerberg R.L., Perkins D.D., Kroken S.,

RA Cogoni C., Macino G., Catcheside D., Li W., Pratt R.J., Oemami S.A.,

RA DeSouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R.,

```

RA Yarden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,
RA Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M.,
RA Paulsen I., Sachs M.S., Landu E.S., Nussbaum C., Birren B.;
RT "The Genome Sequence of the Filamentous Fungus Neurospora crassa.";
RL Nature 0:0-0(2003).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AABX01000364; EAA30441.1; -; Genomic DNA.
SQ SEQUENCE 803 AA; 84723 MW; 99B7FEA4F3E26C5A CRC64;

Query Match 70.4%; Score 38; DB 2; Length 803;
Best Local Similarity 63.6%; Pred. No. 3.5e+02;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SASQDISNYLN 11
|||||:|||||
Db 182 SASRDSTNYVN 192

RESULT 47
ID Q6BPM0 DEBHA PRELIMINARY; PRT; 879 AA.
AC Q6BPM0
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Debaryomyces hansenii chromosome E of strain CBS767 of Debaryomyces
DE hansenii.
GN OrderedLocusNames=DEHA0E13068g;
OS Debaryomyces hansenii (Yeast) (Torulaspora hansenii).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Debaryomycetes.
OX NCBI_TaxID=4959;
KW NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RN 1
RP STRAIN=ATCC 36239 / CBS 767;
RX PubMed=15229592; DOI=10.1038/nature02579;
RA Lafontaine I., Sherman D., Fischer G., Durrens P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marck C., Neveuglise C., Talla E.,
RA Goffard N., Franchin L., Aigle M., Anthouard V., Babour A., Barbe V.,
RA Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,
RA Boisarane A., Boyer J., Cattolico L., Confaniolero F., de Daruvar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA Nicaud J.-M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
RA Pellenz S., Potier S., Richard G.-F., Straub M.-L., Suleau A.,
RA Swennen D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA Zenlou-Meyer M., Zivanovic Y., Boitot-Fukuhara M., Thierry A.,
RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
RA Winkler P., Souciet J.-L.;
RT "Genome evolution in yeasts.";
RL Nature 430:35-44(2004).
DR EMBL; CR382137; CAG8089.1; -; Genomic DNA.
DR GO; GO:0043234; C:protein complex; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0017111; F:nucleoside-triphosphatase activity; IEA.
DR GO; GO:0000166; F:nucleotide binding; IEA.
DR GO; GO:0006260; F:DNA replication; IEA.
DR InterPro; IPR003593; AAA ATPase.
DR InterPro; IPR00862; RFC.
DR SMART; SM00382; AAA; 1.
KW ATP-binding; Complete proteome; Nucleotide-binding; Transport.
SQ SEQUENCE 879 AA; 99687 MW; 00B48C51712DE216 CRC64;

Query Match 70.4%; Score 38; DB 2; Length 879;
Best Local Similarity 88.9%; Pred. No. 3.8e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SASQDISNY 9

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Db 512 SASQDISRY 520
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RESULT 48
Q98QF1 MYCPU PRELIMINARY; PRT; 904 AA.
ID Q98QF1 MYCPU PRELIMINARY;
AC Q98QF1
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE LIPOPROTEIN.
GN OrderedLocusNames=MYPU_4150;
OS Mycoplasma pulmonis.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2107;
RN 1
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=UAB CTIP;
RX MEDLINE=21267165; PubMed=11353084; DOI=10.1093/nar/29.10.2145;
RA Chambaud I., Heilig R., Ferris S., Barbe V., Samson D., Gallisson F.,
RA Moszer I., Dybvig K., Wroblewski H., Viari A., Rocha E.P.C.,
RA Blanchard A.;
RT "The complete genome sequence of the murine respiratory pathogen
RT Mycoplasma pulmonis.";
RL Nucleic Acids Res. 29:2145-2153(2001).
DR EMBL; AL445564; CAC13588.1; -; Genomic DNA.
DR PIR; G90563; G90563.
DR MYPUList; MYPU 4150; -;
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR000914; SBP_bac_5.
DR Pfam; PF00496; SBP_bac_5; 1.
KW Complete proteome; Lipoprotein.
SQ SEQUENCE 904 AA; 103181 MW; 56D2D1B5958A640E CRC64;

Query Match 70.4%; Score 38; DB 2; Length 904;
Best Local Similarity 72.7%; Pred. No. 3.9e+02;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 SASQDISNYLN 11
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Db 195 TASQKIVNYLN 205

RESULT 49
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ID Q5ALR7 CANAL PRELIMINARY;
AC Q5ALR7
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Hypothetical protein ROD1.
GN Name=ROD1; ORFNames=Cao19.9084;
OS Candida albicans SC5314.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX NCBI_TaxID=237561;
RN 1
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=SC5314;
RX PubMed=15123810; DOI=10.1073/pnas.0401648101;
RA Jones T., Federspiel N.A., Chibana H., Ugabian N., Magee P.T.,
RA Magee B.B., Newport G., Thorstensen Y.R., Agabian N., Magee P.T.,
RA Davis R.W., Scherer S.;
RT "The diploid genome sequence of Candida albicans.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:7329-7334(2004).
RN 12
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=SC5314;
RA Dungan J., Kuo A., Newport G., Lan C.-Y., Iijima C., Adegbola O.,
RA Roberts J., Persson K., Donnelly S., Favoreto S., Tzung K.-W.,
RA Jones T., Scherer S., Agabian N.;

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RT "Annotation of the Genome of Candida albicans."  
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.  
CC -!- CAUTION: The sequence shown here is derived from an  
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
CC preliminary data.  
DR EMBL; AACQ01000008; EAL03665.1; -; Genomic\_DNA.  
KW Hypothetical protein.  
SQ SEQUENCE 911 AA; 98662 MW; 52DA93114A37E5AA4 CRC64;

Query Match 70.4%; Score 38; DB 2; Length 911;  
Best Local Similarity 77.8%; Pred. No. 3.9e+02;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 SQDISNYLN 11  
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Db 97 SQEFSNYLN 105

## RESULT 50

Q5AM66 CANAL  
ID Q5AM66 CANAL PRELIMINARY; PRT; 923 AA.  
AC Q5AM66;  
DT 10-MAY-2005 (TrEMBLrel. 30, Created)  
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)  
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)  
DE Hypothetical protein ROD1.  
GN Name=ROD1; ORFNames=CaO19.1509;  
OS Candida albicans SC5314.  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.  
OX NCBI\_TaxID=237561;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=SC5314;  
RX PubMed=15123810; DOI=10.1073/pnas.0401648101;  
RA Jones T., Federspiel N.A., Chibana H., Dungan J., Kalman S., Magee B.B., Magee B.B., Newport G., Thorstenson Y.R., Agabian N., Agabian P.T., Davis R.W., Scherer S.;  
RT "The diploid genome sequence of Candida albicans."  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=SC5314;  
RA Dungan J., Kuo A., Newport G., Lan C.-Y., Iijima C., Adegbola O., Roberts J., Persson K., Donnelly S., Favoreto S., Tzung K.-W., Jones T., Scherer S., Agabian N.;  
RT "Annotation of the Genome of Candida albicans."  
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.  
CC -!- CAUTION: The sequence shown here is derived from an  
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
CC preliminary data.  
DR EMBL; AACQ01000007; EAL03812.1; -; Genomic\_DNA.  
KW Hypothetical protein.  
SQ SEQUENCE 923 AA; 99486 MW; EB484C71C2A6EC68 CRC64;

Query Match 70.4%; Score 38; DB 2; Length 923;  
Best Local Similarity 77.8%; Pred. No. 4e+02;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 SQDISNYLN 11  
||:||||  
Db 97 SQEFSNYLN 105

Search completed: April 6, 2006, 09:13:04  
Job time : 101.251 secs

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GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: April 6, 2006, 08:58:56 ; Search time 14.7288 Seconds  
(without alignments)  
61.745 Million cell updates/sec

Title: US-10-089-500-6

Perfect score: 54

Sequence: 1 SASQDISNYLN 11

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/ptodata/1/iaa/5 COMB.pep:\*  
2: /cgn2\_6/ptodata/1/iaa/6 COMB.pep:\*  
3: /cgn2\_6/ptodata/1/iaa/H COMB.pep:\*  
4: /cgn2\_6/ptodata/1/iaa/PCTUS COMB.pep:\*  
5: /cgn2\_6/ptodata/1/iaa/RE COMB.pep:\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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2	54	100.0	107	2	US-08-908-469-13
3	54	100.0	107	2	US-08-908-469-15
4	54	100.0	108	2	US-08-908-469-8
5	54	100.0	108	2	US-08-908-469-10
6	54	100.0	108	2	US-08-908-469-126
7	54	100.0	110	2	US-09-440-781-94
8	54	100.0	110	2	US-08-908-469-103
9	54	100.0	110	2	US-08-908-469-105
10	54	100.0	110	2	US-08-908-469-107
11	54	100.0	110	2	US-08-908-469-117
12	54	100.0	128	2	US-09-225-322B-10
13	54	100.0	128	2	US-09-225-322B-19
14	54	100.0	128	2	US-09-764-304-10
15	54	100.0	128	2	US-09-764-304-19
16	54	100.0	237	2	US-08-908-469-100
17	54	100.0	491	2	US-10-011-125A-2
18	51	94.4	109	2	US-09-386-658A-4
19	50	92.6	11	1	US-08-480-434-76
20	50	92.6	11	1	US-08-053-451B-76
21	50	92.6	11	2	US-08-649-100-11
22	50	92.6	11	2	US-08-649-100-27
23	50	92.6	31	2	US-08-525-539A-5
24	50	92.6	76	2	US-08-851-362D-20
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26	50	92.6	95	2	US-10-194-975-57
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					Sequence 15, Appl
					Sequence 8, Appl
					Sequence 10, Appl
					Sequence 126, App
					Sequence 94, Appl
					Sequence 103, App
					Sequence 105, App
					Sequence 107, App
					Sequence 117, App
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					Sequence 34, Appl
					Sequence 38, Appl
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					Sequence 21, Appl
					Sequence 10, Appl
					Sequence 37, Appl
					Sequence 37, Appl
					Sequence 17, Appl
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					Sequence 2, Appl
					Sequence 18, Appl
					Sequence 13, Appl
					Sequence 24, Appl
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					Sequence 9, Appl
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					Sequence 2, Appl
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					Sequence 26, Appl
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					Sequence 12, Appl
					Sequence 39, Appl
					Sequence 40, Appl
					Sequence 1, Appl
					Sequence 2, Appl
					Sequence 1, Appl
					Sequence 2, Appl
					Sequence 24, Appl
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					Sequence 39, Appl
					Sequence 40, Appl
					Sequence 25, Appl
					Sequence 25, Appl
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					Sequence 150, App
					Sequence 6, Appl
					Sequence 10, Appl
					Sequence 2, Appl
					Sequence 6, Appl
					Sequence 8, Appl
					Sequence 117, App
					Sequence 117, App
					Sequence 112, App
					Sequence 112, App

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102	45	83.3	104	4	PCT-US95-08743-112	Sequence 112, App	175	42	77.8	107	4	PCT-US95-08743-103	Sequence 103, App
103	45	83.3	107	1	US-08-276-852-107	Sequence 107, App	176	42	77.8	108	1	US-08-378-939-20	Sequence 20, Appl
104	45	83.3	107	1	US-08-276-852-108	Sequence 108, App	177	41	75.9	105	2	US-08-851-362D-30	Sequence 30, Appl
105	45	83.3	107	1	US-08-899-575-108	Sequence 107, App	178	41	75.9	107	1	US-08-290-592E-20	Sequence 20, Appl
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108	45	83.3	107	1	US-08-899-575-108	Sequence 108, App	181	41	75.9	107	2	PCT-US95-10053-17	Sequence 17, Appl
109	45	83.3	107	1	US-07-934-373C-16	Sequence 16, Appl	182	41	75.9	107	4	PCT-US95-10053-18	Sequence 18, Appl
110	45	83.3	107	1	US-07-934-373C-17	Sequence 17, Appl	183	41	75.9	107	4	PCT-US96-09448-20	Sequence 20, Appl
111	45	83.3	107	1	US-08-437-642B-16	Sequence 16, Appl	184	41	75.9	107	4	PCT-US96-09448-21	Sequence 21, Appl
112	45	83.3	107	2	US-08-437-642B-17	Sequence 17, Appl	185	41	75.9	127	1	US-10-268-883-5	Sequence 5, Appli
113	45	83.3	107	2	US-08-146-206C-16	Sequence 16, Appl	186	41	75.9	142	1	US-08-579-940-2	Sequence 2, Appli
114	45	83.3	107	2	US-08-146-206C-17	Sequence 17, Appl	187	41	75.9	142	2	US-08-838-692-4	Sequence 4, Appli
115	45	83.3	107	2	US-09-705-686-16	Sequence 16, Appl	188	41	75.9	355	2	US-08-875-811-41	Sequence 41, Appl
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127	45	83.3	126	1	US-08-436-717-71	Sequence 71, Appl	200	40	74.1	108	2	US-09-240-274-41	Sequence 41, Appl
128	45	83.3	126	1	US-08-436-717-71	Sequence 71, Appl	201	40	74.1	108	2	US-09-155-106-22	Sequence 22, Appl
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131	45	83.3	127	1	US-08-574-699A-2	Sequence 2, Appli	204	40	74.1	108	2	US-09-155-106-28	Sequence 28, Appl
132	45	83.3	247	2	US-10-620-049-21	Sequence 21, Appl	205	40	74.1	108	2	US-09-155-106-30	Sequence 30, Appl
133	45	83.3	247	2	US-10-620-049-23	Sequence 23, Appl	206	40	74.1	108	2	US-09-848-798-41	Sequence 41, Appl
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137	45	83.3	302	1	US-08-121-054C-18	Sequence 18, Appl	210	39.5	73.1	108	2	US-08-964-690-24	Sequence 24, Appl
138	45	83.3	302	1	US-08-121-054C-30	Sequence 30, Appl	211	39.5	73.1	109	2	US-08-561-521-42	Sequence 42, Appl
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142	45	83.3	302	2	US-09-813-659-32	Sequence 32, Appl	215	39.5	73.1	109	4	PCT-US95-01219-42	Sequence 42, Appl
143	45	83.3	302	2	US-09-549-067A-18	Sequence 18, Appl	216	39	72.2	11	2	US-09-192-854-6	Sequence 6, Appli
144	45	83.3	302	2	US-09-549-067A-32	Sequence 32, Appl	217	39	72.2	11	2	US-09-511-939-10	Sequence 10, Appl
145	44	81.5	102	2	US-09-726-219A-173	Sequence 173, App	218	39	72.2	11	2	US-09-511-939-16	Sequence 16, Appl
146	44	81.5	102	2	US-09-196-522-173	Sequence 173, App	219	39	72.2	11	2	US-09-511-939-22	Sequence 22, Appl
147	44	81.5	107	1	US-08-652-558-36	Sequence 36, App	220	39	72.2	11	2	US-09-511-939-28	Sequence 28, Appl
148	44	81.5	107	1	US-08-378-939-14	Sequence 14, Appl	221	39	72.2	11	2	US-09-511-939-34	Sequence 34, Appl
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157	44	81.5	108	2	US-09-490-153-14	Sequence 14, Appl	230	39	72.2	11	2	US-09-511-939-136	Sequence 136, App
158	44	81.5	108	2	US-09-232-290-16	Sequence 16, Appl	231	39	72.2	11	2	US-09-511-939-154	Sequence 154, App
159	44	81.5	108	2	US-09-490-324-14	Sequence 14, Appl	232	39	72.2	11	2	US-09-511-939-160	Sequence 160, App
160	44	81.5	108	4	PCT-US95-08743-102	Sequence 102, App	233	39	72.2	11	2	US-09-511-939-166	Sequence 166, App
161	44	81.5	109	2	US-10-330-613A-10	Sequence 10, Appl	234	39	72.2	11	2	US-09-511-939-172	Sequence 172, App
162	43	79.6	11	1	US-07-942-245-496	Sequence 496, App	235	39	72.2	11	2	US-09-511-939-178	Sequence 178, App
163	43	79.6	30	2	US-08-525-539A-7	Sequence 7, Appli	236	39	72.2	11	2	US-09-511-939-202	Sequence 202, App
164	43	79.6	102	2	US-09-199-149-10	Sequence 10, Appl	237	39	72.2	11	2	US-09-511-939-208	Sequence 208, App
165	43	79.6	102	2	US-09-199-149-29	Sequence 29, Appl	238	39	72.2	11	2	US-09-511-939-226	Sequence 226, App
166	43	79.6	105	2	US-09-199-149-31	Sequence 31, Appl	239	39	72.2	11	2	US-09-511-939-232	Sequence 232, App
167	43	79.6	107	2	US-09-232-290-29	Sequence 29, Appl	240	39	72.2	11	2	US-09-511-939-244	Sequence 244, App
168	43	79.6	108	2	US-09-199-149-7	Sequence 7, Appli	241	39	72.2	11	2	US-09-511-939-250	Sequence 250, App
169	43	79.6	108	2	US-09-199-149-14	Sequence 14, Appl	242	39	72.2	11	2	US-09-511-939-256	Sequence 256, App
170	43	79.6	108	2	US-09-905-243-73	Sequence 73, Appl	243	39	72.2	11	2	US-09-511-939-280	Sequence 280, App
171	43	79.6	109	1	US-07-942-245-11	Sequence 11, Appl	244	39	72.2	11	2	US-09-511-939-292	Sequence 292, App
172	42	77.8	107	1	US-08-276-852-103	Sequence 103, App	245	39	72.2	11	2	US-09-511-939-304	Sequence 304, App
173	42	77.8	107	1	US-08-899-575-103	Sequence 103, App	246	39	72.2	11	2		

247	39	72.2	76	2	US-08-851-362D-21	Sequence 21, Appl	320	38	70.4	107	1	US-08-561-521-6	Sequence 6, Appl1
248	39	72.2	88	2	US-09-905-243-31	Sequence 31, Appl	321	38	70.4	107	1	US-08-561-521-8	Sequence 8, Appl1
249	39	72.2	88	2	US-09-905-243-36	Sequence 36, Appl	322	38	70.4	107	1	US-08-652-558-34	Sequence 34, Appl
250	39	72.2	95	2	US-09-472-087-94	Sequence 94, Appl	323	38	70.4	107	1	US-08-652-558-47	Sequence 47, Appl
251	39	72.2	95	2	US-10-194-975-54	Sequence 54, Appl	324	38	70.4	107	1	US-08-318-157B-6	Sequence 6, Appl1
252	39	72.2	95	2	US-10-194-975-55	Sequence 55, Appl	325	38	70.4	107	1	US-08-437-642B-18	Sequence 18, Appl
253	39	72.2	95	2	US-10-330-613A-43	Sequence 43, Appl	326	38	70.4	107	2	US-09-240-274-44	Sequence 44, Appl
254	39	72.2	103	2	US-09-240-274-42	Sequence 42, Appl	327	38	70.4	107	2	US-09-240-274-162	Sequence 162, App
255	39	72.2	103	2	US-09-848-798-42	Sequence 42, Appl	328	38	70.4	107	2	US-08-025-203-15	Sequence 15, Appl
256	39	72.2	107	1	US-08-276-852-104	Sequence 104, App	329	38	70.4	107	2	US-08-146-206C-18	Sequence 18, Appl
257	39	72.2	107	1	US-08-276-852-105	Sequence 105, App	330	38	70.4	107	2	US-09-648-067A-14	Sequence 14, Appl
258	39	72.2	107	1	US-08-899-575-104	Sequence 104, App	331	38	70.4	107	2	US-09-705-686A-18	Sequence 18, Appl
259	39	72.2	107	1	US-08-899-575-105	Sequence 105, App	332	38	70.4	107	2	US-09-253-794-6	Sequence 6, Appl1
260	39	72.2	107	1	US-08-899-575-104	Sequence 104, App	333	38	70.4	107	2	US-09-705-392A-18	Sequence 18, Appl
261	39	72.2	107	1	US-08-899-575-105	Sequence 105, App	334	38	70.4	107	2	US-09-999-021-15	Sequence 15, Appl
262	39	72.2	107	2	US-08-851-362D-32	Sequence 32, Appl	335	38	70.4	107	2	US-09-999-025-15	Sequence 15, Appl
263	39	72.2	107	2	US-09-240-274-33	Sequence 33, Appl	336	38	70.4	107	2	US-10-040-997-15	Sequence 15, Appl
264	39	72.2	107	2	US-09-240-274-37	Sequence 37, Appl	337	38	70.4	107	2	US-09-999-040-15	Sequence 15, Appl
265	39	72.2	107	2	US-09-240-274-38	Sequence 38, Appl	338	38	70.4	107	2	US-09-998-817-15	Sequence 15, Appl
266	39	72.2	107	2	US-09-240-274-39	Sequence 39, Appl	339	38	70.4	107	2	US-09-705-398-18	Sequence 18, Appl
267	39	72.2	107	2	US-09-240-274-40	Sequence 40, Appl	340	38	70.4	107	2	US-08-848-798-44	Sequence 44, Appl
268	39	72.2	107	2	US-09-240-274-156	Sequence 156, App	341	38	70.4	107	2	US-09-848-798-162	Sequence 162, App
269	39	72.2	107	2	US-09-240-274-158	Sequence 158, App	342	38	70.4	107	2	US-09-602-812A-5	Sequence 5, Appl1
270	39	72.2	107	2	US-09-240-274-168	Sequence 168, App	343	38	70.4	107	4	PCT-US93-07832-18	Sequence 18, Appl
271	39	72.2	107	2	US-09-240-274-175	Sequence 175, App	344	38	70.4	107	4	PCT-US95-01219-6	Sequence 6, Appl1
272	39	72.2	107	2	US-09-240-274-176	Sequence 176, App	345	38	70.4	107	4	PCT-US95-01219-8	Sequence 8, Appl1
273	39	72.2	107	2	US-09-848-798-33	Sequence 33, Appl	346	38	70.4	108	1	US-08-070-116A-7	Sequence 7, Appl1
274	39	72.2	107	2	US-09-848-798-37	Sequence 37, Appl	347	38	70.4	108	1	US-08-116-247-9	Sequence 9, Appl1
275	39	72.2	107	2	US-09-848-798-38	Sequence 38, Appl	348	38	70.4	108	2	US-08-974-899-3	Sequence 3, Appl1
276	39	72.2	107	2	US-09-848-798-39	Sequence 39, Appl	349	38	70.4	108	2	US-09-240-274-181	Sequence 181, App
277	39	72.2	107	2	US-09-848-798-40	Sequence 40, Appl	350	38	70.4	108	2	US-08-557-050-7	Sequence 7, Appl1
278	39	72.2	107	2	US-09-848-798-156	Sequence 156, App	351	38	70.4	108	2	US-08-454-899G-100	Sequence 100, App
279	39	72.2	107	2	US-09-848-798-158	Sequence 158, App	352	38	70.4	108	2	US-09-795-798-3	Sequence 3, Appl1
280	39	72.2	107	2	US-09-848-798-168	Sequence 168, App	353	38	70.4	108	2	US-09-348-224-9	Sequence 9, Appl1
281	39	72.2	107	2	US-09-848-798-175	Sequence 175, App	354	38	70.4	108	2	US-08-908-469-12	Sequence 12, Appl
282	39	72.2	107	2	US-09-848-798-176	Sequence 176, App	355	38	70.4	108	2	US-08-908-469-12	Sequence 12, Appl
283	39	72.2	107	4	PCT-US95-08743-104	Sequence 104, App	356	38	70.4	109	1	US-07-934-373C-3	Sequence 3, Appl1
284	39	72.2	107	4	PCT-US95-08743-105	Sequence 105, App	357	38	70.4	109	2	US-08-437-642B-3	Sequence 3, Appl1
285	39	72.2	108	1	US-08-379-057-29	Sequence 29, Appl	358	38	70.4	109	2	US-08-146-206C-3	Sequence 3, Appl1
286	39	72.2	108	2	US-08-983-607-29	Sequence 29, Appl	359	38	70.4	109	2	US-09-705-686A-3	Sequence 3, Appl1
287	39	72.2	108	2	US-08-983-607-37	Sequence 37, Appl	360	38	70.4	109	2	US-09-705-392A-3	Sequence 3, Appl1
288	39	72.2	108	2	US-09-240-274-32	Sequence 32, Appl	361	38	70.4	109	4	PCT-US93-07832-3	Sequence 3, Appl1
289	39	72.2	108	2	US-09-240-274-43	Sequence 43, Appl	362	38	70.4	109	4	PCT-US93-07832-3	Sequence 3, Appl1
290	39	72.2	108	2	US-09-240-274-163	Sequence 163, App	363	38	70.4	487	2	US-09-248-796A-20378	Sequence 20378, A
291	39	72.2	108	2	US-09-240-274-167	Sequence 167, App	364	37	68.5	11	2	US-08-836-561-43	Sequence 43, Appl
292	39	72.2	108	2	US-09-848-798-32	Sequence 32, Appl	365	37	68.5	11	2	US-09-434-122-43	Sequence 43, Appl
293	39	72.2	108	2	US-09-848-798-43	Sequence 43, Appl	366	37	68.5	11	2	US-08-802-083-10	Sequence 10, Appl
294	39	72.2	108	2	US-09-848-798-163	Sequence 163, Appl	367	37	68.5	51	1	US-08-472-788A-73	Sequence 73, Appl
295	39	72.2	108	2	US-09-848-798-167	Sequence 167, App	368	37	68.5	51	1	US-08-472-788A-74	Sequence 74, Appl
296	39	72.2	134	2	US-09-472-087-23	Sequence 23, Appl	369	37	68.5	51	1	US-08-082-842A-73	Sequence 73, Appl
297	39	72.2	134	2	US-09-472-087-97	Sequence 97, Appl	370	37	68.5	51	1	US-08-082-842A-74	Sequence 74, Appl
298	39	72.2	137	2	US-09-582-337-24	Sequence 24, Appl	371	37	68.5	88	2	US-09-905-243-39	Sequence 29, Appl
299	39	72.2	150	2	US-09-472-087-24	Sequence 24, Appl	372	37	68.5	88	2	US-09-905-243-33	Sequence 33, Appl
300	39	72.2	150	2	US-09-472-087-98	Sequence 98, Appl	373	37	68.5	92	1	US-08-273-146-47	Sequence 27, Appl
301	39	72.2	224	2	US-09-456-090A-48	Sequence 48, Appl	374	37	68.5	95	2	US-05-627-896B-27	Sequence 27, Appl
302	39	72.2	224	2	US-09-453-234-48	Sequence 48, Appl	375	37	68.5	95	2	US-10-194-975-58	Sequence 58, Appl
303	39	72.2	240	2	US-09-192-854-2	Sequence 2, Appl1	376	37	68.5	95	2	US-10-194-975-61	Sequence 61, Appl
304	39	72.2	240	2	US-09-511-939-2	Sequence 2, Appl1	377	37	68.5	95	2	US-09-339-596A-42	Sequence 42, Appl
305	39	72.2	459	2	US-09-328-352-4333	Sequence 4333, Ap	378	37	68.5	95	2	US-10-330-613A-63	Sequence 36, Appl
306	39	72.2	466	2	US-09-134-000C-6667	Sequence 6667, Ap	379	37	68.5	105	2	US-08-851-362D-36	Sequence 36, Appl
307	39	72.2	49	1	US-08-478-039-87	Sequence 87, Appl	380	37	68.5	107	1	US-08-425-336-123	Sequence 123, App
308	38	70.4	49	1	US-08-478-039-87	Sequence 87, Appl	381	37	68.5	107	1	US-08-425-336-125	Sequence 125, App
309	38	70.4	85	1	US-08-303-569B-8	Sequence 8, Appl1	382	37	68.5	107	1	US-08-276-852-82	Sequence 82, Appl
310	38	70.4	85	1	US-08-303-569B-8	Sequence 8, Appl1	383	37	68.5	107	1	US-08-276-852-84	Sequence 84, Appl
311	38	70.4	85	2	US-09-795-515-8	Sequence 15, Appl	384	37	68.5	107	1	US-08-300-386A-66	Sequence 66, Appl
312	38	70.4	90	2	US-09-199-149-15	Sequence 35, Appl	385	37	68.5	107	1	US-08-488-113B-123	Sequence 123, App
313	38	70.4	103	2	US-09-460-384-35	Sequence 106, App	386	37	68.5	107	1	US-08-488-113B-125	Sequence 125, App
314	38	70.4	104	1	US-08-276-852-106	Sequence 106, App	387	37	68.5	107	1	US-08-477-484B-123	Sequence 123, App
315	38	70.4	104	1	US-08-899-575-106	Sequence 106, App	388	37	68.5	107	1	US-08-477-484B-125	Sequence 125, App
316	38	70.4	104	1	US-08-899-575-106	Sequence 106, App	389	37	68.5	107	1	US-08-107-669D-26	Sequence 26, Appl
317	38	70.4	104	4	PCT-US95-08743-106	Sequence 106, App	390	37	68.5	107	1	US-08-107-669D-27	Sequence 27, Appl
318	38	70.4	105	2	US-08-851-362D-26	Sequence 26, Appl	391	37	68.5	107	1	US-08-107-669D-27	Sequence 27, Appl
319	38	70.4	107	1	US-07-934-373C-18	Sequence 18, Appl	392	37	68.5	107	1	US-08-472-788A-26	Sequence 26, Appl

393	37	68.5	107	1	US-08-472-788A-27	Sequence 27, Appl	466	36	66.7	108	1	US-08-162-102C-25	Sequence 25, Appl
394	37	68.5	107	1	US-08-472-788A-87	Sequence 87, Appl	467	36	66.7	108	2	US-08-920-100B-25	Sequence 25, Appl
395	37	68.5	107	1	US-08-899-575-82	Sequence 82, Appl	468	36	66.7	108	4	PCT-US93-08786-25	Sequence 25, Appl
396	37	68.5	107	1	US-08-899-575-84	Sequence 84, Appl	469	36	66.7	110	2	US-09-440-781-95	Sequence 95, Appl
397	37	68.5	107	1	US-08-899-575-82	Sequence 82, Appl	470	36	66.7	110	2	US-08-908-469-109	Sequence 109, App
398	37	68.5	107	1	US-08-899-575-84	Sequence 84, Appl	471	36	66.7	110	2	US-08-908-469-111	Sequence 111, App
399	37	68.5	107	1	US-08-477-531B-26	Sequence 26, Appl	472	36	66.7	110	2	US-08-908-469-113	Sequence 113, App
400	37	68.5	107	1	US-08-477-531B-27	Sequence 27, Appl	473	36	66.7	110	2	US-08-908-469-115	Sequence 115, App
401	37	68.5	107	1	US-08-477-531B-65	Sequence 65, Appl	474	36	66.7	138	1	US-08-480-434-63	Sequence 63, Appl
402	37	68.5	107	1	US-08-646-360-123	Sequence 123, App	475	36	66.7	138	1	US-08-053-451B-63	Sequence 63, Appl
403	37	68.5	107	1	US-08-646-360-123	Sequence 123, App	476	36	66.7	407	2	US-09-270-767-57916	Sequence 57916, A
404	37	68.5	107	1	US-08-082-842A-26	Sequence 26, Appl	477	35	65.7	92	2	US-10-330-613A-60	Sequence 60, Appl
405	37	68.5	107	1	US-08-082-842A-27	Sequence 27, Appl	478	35	64.8	11	1	US-07-942-245-494	Sequence 494, App
406	37	68.5	107	1	US-08-082-842A-87	Sequence 87, Appl	479	35	64.8	11	2	US-09-339-922A-110	Sequence 110, App
407	37	68.5	107	2	US-08-931-645-66	Sequence 66, Appl	480	35	64.8	11	2	US-08-407-620A-4	Sequence 4, Appl
408	37	68.5	107	2	US-08-839-765-123	Sequence 123, App	481	35	64.8	11	2	US-09-192-854-105	Sequence 105, App
409	37	68.5	107	2	US-08-839-765-123	Sequence 123, App	482	35	64.8	11	2	US-09-511-939-184	Sequence 184, App
410	37	68.5	107	2	US-09-136-389-123	Sequence 123, App	483	35	64.8	13	2	US-09-339-922A-82	Sequence 82, Appl
411	37	68.5	107	2	US-09-136-389-123	Sequence 123, App	484	35	64.8	13	2	US-09-016-061-82	Sequence 82, Appl
412	37	68.5	107	2	US-09-610-838-123	Sequence 123, App	485	35	64.8	84	2	US-09-471-276-816	Sequence 816, App
413	37	68.5	107	2	US-09-610-838-123	Sequence 123, App	486	35	64.8	107	1	US-08-300-386A-67	Sequence 67, Appl
414	37	68.5	107	2	US-09-711-485-123	Sequence 123, App	487	35	64.8	107	2	US-08-931-645-67	Sequence 67, Appl
415	37	68.5	107	2	US-09-711-485-123	Sequence 123, App	488	35	64.8	107	4	PCT-US95-11235-67	Sequence 67, Appl
416	37	68.5	107	4	PCT-US95-08743-82	Sequence 82, Appl	489	35	64.8	108	1	US-08-378-939-26	Sequence 26, Appl
417	37	68.5	107	4	PCT-US95-08743-84	Sequence 84, Appl	490	35	64.8	108	2	US-08-407-620A-8	Sequence 8, Appl
418	37	68.5	107	4	PCT-US95-11235-66	Sequence 66, Appl	491	35	64.8	108	2	US-08-407-620A-10	Sequence 10, Appl
419	37	68.5	109	2	US-09-802-083B-4	Sequence 4, Appl	492	35	64.8	108	2	US-10-268-883-12	Sequence 12, Appl
420	37	68.5	112	2	US-09-627-218B-1	Sequence 1, Appl	493	35	64.8	109	1	US-07-942-245-1	Sequence 1, Appl
421	37	68.5	114	4	PCT-US95-061521-43	Sequence 43, Appl	494	35	64.8	127	2	US-08-284-516C-57	Sequence 57, Appl
422	37	68.5	114	4	PCT-US95-061521-43	Sequence 43, Appl	495	35	64.8	127	2	US-09-537-911A-57	Sequence 57, Appl
423	37	68.5	127	2	US-08-836-561-29	Sequence 29, Appl	496	35	64.8	129	1	US-08-860-174A-5	Sequence 5, Appl
424	37	68.5	127	2	US-08-836-561-71	Sequence 71, Appl	497	35	64.8	130	2	US-10-268-883-11	Sequence 11, Appl
425	37	68.5	127	2	US-08-836-561-88	Sequence 88, Appl	498	35	64.8	218	2	US-09-328-352-4680	Sequence 4680, App
426	37	68.5	127	2	US-08-836-561-92	Sequence 92, Appl	499	35	64.8	258	1	US-08-860-174A-13	Sequence 13, Appl
427	37	68.5	127	2	US-08-836-561-98	Sequence 98, Appl	500	35	64.8	259	2	US-09-419-788-29	Sequence 29, Appl
428	37	68.5	127	2	US-08-836-561-103	Sequence 103, App	501	35	64.8	302	2	US-09-248-796A-14539	Sequence 14539, A
429	37	68.5	127	2	US-09-434-122-29	Sequence 29, Appl	502	35	64.8	1040	1	US-08-254-989-2	Sequence 2, Appl
430	37	68.5	127	2	US-09-434-122-71	Sequence 71, Appl	503	35	64.8	1043	2	US-09-538-092-935	Sequence 935, App
431	37	68.5	127	2	US-09-434-122-88	Sequence 88, Appl	504	34	63.0	11	1	US-08-182-067-4	Sequence 4, Appl
432	37	68.5	127	2	US-09-434-122-92	Sequence 92, Appl	505	34	63.0	11	1	US-08-465-313-4	Sequence 4, Appl
433	37	68.5	127	2	US-09-434-122-98	Sequence 98, Appl	506	34	63.0	11	2	US-09-339-922A-108	Sequence 108, App
434	37	68.5	127	2	US-09-434-122-103	Sequence 103, App	507	34	63.0	11	2	US-09-809-739-2	Sequence 2, Appl
435	37	68.5	129	2	US-09-019-441A-6	Sequence 6, Appl	508	34	63.0	11	2	US-09-378-967-4	Sequence 4, Appl
436	37	68.5	235	2	US-08-812-586-16	Sequence 16, Appl	509	34	63.0	11	2	US-09-192-854-153	Sequence 153, App
437	37	68.5	235	2	US-09-535-832A-17	Sequence 17, Appl	510	34	63.0	11	2	US-09-511-939-268	Sequence 268, App
438	37	68.5	240	1	US-08-488-113B-147	Sequence 147, App	511	34	63.0	11	2	US-09-798-058-8	Sequence 8, Appl
439	37	68.5	240	1	US-08-488-113B-148	Sequence 148, App	512	34	63.0	13	2	US-09-339-922A-42	Sequence 42, Appl
440	37	68.5	240	1	US-08-477-484B-147	Sequence 147, App	513	34	63.0	13	2	US-09-016-061-42	Sequence 42, Appl
441	37	68.5	240	1	US-08-477-484B-148	Sequence 148, App	514	34	63.0	96	1	US-08-737-560A-9	Sequence 9, Appl
442	37	68.5	240	1	US-08-646-360-147	Sequence 147, App	515	34	63.0	105	1	US-08-276-852-89	Sequence 89, Appl
443	37	68.5	240	1	US-08-646-360-148	Sequence 148, App	516	34	63.0	105	1	US-08-899-575-89	Sequence 89, Appl
444	37	68.5	240	2	US-08-839-765-147	Sequence 147, App	517	34	63.0	105	1	US-08-899-575-85	Sequence 85, Appl
445	37	68.5	240	2	US-08-839-765-148	Sequence 148, App	518	34	63.0	105	4	PCT-US95-08743-89	Sequence 89, Appl
446	37	68.5	240	2	US-09-136-389-147	Sequence 147, App	519	34	63.0	106	1	US-08-276-852-83	Sequence 83, Appl
447	37	68.5	240	2	US-09-136-389-148	Sequence 148, App	520	34	63.0	106	1	US-08-276-852-85	Sequence 85, Appl
448	37	68.5	240	2	US-09-610-838-147	Sequence 147, App	521	34	63.0	106	1	US-08-899-575-83	Sequence 83, Appl
449	37	68.5	240	2	US-09-610-838-148	Sequence 148, App	522	34	63.0	106	1	US-08-899-575-85	Sequence 85, Appl
450	37	68.5	240	2	US-09-711-485-147	Sequence 147, App	523	34	63.0	106	1	US-08-899-575-85	Sequence 85, Appl
451	37	68.5	240	2	US-09-711-485-148	Sequence 148, App	524	34	63.0	106	1	US-08-899-575-85	Sequence 85, Appl
452	37	66.7	11	1	US-09-328-352-6613	Sequence 6613, App	525	34	63.0	106	4	PCT-US95-08743-85	Sequence 85, Appl
453	36	66.7	11	1	US-08-480-434-66	Sequence 66, Appl	526	34	63.0	106	4	PCT-US95-08743-85	Sequence 85, Appl
454	36	66.7	11	1	US-08-480-434-75	Sequence 75, Appl	527	34	63.0	107	2	US-09-240-274-179	Sequence 179, App
455	36	66.7	11	1	US-08-053-451B-66	Sequence 66, Appl	528	34	63.0	107	2	US-09-247-352-8	Sequence 8, Appl
456	36	66.7	11	1	US-08-053-451B-75	Sequence 75, Appl	529	34	63.0	107	2	US-09-247-352-12	Sequence 12, Appl
457	36	66.7	56	1	US-08-162-102C-40	Sequence 40, Appl	530	34	63.0	107	2	US-09-438-954-3	Sequence 3, Appl
458	36	66.7	107	1	US-08-480-434-73	Sequence 73, Appl	531	34	63.0	107	2	US-09-339-922A-4	Sequence 4, Appl
459	36	66.7	107	1	US-08-053-451B-73	Sequence 73, Appl	532	34	63.0	107	2	US-09-339-922A-8	Sequence 8, Appl
460	36	66.7	107	1	US-08-053-451B-174	Sequence 174, App	533	34	63.0	107	2	US-09-339-922A-32	Sequence 32, Appl
461	36	66.7	107	1	US-08-483-749A-28	Sequence 28, Appl	534	34	63.0	107	2	US-08-791-391A-4	Sequence 4, Appl
462	36	66.7	107	2	US-09-240-274-172	Sequence 172, App	535	34	63.0	107	2	US-08-791-391A-8	Sequence 8, Appl
463	36	66.7	107	2	US-09-240-274-174	Sequence 174, App	536	34	63.0	107	2	US-08-791-391A-32	Sequence 32, Appl
464	36	66.7	107	2	US-09-848-798-172	Sequence 172, App	537	34	63.0	107	2	US-09-016-061-4	Sequence 4, Appl
465	36	66.7	107	2	US-09-848-798-174	Sequence 174, App	538	34	63.0	107	2	US-09-016-061-8	Sequence 8, Appl



539	34	63.0	107	2	US-09-016-061-32	Sequence 32, Appl	612	33	61.1	404	1	US-08-440-179-2	Sequence 2, Appl1
540	34	63.0	107	2	US-09-434-870-1	Sequence 1, Appl1	613	33	61.1	404	1	US-08-450-130A-1	Sequence 1, Appl1
541	34	63.0	107	2	US-09-848-798-179	Sequence 179, App	614	33	61.1	404	1	US-08-331-316A-2	Sequence 2, Appl1
542	34	63.0	108	2	US-09-247-352-1	Sequence 1, Appl1	615	33	61.1	404	1	US-08-573-890-2	Sequence 4, Appl1
543	34	63.0	108	2	US-09-466-635-1	Sequence 4, Appl1	616	33	61.1	404	1	US-08-394-189B-4	Sequence 1, Appl1
544	34	63.0	109	2	US-09-798-058-4	Sequence 4, Appl1	617	33	61.1	404	2	US-08-450-362A-1	Sequence 39, Appl1
545	34	63.0	125	1	US-08-039-198B-12	Sequence 12, Appl	618	33	61.1	404	2	US-08-258-287B-39	Sequence 39, Appl1
546	34	63.0	125	1	US-08-182-067-2	Sequence 2, Appl1	619	33	61.1	404	2	US-08-368-704C-39	Sequence 18, Appl1
547	34	63.0	125	1	US-08-465-313-2	Sequence 2, Appl1	620	33	61.1	404	2	US-08-954-536-18	Sequence 2, Appl1
548	34	63.0	125	2	US-09-809-739-1	Sequence 1, Appl1	621	33	61.1	404	2	US-09-039-657-2	Sequence 2, Appl1
549	34	63.0	125	2	US-09-378-967-2	Sequence 2, Appl1	622	33	61.1	404	2	US-08-748-547-2	Sequence 2, Appl1
550	34	63.0	127	2	US-09-809-739-10	Sequence 10, Appl	623	33	61.1	404	2	US-08-908-436-3	Sequence 3, Appl1
551	34	63.0	129	2	US-08-943-136-2	Sequence 2, Appl1	624	33	61.1	404	2	US-09-248-179-2	Sequence 2, Appl1
552	34	63.0	129	2	US-08-973-518-2	Sequence 2, Appl1	625	33	61.1	404	2	US-09-069-023-30	Sequence 30, Appl1
553	34	63.0	148	2	US-09-318-786-25	Sequence 25, Appl	626	33	61.1	404	2	US-09-561-756-6	Sequence 6, Appl1
554	34	63.0	214	2	US-09-247-352-4	Sequence 4, Appl1	627	33	61.1	404	2	US-09-227-721-6	Sequence 13, Appl1
555	34	63.0	214	2	US-09-466-635-4	Sequence 4, Appl1	628	33	61.1	404	2	US-08-983-502-13	Sequence 7, Appl1
556	34	63.0	220	2	US-09-328-352-4197	Sequence 4197, Ap	629	33	61.1	404	2	US-08-724-378D-7	Sequence 2, Appl1
557	34	63.0	234	1	US-07-690-192-2	Sequence 2, Appl1	630	33	61.1	404	2	US-09-827-708A-2	Sequence 7, Appl1
558	34	63.0	284	2	US-08-564-164A-2	Sequence 2, Appl1	631	33	61.1	404	2	US-09-516-747-13	Sequence 13, Appl1
559	34	63.0	287	2	US-09-318-786-37	Sequence 37, Appl	632	33	61.1	404	2	US-09-954-697-6	Sequence 6, Appl1
560	34	63.0	360	2	US-09-668-097A-32	Sequence 32, Appl	633	33	61.1	404	2	US-09-291-289-5	Sequence 5, Appl1
561	34	63.0	419	2	US-09-328-352-7844	Sequence 7844, Ap	634	33	61.1	404	2	US-09-895-263B-14	Sequence 14, Appl1
562	34	63.0	492	2	US-09-248-796A-14755	Sequence 14755, A	635	33	61.1	404	2	US-09-851-873-80	Sequence 80, Appl1
563	34	63.0	557	2	US-09-134-001C-4392	Sequence 4392, Ap	636	33	61.1	404	2	US-09-613-508B-14	Sequence 14, Appl1
564	34	63.0	994	2	US-09-248-796A-15273	Sequence 15273, A	637	33	61.1	404	2	US-09-888-243-4	Sequence 4, Appl1
565	33	61.1	55	2	US-08-953-937A-9	Sequence 9, Appl1	638	33	61.1	404	2	US-09-888-243-30	Sequence 30, Appl1
566	33	61.1	55	2	US-09-300-985-9	Sequence 9, Appl1	639	33	61.1	404	4	PCT-US93-05705-4	Sequence 4, Appl1
567	33	61.1	100	2	US-09-899-896-8	Sequence 8, Appl1	640	33	61.1	404	4	PCT-US95-06132-2	Sequence 2, Appl1
568	33	61.1	106	1	US-08-276-852-101	Sequence 101, App	641	33	61.1	404	4	PCT-US95-07619-1	Sequence 1, Appl1
569	33	61.1	106	1	US-08-899-575-101	Sequence 101, App	642	33	61.1	404	4	PCT-US96-10521-13	Sequence 13, Appl1
570	33	61.1	106	1	US-08-899-575-101	Sequence 101, App	643	33	61.1	416	2	US-09-270-767-45965	Sequence 45965, A
571	33	61.1	106	2	US-09-740-002-22	Sequence 22, Appl	644	33	61.1	421	2	US-08-807-263-4	Sequence 4, Appl1
572	33	61.1	106	4	PCT-US95-08743-101	Sequence 101, App	645	33	61.1	458	6	5217891-15	Patent No. 5217891
573	33	61.1	107	1	US-07-634-278-34	Sequence 34, Appl	646	33	61.1	470	2	US-09-071-709-12	Sequence 12, Appl1
574	33	61.1	107	1	US-08-477-728-34	Sequence 34, Appl	647	33	61.1	470	2	US-09-713-669-12	Sequence 12, Appl1
575	33	61.1	107	1	US-08-474-040-34	Sequence 34, Appl	648	33	61.1	505	2	US-09-248-796A-27244	Sequence 27244, A
576	33	61.1	107	1	US-08-487-200-34	Sequence 34, Appl	649	33	61.1	511	1	US-08-462-484-8	Sequence 8, Appl1
577	33	61.1	107	1	US-08-888-366-22	Sequence 22, Appl	650	33	61.1	511	1	US-08-441-147-8	Sequence 8, Appl1
578	33	61.1	107	2	US-08-484-537-34	Sequence 34, Appl	651	33	61.1	511	4	PCT-US95-07536-8	Sequence 8, Appl1
579	33	61.1	107	2	US-09-240-274-36	Sequence 36, Appl	652	33	61.1	532	1	US-08-899-324-33	Sequence 33, Appl1
580	33	61.1	107	2	US-09-240-274-169	Sequence 169, App	653	33	61.1	532	2	US-08-329-892B-33	Sequence 33, Appl1
581	33	61.1	107	2	US-09-438-954-1	Sequence 1, Appl1	654	33	61.1	809	2	US-09-252-991A-29280	Sequence 29280, A
582	33	61.1	107	2	US-09-438-954-38	Sequence 38, Appl	655	32.5	60.2	116	1	US-08-478-039-83	Sequence 83, Appl1
583	33	61.1	107	2	US-09-848-798-36	Sequence 36, Appl	656	32.5	60.2	116	1	US-08-476-349A-83	Sequence 83, Appl1
584	33	61.1	107	2	US-09-848-798-169	Sequence 169, App	657	32	59.3	11	1	US-07-942-245-522	Sequence 522, App
585	33	61.1	108	1	US-08-378-939-16	Sequence 16, Appl	658	32	59.3	11	2	US-08-599-226-7	Sequence 7, Appl1
586	33	61.1	108	1	US-08-378-939-24	Sequence 24, Appl	659	32	59.3	11	2	US-09-125-098-7	Sequence 7, Appl1
587	33	61.1	108	1	US-08-737-560A-11	Sequence 11, Appl	660	32	59.3	11	2	US-09-540-018-7	Sequence 7, Appl1
588	33	61.1	108	2	US-09-157-370-4	Sequence 4, Appl1	661	32	59.3	11	2	US-09-647-468-136	Sequence 136, App
589	33	61.1	109	2	US-09-157-370-3	Sequence 3, Appl1	662	32	59.3	88	2	US-09-905-243-63	Sequence 63, Appl1
590	33	61.1	110	1	US-08-300-386A-70	Sequence 70, Appl	663	32	59.3	92	1	US-08-273-146-45	Sequence 45, Appl1
591	33	61.1	110	2	US-08-931-645-70	Sequence 70, Appl	664	32	59.3	92	1	US-08-273-146-53	Sequence 53, Appl1
592	33	61.1	110	2	US-09-543-681A-5117	Sequence 5117, Ap	665	32	59.3	93	2	US-09-107-532A-5782	Sequence 5782, Ap
593	33	61.1	110	4	PCT-US95-11235-70	Sequence 70, Appl	666	32	59.3	95	2	US-10-194-975-60	Sequence 60, Appl1
594	33	61.1	128	1	US-08-338-582-4	Sequence 4, Appl1	667	32	59.3	95	2	US-10-194-975-67	Sequence 67, Appl1
595	33	61.1	129	2	US-09-582-337-22	Sequence 22, Appl	668	32	59.3	95	2	US-10-194-975-68	Sequence 68, Appl1
596	33	61.1	199	2	US-09-328-352-7802	Sequence 7802, Ap	669	32	59.3	95	2	US-10-194-975-69	Sequence 69, Appl1
597	33	61.1	215	1	US-08-737-129A-8	Sequence 8, Appl1	670	32	59.3	95	2	US-10-194-975-86	Sequence 86, Appl1
598	33	61.1	234	2	US-09-740-002-26	Sequence 26, Appl	671	32	59.3	100	2	US-09-899-896-4	Sequence 4, Appl1
599	33	61.1	235	2	US-09-489-039A-9599	Sequence 9599, Ap	672	32	59.3	107	1	US-08-107-669D-14	Sequence 14, Appl1
600	33	61.1	236	1	US-08-157-101A-5	Sequence 5, Appl1	673	32	59.3	107	1	US-08-472-788A-14	Sequence 14, Appl1
601	33	61.1	243	2	US-09-248-796A-16273	Sequence 16273, A	674	32	59.3	107	1	US-08-477-531B-14	Sequence 14, Appl1
602	33	61.1	248	2	US-09-710-279-464	Sequence 464, App	675	32	59.3	107	1	US-08-082-842A-14	Sequence 14, Appl1
603	33	61.1	276	2	US-09-270-767-61503	Sequence 61503, A	676	32	59.3	107	1	US-08-888-366-14	Sequence 14, Appl1
604	33	61.1	345	2	US-10-155-947-4	Sequence 4, Appl1	677	32	59.3	107	1	US-08-888-366-20	Sequence 20, Appl1
605	33	61.1	348	2	US-09-198-452A-922	Sequence 922, App	678	32	59.3	107	1	US-08-888-366-26	Sequence 26, Appl1
606	33	61.1	348	2	US-09-438-185A-856	Sequence 856, App	679	32	59.3	107	2	US-08-599-226-1	Sequence 1, Appl1
607	33	61.1	359	2	US-09-646-028-16	Sequence 16, Appl	680	32	59.3	107	2	US-08-599-226-9	Sequence 9, Appl1
608	33	61.1	361	2	US-09-646-028-13	Sequence 13, Appl	681	32	59.3	107	2	US-09-125-098-1	Sequence 1, Appl1
609	33	61.1	374	2	US-09-646-028-15	Sequence 15, Appl	682	32	59.3	107	2	US-09-125-098-9	Sequence 9, Appl1
610	33	61.1	404	1	US-08-203-716-2	Sequence 2, Appl1	683	32	59.3	107	2	US-09-438-954-40	Sequence 40, Appl1
611	33	61.1	404	1	US-08-242-663A-2	Sequence 2, Appl1	684	32	59.3	107	2	US-09-540-018-1	Sequence 1, Appl1

685	32	59.3	107	2	US-09-540-018-9	Sequence 9, Appli	758	32	59.3	548	1	US-08-993-118A-4	Sequence 4, Appli
686	32	59.3	107	2	US-09-647-468-93	Sequence 93, Appli	759	32	59.3	548	2	US-09-399-886-4	Sequence 4, Appli
687	32	59.3	107	2	US-09-647-468-99	Sequence 99, Appli	760	32	59.3	548	2	US-09-396-260-4	Sequence 4, Appli
688	32	59.3	107	2	US-09-647-468-101	Sequence 101, Appl	761	32	59.3	548	2	US-09-576-281-4	Sequence 4, Appli
689	32	59.3	107	2	US-09-647-468-107	Sequence 107, Appl	762	32	59.3	584	2	US-09-270-767-43419	Sequence 43419, A
690	32	59.3	107	2	US-09-647-468-109	Sequence 109, Appl	763	32	59.3	637	1	US-08-235-838-16	Sequence 16, Appl
691	32	59.3	107	2	US-09-647-468-148	Sequence 148, Appl	764	32	59.3	637	1	US-08-465-473B-16	Sequence 16, Appl
692	32	59.3	107	2	US-09-434-870-2	Sequence 2, Appli	765	32	59.3	887	1	US-08-215-709-1	Sequence 1, Appli
693	32	59.3	107	2	US-10-330-613A-30	Sequence 30, Appli	766	32	59.3	1155	2	US-09-543-681A-6286	Sequence 6286, Ap
694	32	59.3	107	2	US-08-766-350B-47	Sequence 47, Appl	767	32	59.3	1234	4	US-08-317-310A-15	Sequence 15, Appl
695	32	59.3	108	1	US-08-378-939-18	Sequence 18, Appl	768	32	59.3	1234	4	PCT-US95-13041-15	Sequence 15, Appl
696	32	59.3	108	1	US-08-602-725-29	Sequence 29, Appl	769	32	59.3	1239	1	US-08-937-931-2	Sequence 2, Appli
697	32	59.3	108	2	US-09-726-219A-267	Sequence 267, Appl	770	32	59.3	1239	2	US-09-285-502-2	Sequence 2, Appli
698	32	59.3	108	2	US-09-196-522-267	Sequence 267, Appl	771	32	59.3	1239	2	US-09-709-126-2	Sequence 2, Appli
699	32	59.3	109	1	US-08-713-939A-74	Sequence 74, Appl	772	32	59.3	1239	2	US-09-871-385A-2	Sequence 2, Appli
700	32	59.3	109	2	US-09-036-579-74	Sequence 74, Appl	773	32	59.3	1282	2	US-09-134-000C-5785	Sequence 5785, Ap
701	32	59.3	109	2	US-09-025-769B-28	Sequence 28, Appl	774	31.5	58.3	110	2	US-09-726-219A-254	Sequence 254, App
702	32	59.3	109	2	US-09-025-769B-43	Sequence 43, Appl	775	31.5	58.3	110	2	US-09-726-219A-255	Sequence 255, App
703	32	59.3	109	2	US-09-550-37A-74	Sequence 74, Appl	776	31.5	58.3	110	2	US-09-196-522-254	Sequence 254, App
704	32	59.3	109	2	US-09-943-906-74	Sequence 74, Appl	777	31.5	58.3	110	2	US-09-196-522-255	Sequence 255, App
705	32	59.3	109	2	US-09-490-070A-28	Sequence 28, Appl	778	31	57.4	69	2	US-09-270-767-33598	Sequence 33598, A
706	32	59.3	109	2	US-09-490-070A-43	Sequence 43, Appl	779	31	57.4	69	2	US-09-270-767-48815	Sequence 48815, A
707	32	59.3	109	2	US-09-802-083-3	Sequence 3, Appli	780	31	57.4	88	2	US-09-905-243-32	Sequence 32, Appl
708	32	59.3	109	2	US-09-490-153-28	Sequence 28, Appl	781	31	57.4	95	2	US-10-194-975-87	Sequence 87, Appl
709	32	59.3	109	2	US-09-490-153-43	Sequence 43, Appl	782	31	57.4	107	2	US-08-483-749A-26	Sequence 26, Appl
710	32	59.3	109	2	US-09-490-324-28	Sequence 28, Appl	783	31	57.4	107	2	US-09-647-468-147	Sequence 147, App
711	32	59.3	109	2	US-09-490-324-43	Sequence 43, Appl	784	31	57.4	109	1	US-08-300-386A-69	Sequence 69, Appl
712	32	59.3	109	2	US-10-435-602-74	Sequence 74, Appl	785	31	57.4	109	2	US-08-931-645-69	Sequence 69, Appl
713	32	59.3	115	1	US-08-053-131-179	Sequence 179, App	786	31	57.4	109	2	US-09-905-243-67	Sequence 67, Appl
714	32	59.3	115	1	US-08-096-762-179	Sequence 179, App	787	31	57.4	109	4	PCT-US95-11235-69	Sequence 69, Appl
715	32	59.3	115	2	US-09-042-353-42	Sequence 42, Appl	788	31	57.4	115	1	US-08-053-131-181	Sequence 181, App
716	32	59.3	115	2	US-08-758-417A-307	Sequence 307, App	789	31	57.4	115	1	US-08-096-762-181	Sequence 181, App
717	32	59.3	122	2	US-09-248-796A-26958	Sequence 26958, A	790	31	57.4	115	2	US-09-042-353-44	Sequence 44, Appl
718	32	59.3	127	2	US-09-647-468-162	Sequence 162, App	791	31	57.4	115	2	US-08-758-417A-309	Sequence 309, App
719	32	59.3	127	2	US-09-647-468-179	Sequence 179, App	792	31	57.4	129	2	US-09-647-468-161	Sequence 161, App
720	32	59.3	127	2	US-09-647-468-180	Sequence 180, App	793	31	57.4	139	2	US-09-472-087-22	Sequence 22, Appl
721	32	59.3	127	2	US-09-647-468-181	Sequence 181, App	794	31	57.4	139	2	US-09-472-087-96	Sequence 96, Appl
722	32	59.3	127	2	US-09-647-468-182	Sequence 182, App	795	31	57.4	139	2	US-09-270-767-33358	Sequence 33358, A
723	32	59.3	127	2	US-09-647-468-183	Sequence 183, App	796	31	57.4	139	2	US-09-270-767-48575	Sequence 48575, A
724	32	59.3	134	2	US-09-621-976-5076	Sequence 5076, Ap	797	31	57.4	158	1	US-07-778-156-3	Sequence 3, Appli
725	32	59.3	139	2	US-09-472-087-16	Sequence 16, Appl	798	31	57.4	158	1	US-08-422-166-3	Sequence 3, Appli
726	32	59.3	139	2	US-09-472-087-90	Sequence 90, Appl	799	31	57.4	175	1	US-08-401-530A-3	Sequence 3, Appli
727	32	59.3	142	2	US-09-472-087-91	Sequence 91, Appl	800	31	57.4	175	1	US-08-709-662-3	Sequence 3, Appli
728	32	59.3	146	2	US-09-472-087-91	Sequence 91, Appl	801	31	57.4	175	2	US-09-270-767-38110	Sequence 38110, A
729	32	59.3	146	2	US-09-472-087-93	Sequence 93, Appl	802	31	57.4	175	2	US-09-270-767-53327	Sequence 53327, A
730	32	59.3	174	1	US-08-401-530A-6	Sequence 6, Appli	803	31	57.4	178	2	US-09-248-796A-27780	Sequence 27780, A
731	32	59.3	174	1	US-08-709-662-6	Sequence 6, Appli	804	31	57.4	184	1	US-07-778-156-2	Sequence 2, Appli
732	32	59.3	190	2	US-09-270-767-46639	Sequence 46639, A	805	31	57.4	184	1	US-08-422-166-2	Sequence 2, Appli
733	32	59.3	224	2	US-09-456-090A-46	Sequence 46, Appl	806	31	57.4	208	2	US-09-977-653-10	Sequence 10, Appl
734	32	59.3	224	2	US-09-456-090A-82	Sequence 82, Appl	807	31	57.4	214	2	US-09-472-087-71	Sequence 71, Appl
735	32	59.3	224	2	US-09-456-090A-84	Sequence 84, Appl	808	31	57.4	224	2	US-09-456-090A-36	Sequence 36, Appl
736	32	59.3	224	2	US-09-456-090A-88	Sequence 88, Appl	809	31	57.4	224	2	US-09-453-234-36	Sequence 36, Appl
737	32	59.3	224	2	US-09-456-090A-90	Sequence 90, Appl	810	31	57.4	226	2	US-09-134-001C-5562	Sequence 5562, Ap
738	32	59.3	224	2	US-09-453-234-46	Sequence 46, Appl	811	31	57.4	243	1	US-08-133-804-6	Sequence 6, Appli
739	32	59.3	224	2	US-09-453-234-82	Sequence 82, Appl	812	31	57.4	243	1	US-08-461-838-6	Sequence 6, Appli
740	32	59.3	224	2	US-09-453-234-84	Sequence 84, Appl	813	31	57.4	243	1	US-08-461-838-6	Sequence 6, Appli
741	32	59.3	224	2	US-09-453-234-88	Sequence 88, Appl	814	31	57.4	243	1	US-08-356-786-4	Sequence 4, Appli
742	32	59.3	224	2	US-09-453-234-90	Sequence 90, Appl	815	31	57.4	274	2	US-09-248-796A-20766	Sequence 20766, A
743	32	59.3	234	2	US-09-472-087-17	Sequence 17, Appl	816	31	57.4	280	2	US-09-248-796A-20765	Sequence 20765, A
744	32	59.3	234	2	US-09-472-087-69	Sequence 69, Appl	817	31	57.4	315	2	US-09-543-681A-6161	Sequence 6161, Ap
745	32	59.3	241	1	US-08-235-838-11	Sequence 11, Appl	818	31	57.4	322	2	US-09-252-991A-29347	Sequence 29347, A
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753	32	59.3	368	2	US-09-252-991A-18904	Sequence 18904, A	826	31	57.4	386	2	US-09-107-532A-4088	Sequence 4088, Ap
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ALIGNMENTS

US-08-908-469-4
; Sequence 4, Application US/08908469
; Patent No. 6884879
; GENERAL INFORMATION:
; APPLICANT: Baca, Manuel
; Wells, James A.
; Presta, Leonard G.
; Lowman, Henry B.
; Chen, Yvonne M.
; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
; NUMBER OF SEQUENCES: 131
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; City: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/908,469
; FILING DATE: 21-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/833,504
; FILING DATE: 07-APR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Cui, Steven X.
; REGISTRATION NUMBER: 44,637
; REFERENCE/DOCKET NUMBER: P1093P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-8674
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
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Best Local Similarity 100.0%; Pred. No. 0.0018;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 SASQDISNYLN 11

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; Patent No. 6884879
; GENERAL INFORMATION:
; APPLICANT: Baca, Manuel
; Wells, James A.
; Presta, Leonard G.
; Lowman, Henry B.
; Chen, Yvonne M.
; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
; NUMBER OF SEQUENCES: 131
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; Patent No. 6884879
; GENERAL INFORMATION:
; APPLICANT: Baca, Manuel
; Wells, James A.
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; ; Presta, Leonard G.
; ; Lowman, Henry B.
; ; Chen, Yvonne M.
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; ; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
; ; NUMBER OF SEQUENCES: 131
; ; CORRESPONDENCE ADDRESS:
; ; ADDRESSEE: Genentech, Inc.
; ; STREET: 1 DNA Way
; ; CITY: South San Francisco
; ; STATE: California
; ; COUNTRY: USA
; ; ZIP: 94080
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; ; COMPUTER READABLE FORM:
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; ; CURRENT APPLICATION DATA:
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; ; FILING DATE: 21-May-2001
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; ; PRIOR APPLICATION DATA:
; ; APPLICATION NUMBER: 08/833,504
; ; FILING DATE: 07-APR-1997
; ; ATTORNEY/AGENT INFORMATION:
; ; NAME: Cui, Steven X.
; ; REGISTRATION NUMBER: 44,637
; ; REFERENCE/DOCKET NUMBER: P1093P1
; ; TELECOMMUNICATION INFORMATION:
; ; TELEPHONE: 650/225-8674
; ; TELEFAX: 650/952-9881
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; ; INFORMATION FOR SEQ ID NO: 15:
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; ; LENGTH: 107 amino acids
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; ; TOPOLOGY: Linear
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RESULT 4
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; Patent No. 6884879
; GENERAL INFORMATION:
; APPLICANT: Baca, Manuel
; Wells, James A.
; Presta, Leonard G.
; Lowman, Henry B.
; Chen, Yvonne M.
;
; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
; NUMBER OF SEQUENCES: 131
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
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; COMPUTER READABLE FORM:
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; COMPUTER: IBM PC compatible
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; SOFTWARE: WinPatIn (Genentech)
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; FILING DATE: 21-May-2001
; CLASSIFICATION: <Unknown>
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/833,504
; FILING DATE: 07-APR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Cui, Steven X.
; REGISTRATION NUMBER: 44,637
; REFERENCE/DOCKET NUMBER: P1093P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-8674
; TELEFAX: 650/952-9881
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; LENGTH: 107 amino acids
; TYPE: Amino Acid
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; ; ATTORNEY/AGENT INFORMATION:
; ; NAME: Cui, Steven X.
; ; REGISTRATION NUMBER: 44,637
; ; REFERENCE/DOCKET NUMBER: P1093P1
; ; TELECOMMUNICATION INFORMATION:
; ; TELEPHONE: 650/225-8674
; ; TELEFAX: 650/952-9881
; ;
; ; INFORMATION FOR SEQ ID NO: 8:
; ; SEQUENCE CHARACTERISTICS:
; ; LENGTH: 108 amino acids
; ; TYPE: Amino Acid
; ; TOPOLOGY: Linear
; ;
; ; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-08-908-469-8
Query Match 100.0%; Score 54; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.023;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SASQDISNYLN 11
Db 24 SASQDISNYLN 34

RESULT 5
US-08-908-469-10
; Sequence 10, Application US/08908469
; Patent No. 6884879
; GENERAL INFORMATION:
; APPLICANT: Baca, Manuel
; Wells, James A.
; Presta, Leonard G.
; Lowman, Henry B.
; Chen, Yvonne M.
;
; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
; NUMBER OF SEQUENCES: 131
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/908,469
; FILING DATE: 21-May-2001
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/833,504
; FILING DATE: 07-APR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Cui, Steven X.
; REGISTRATION NUMBER: 44,637
; REFERENCE/DOCKET NUMBER: P1093P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-8674
; TELEFAX: 650/952-9881
;
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
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;
; SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-08-908-469-10

Query Match      100.0%; Score 54; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.023;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SASQDISNYLN 11
Db      24 SASQDISNYLN 34

RESULT 6
US-08-908-469-126
; Sequence 126, Application US/08908469
; Patent No. 6884879
; GENERAL INFORMATION:
; APPLICANT: Baca, Manuel
;               Wells, James A.
;               Presta, Leonard G.
;               Lowman, Henry B.
;               Chen, Yvonne M.
; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
; NUMBER OF SEQUENCES: 131
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/908,469
; FILING DATE: 21-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/833,504
; FILING DATE: 07-APR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Cui, Steven X.
; REGISTRATION NUMBER: 44,637
; REFERENCE/DOCKET NUMBER: P1093P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-8674
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 126:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 126:
US-08-908-469-126

Query Match      100.0%; Score 54; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.023;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SASQDISNYLN 11
Db      24 SASQDISNYLN 34

RESULT 7
US-09-440-781-94
; Sequence 94, Application US/09440781
; Patent No. 6632926
; GENERAL INFORMATION:
; APPLICANT: Yvonne Man-ye Chen et al.
; TITLE OF INVENTION: ANTIBODY VARIANTS
; FILE REFERENCE: P1469R1
; CURRENT APPLICATION NUMBER: US/09/440,781
; CURRENT FILING DATE: 1999-11-16
; NUMBER OF SEQ ID NOS: 99
; SEQ ID NO 94
; LENGTH: 110
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: artificial
; LOCATION: 1-110
; OTHER INFORMATION: humanized antibody light chain variable domain
US-09-440-781-94

Query Match      100.0%; Score 54; DB 2; Length 110;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SASQDISNYLN 11
Db      24 SASQDISNYLN 34

RESULT 8
US-08-908-469-103
; Sequence 103, Application US/08908469
; Patent No. 6884879
; GENERAL INFORMATION:
; APPLICANT: Baca, Manuel
;               Wells, James A.
;               Presta, Leonard G.
;               Lowman, Henry B.
;               Chen, Yvonne M.
; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
; NUMBER OF SEQUENCES: 131
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/908,469
; FILING DATE: 21-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/833,504
; FILING DATE: 07-APR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Cui, Steven X.
; REGISTRATION NUMBER: 44,637
; REFERENCE/DOCKET NUMBER: P1093P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-8674
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 103:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 110 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 103:
US-08-908-469-103

Query Match      100.0%; Score 54; DB 2; Length 110;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 1 SASQDISNYLN 11  
DB 24 SASQDISNYLN 34

## RESULT 9

US-08-908-469-105  
; Sequence 105, Application US/08908469  
; Patent No. 6884879  
; GENERAL INFORMATION:  
; APPLICANT: Baca, Manuel  
; Wells, James A.  
; Presta, Leonard G.  
; Lowman, Henry B.  
; Chen, Yvonne M.

; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES  
; NUMBER OF SEQUENCES: 131  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/908,469  
; FILING DATE: 21-May-2001  
; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/833,504  
; FILING DATE: 07-APR-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Cui, Steven X.  
; REGISTRATION NUMBER: 44,637  
; REFERENCE/DOCKET NUMBER: P1093P1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-8674  
; TELEFAX: 650/952-9881

; INFORMATION FOR SEQ ID NO: 105:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 110 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear

; SEQUENCE DESCRIPTION: SEQ ID NO: 105:  
US-08-908-469-105  
Query Match 100.0%; Score 54; DB 2; Length 110;  
Best Local Similarity 100.0%; Pred. No. 0.024;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASQDISNYLN 11  
DB 24 SASQDISNYLN 34

## RESULT 10

US-08-908-469-107  
; Sequence 107, Application US/08908469  
; Patent No. 6884879  
; GENERAL INFORMATION:  
; APPLICANT: Baca, Manuel  
; Wells, James A.  
; Presta, Leonard G.  
; Lowman, Henry B.  
; Chen, Yvonne M.

; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES  
; NUMBER OF SEQUENCES: 131

; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/908,469  
; FILING DATE: 21-May-2001  
; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/833,504  
; FILING DATE: 07-APR-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Cui, Steven X.  
; REGISTRATION NUMBER: 44,637  
; REFERENCE/DOCKET NUMBER: P1093P1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-8674  
; TELEFAX: 650/952-9881

; INFORMATION FOR SEQ ID NO: 107:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 110 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear

; SEQUENCE DESCRIPTION: SEQ ID NO: 107:  
US-08-908-469-107

Query Match 100.0%; Score 54; DB 2; Length 110;  
Best Local Similarity 100.0%; Pred. No. 0.024;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASQDISNYLN 11  
DB 24 SASQDISNYLN 34

## RESULT 11

US-08-908-469-117  
; Sequence 117, Application US/08908469  
; Patent No. 6884879  
; GENERAL INFORMATION:  
; APPLICANT: Baca, Manuel  
; Wells, James A.  
; Presta, Leonard G.  
; Lowman, Henry B.  
; Chen, Yvonne M.

; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES  
; NUMBER OF SEQUENCES: 131  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/908,469  
; FILING DATE: 21-May-2001  
; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/833,504

```
;
; FILING DATE: 07-APR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Cui, Steven X.
; REGISTRATION NUMBER: 44,637
; REFERENCE/DOCKET NUMBER: P1093P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-8674
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 117:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 110 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 117:
US-08-908-469-117

Query Match 100.0%; Score 54; DB 2; Length 110;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SASQDISNYLN 11
Db 24 SASQDISNYLN 34

RESULT 12
US-09-225-322B-10
; Sequence 10, Application US/09225322B
; Patent No. 6437098
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUWANA, YOSHIHISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/09/225,322B
; CURRENT FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: US 08/454,680
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
; PRIOR APPLICATION NUMBER: US07/947,674
; PRIOR FILING DATE: 1992-09-17
; PRIOR APPLICATION NUMBER: JP 3-238375
; PRIOR FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:light chain
US-09-225-322B-19

Query Match 100.0%; Score 54; DB 2; Length 128;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SASQDISNYLN 11
Db 44 SASQDISNYLN 54

RESULT 14
US-09-764-304-10
; Sequence 10, Application US/09764304
; Patent No. 6495666
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUWANA, YOSHIHISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/09/764,304
; CURRENT FILING DATE: 2001-01-19
; EARLIER APPLICATION NUMBER: 09/225,322
; EARLIER FILING DATE: 1999-01-05
; EARLIER APPLICATION NUMBER: US 08/454,680
; EARLIER FILING DATE: 1995-05-31
; EARLIER APPLICATION NUMBER: US 08/408,133
; EARLIER FILING DATE: 1995-03-21
; EARLIER APPLICATION NUMBER: US 08/292,178
; EARLIER FILING DATE: 1994-08-17
; EARLIER APPLICATION NUMBER: US07/947,674
; EARLIER FILING DATE: 1992-09-17
; EARLIER APPLICATION NUMBER: JP 3-238375
; EARLIER FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: cDNA KM-641
US-09-225-322B-10

Query Match 100.0%; Score 54; DB 2; Length 128;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SASQDISNYLN 11
Db 44 SASQDISNYLN 54

RESULT 13
US-09-225-322B-19
; Sequence 19, Application US/09225322B
; Patent No. 6437098
; GENERAL INFORMATION:
```



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US-09-764-304-10
Query Match      100.0%; Score 54; DB 2; Length 128;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SASQDISNYLN 11
Db      44 SASQDISNYLN 54

RESULT 15
US-09-764-304-19
; Sequence 19, Application US/09764304
; Patent No. 6495666
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUWANA, YOSHIHISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/09/764,304
; EARLIER FILING DATE: 2001-01-19
; EARLIER APPLICATION NUMBER: 09/225,322
; EARLIER FILING DATE: 1999-01-05
; EARLIER APPLICATION NUMBER: US 08/454,680
; EARLIER FILING DATE: 1995-05-31
; EARLIER APPLICATION NUMBER: US 08/408,133
; EARLIER FILING DATE: 1995-03-21
; EARLIER APPLICATION NUMBER: US 08/292,178
; EARLIER FILING DATE: 1994-08-17
; EARLIER APPLICATION NUMBER: US07/947,674
; EARLIER FILING DATE: 1992-09-17
; EARLIER APPLICATION NUMBER: JP 3-238375
; EARLIER FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 19
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: light chain
; OTHER INFORMATION: variable region
US-09-764-304-19

Query Match      100.0%; Score 54; DB 2; Length 128;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SASQDISNYLN 11
Db      44 SASQDISNYLN 54

RESULT 16
US-08-908-469-100
; Sequence 100, Application US/08908469
; Patent No. 6884879
; GENERAL INFORMATION:
; APPLICANT: Baca, Manuel
; Wells, James A.
; Presta, Leonard G.
; Lowman, Henry B.
; Chen, Yvonne M.
; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
; NUMBER OF SEQUENCES: 131
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
```

```
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/908,469
; FILING DATE: 21-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/833,504
; FILING DATE: 07-APR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Cui, Steven X.
; REGISTRATION NUMBER: 44,637
; REFERENCE/DOCKET NUMBER: P1093P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-8674
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 100:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 237 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 100:
US-08-908-469-100

Query Match      100.0%; Score 54; DB 2; Length 237;
Best Local Similarity 100.0%; Pred. No. 0.056;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SASQDISNYLN 11
Db      47 SASQDISNYLN 57

RESULT 17
US-10-011-125A-2
; Sequence 2, Application US/10011125A
; Patent No. 6828121
; GENERAL INFORMATION:
; APPLICANT: Chen, Christina Yu-Ching
; TITLE OF INVENTION: BACTERIAL HOST STRAINS
; FILE REFERENCE: P1804R1
; CURRENT APPLICATION NUMBER: US/10/011,125A
; CURRENT FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: US 60/256,162
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 12
; SEQ ID NO 2
; LENGTH: 491
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized.
; Patent No. 6828121
US-10-011-125A-2

Query Match      100.0%; Score 54; DB 2; Length 491;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SASQDISNYLN 11
Db      47 SASQDISNYLN 57

RESULT 18
US-09-386-658A-4
; Sequence 4, Application US/09386658A
```

Patent No. 6593137  
; GENERAL INFORMATION:  
; APPLICANT: Erlanger, Bernard F.  
; APPLICANT: Chen, Bi-Xing  
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR FULLERENES  
; FILE REFERENCE: 0575/54182  
; CURRENT APPLICATION NUMBER: US/09/386,658A  
; CURRENT FILING DATE: 1999-08-31  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 4  
; LENGTH: 109  
; TYPE: PRT  
; ORGANISM: Mouse  
US-09-386-658A-4

Query Match 94.4%; Score 51; DB 2; Length 109;  
Best Local Similarity 90.9%; Pred. No. 0.079;  
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SASQDISNYLN 11  
Db 24 SASQDINNYLN 34

RESULT 19  
US-08-480-434-76  
; Sequence 76, Application US/08480434  
; Patent No. 5811248  
; GENERAL INFORMATION:  
; APPLICANT: Charles C. Dittlow, et al.  
; TITLE OF INVENTION: ATHEROSCLEROTIC PLAQUE SPECIFIC ANTIGENS,  
; TITLE OF INVENTION: ANTIBODIES THERETO, AND USES THEREOF  
; NUMBER OF SEQUENCES: 88  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.24  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/480,434  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:  
; NAME: Albert P. Halluin  
; REGISTRATION NUMBER: 25,227  
; REFERENCE/DOCKET NUMBER: 7606-053  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 854-3660  
; TELEFAX: (415) 854-3694  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 76:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHETICAL: N  
; ANTI-SENSE: N

US-08-480-434-76  
Query Match 92.6%; Score 50; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.009;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ASQDISNYLN 11  
Db 2 ASQDISNYLN 11  
RESULT 20  
US-08-053-451B-76  
; Sequence 76, Application US/08053451B  
; Patent No. 5955584  
; GENERAL INFORMATION:  
; APPLICANT: Chen, Francis W.  
; APPLICANT: Dittlow, Charles C.  
; APPLICANT: Calenoff, Emanuel  
; TITLE OF INVENTION: ATHEROSCLEROTIC PLAQUE SPECIFIC  
; TITLE OF INVENTION: ANTIGENS, ANTIBODIES THERETO, AND USES THEREOF  
; NUMBER OF SEQUENCES: 176  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/053,451B  
; FILING DATE: 26-APR-1993  
; CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:  
; NAME: Halluin, Albert P.  
; REGISTRATION NUMBER: 25,227  
; REFERENCE/DOCKET NUMBER: 7606-033-999  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-854-3660  
; TELEFAX: 415-854-3694  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 76:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; MOLECULE TYPE: DNA  
; HYPOTHETICAL: N  
; ANTI-SENSE: N

US-08-053-451B-76  
Query Match 92.6%; Score 50; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.009;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ASQDISNYLN 11  
Db 2 ASQDISNYLN 11

RESULT 21  
US-08-649-100-11  
; Sequence 11, Application US/08649100  
; Patent No. 6114507  
; GENERAL INFORMATION:  
; APPLICANT: SHIRAKAWA, KAMON  
; APPLICANT: MATSUE, TOMOKAZU  
; APPLICANT: NAGATA, SHIGEKAZU  
; APPLICANT: CO, MAN SUNG  
; APPLICANT: VASQUEZ, MAXIMILIANO  
; TITLE OF INVENTION: ANTI-FAS LIGAND ANTIBODY AND ASSAY  
; TITLE OF INVENTION: METHOD USING THE ANTI-FAS LIGAND ANTIBODY  
; NUMBER OF SEQUENCES: 41

;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH  
;; STREET: PO BOX 747  
;; CITY: FALLS CHURCH  
;; STATE: VA  
;; COUNTRY: USA  
;; ZIP: 22040-0747  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/649,100  
;; FILING DATE:  
;; CLASSIFICATION: 435  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: MURPHY JR, GERALD M  
;; REGISTRATION NUMBER: 28,977  
;; REFERENCE/DOCKET NUMBER: 1110-160  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (703) 205-8000  
;; TELEFAX: (703) 205-8050  
;; INFORMATION FOR SEQ ID NO: 11:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 11 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
US-08-649-100-11

Query Match 92.6%; Score 50; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.009;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ASQDISNYLN 11  
Db 2 ASQDISNYLN 11

RESULT 22  
US-08-649-100-27  
; Sequence 27, Application US/08649100  
; Patent No. 6114507  
; GENERAL INFORMATION:  
; APPLICANT: SHIRAKAWA, KAMON  
; APPLICANT: MATSUE, TOMOKAZU  
; APPLICANT: NAGATA, SHIGEKAZU  
; APPLICANT: CO, MAN SUNG  
; APPLICANT: VASQUEZ, MAXIMILIANO  
; TITLE OF INVENTION: ANTI-FAS LIGAND ANTIBODY AND ASSAY  
; TITLE OF INVENTION: METHOD USING THE ANTI-FAS LIGAND ANTIBODY  
; NUMBER OF SEQUENCES: 41  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH  
; STREET: PO BOX 747  
; CITY: FALLS CHURCH  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22040-0747  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/649,100  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MURPHY JR, GERALD M  
; REGISTRATION NUMBER: 28,977

;; REFERENCE/DOCKET NUMBER: 1110-160  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (703) 205-8000  
;; TELEFAX: (703) 205-8050  
;; INFORMATION FOR SEQ ID NO: 27:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 11 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
US-08-649-100-27

Query Match 92.6%; Score 50; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.009;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ASQDISNYLN 11  
Db 2 ASQDISNYLN 11

RESULT 23  
US-08-525-539A-5  
; Sequence 5, Application US/08525539A  
; Patent No. 6309636  
; GENERAL INFORMATION:  
; APPLICANT: DO COUTO, FERNANDO J.R.  
; APPLICANT: CERIANI, ROBERTO L.  
; APPLICANT: PETERSON, JERRY A.  
; TITLE OF INVENTION: RECOMBINANT PEPTIDES DERIVED FROM THE  
; TITLE OF INVENTION: MC3 ANTI-BA46 ANTIBODY, METHODS OF USE THEREOF, AND  
; NUMBER OF SEQUENCES: 81  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 755 Page Mill Road  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/525,539A  
; FILING DATE: 14-SEP-1995  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: DYLAN, TYLER  
; REGISTRATION NUMBER: 37,612  
; REFERENCE/DOCKET NUMBER: 27633-20001.21  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 813-5600  
; TELEFAX: (415) 494-0792  
; TELEX: 706141  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 31 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-525-539A-5

Query Match 92.6%; Score 50; DB 2; Length 31;  
Best Local Similarity 100.0%; Pred. No. 0.029;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ASQDISNYLN 11  
Db 12 ASQDISNYLN 21

```
RESULT 24
US-08-851-362D-20
; Sequence 20, Application US/08851362D
; Patent No. 6235883
; GENERAL INFORMATION:
; APPLICANT: Jakobovits, Aya
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Gallo, Michael
; APPLICANT: Jia, Xiao-Chi
; TITLE OF INVENTION: Human Monoclonal Antibodies to Epidermal
; FILE REFERENCE: Cell 4.20
; CURRENT APPLICATION NUMBER: US/08/851,362D
; CURRENT FILING DATE: 1997-05-05
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 76
; TYPE: PRT
; ORGANISM: human
US-08-851-362D-20

Query Match          92.6%; Score 50; DB 2; Length 76;
Best Local Similarity 100.0%; Pred. No. 0.08;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 ASQDISNYLN 11
      |||||
Db      6 ASQDISNYLN 15

RESULT 25
US-10-194-975-56
; Sequence 56, Application US/10194975
; Patent No. 6881557
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: Super Humanized Antibodies
; FILE REFERENCE: 501231.01
; CURRENT APPLICATION NUMBER: US/10/194,975
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 56
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-194-975-56

Query Match          92.6%; Score 50; DB 2; Length 95;
Best Local Similarity 100.08; Pred. No. 0.1;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 ASQDISNYLN 11
      |||||
Db      25 ASQDISNYLN 34

RESULT 26
US-10-194-975-57
; Sequence 57, Application US/10194975
; Patent No. 6881557
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: Super Humanized Antibodies
; FILE REFERENCE: 501231.01
; CURRENT APPLICATION NUMBER: US/10/194,975
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/305,111
```

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; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 57
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-194-975-57

Query Match          92.6%; Score 50; DB 2; Length 95;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 ASQDISNYLN 11
      |||||
Db      25 ASQDISNYLN 34

RESULT 27
US-10-330-613A-59
; Sequence 59, Application US/10330613A
; Patent No. 6924360
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
; FILE REFERENCE: AGENIX.022A
; CURRENT APPLICATION NUMBER: US/10/330,613A
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: 60/346299
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 59
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-330-613A-59

Query Match          92.6%; Score 50; DB 2; Length 95;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 ASQDISNYLN 11
      |||||
Db      25 ASQDISNYLN 34

RESULT 28
US-08-851-362D-28
; Sequence 28, Application US/08851362D
; Patent No. 6235883
; GENERAL INFORMATION:
; APPLICANT: Jakobovits, Aya
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Gallo, Michael
; APPLICANT: Jia, Xiao-Chi
; TITLE OF INVENTION: Human Monoclonal Antibodies to Epidermal
; FILE REFERENCE: Cell 4.20
; CURRENT APPLICATION NUMBER: US/08/851,362D
; CURRENT FILING DATE: 1997-05-05
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 105
; TYPE: PRT
; ORGANISM: human
US-08-851-362D-28

Query Match          92.6%; Score 50; DB 2; Length 105;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Oy 2 ASQDISNYLN 11  
| | | | | | | |  
Db 6 ASQDISNYLN 15

## RESULT 29

US-08-851-362D-34  
; Sequence 34, Application US/08851362D  
; Patent No. 6235883  
; GENERAL INFORMATION:  
; APPLICANT: Jakobovits, Aya  
; APPLICANT: Yang, Xiao-Dong  
; APPLICANT: Gallo, Michael  
; APPLICANT: Jia, Xiao-Chi  
; TITLE OF INVENTION: Human Monoclonal Antibodies to Epidermal  
; TITLE OF INVENTION: Growth Factor Receptor  
; FILE REFERENCE: Cell 4.20  
; CURRENT APPLICATION NUMBER: US/08/851,362D  
; CURRENT FILING DATE: 1997-05-05  
; NUMBER OF SEQ ID NOS: 49  
; SOFTWARE: FASTSEQ for Windows Version 4.0  
; SEQ ID NO 34  
; LENGTH: 105  
; TYPE: PRT  
; ORGANISM: human  
US-08-851-362D-34

Query Match 92.6%; Score 50; DB 2; Length 105;  
Best Local Similarity 100.0%; Pred. No. 0.11;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 ASQDISNYLN 11  
| | | | | | | |  
Db 6 ASQDISNYLN 15

## RESULT 30

US-08-851-362D-38  
; Sequence 38, Application US/08851362D  
; Patent No. 6235883  
; GENERAL INFORMATION:  
; APPLICANT: Jakobovits, Aya  
; APPLICANT: Yang, Xiao-Dong  
; APPLICANT: Gallo, Michael  
; APPLICANT: Jia, Xiao-Chi  
; TITLE OF INVENTION: Human Monoclonal Antibodies to Epidermal  
; TITLE OF INVENTION: Growth Factor Receptor  
; FILE REFERENCE: Cell 4.20  
; CURRENT APPLICATION NUMBER: US/08/851,362D  
; CURRENT FILING DATE: 1997-05-05  
; NUMBER OF SEQ ID NOS: 49  
; SOFTWARE: FASTSEQ for Windows Version 4.0  
; SEQ ID NO 38  
; LENGTH: 105  
; TYPE: PRT  
; ORGANISM: human  
US-08-851-362D-38

Query Match 92.6%; Score 50; DB 2; Length 105;  
Best Local Similarity 100.0%; Pred. No. 0.11;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 ASQDISNYLN 11  
| | | | | | | |  
Db 6 ASQDISNYLN 15

## RESULT 31

US-08-480-434-74  
; Sequence 74, Application US/08480434  
; Patent No. 5811248  
; GENERAL INFORMATION:  
; APPLICANT: Charles C. Dittlow, et al.

; TITLE OF INVENTION: ATHEROSCLEROTIC PLAQUE SPECIFIC ANTIGENS,  
; TITLE OF INVENTION: ANTIBODIES THERETO, AND USES THEREOF  
; NUMBER OF SEQUENCES: 88  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.24  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/480,434  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Albert P. Halluin  
; REGISTRATION NUMBER: 25,227  
; REFERENCE/DOCKET NUMBER: 7606-053  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 854-3660  
; TELEFAX: (415) 854-3694  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 74:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 107 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHETICAL: N  
; ANTI-SENSE: N  
US-08-480-434-74

Query Match 92.6%; Score 50; DB 1; Length 107;  
Best Local Similarity 100.0%; Pred. No. 0.12;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 ASQDISNYLN 11  
| | | | | | | |  
Db 25 ASQDISNYLN 34

## RESULT 32

US-08-053-451B-74  
; Sequence 74, Application US/08053451B  
; Patent No. 5955584  
; GENERAL INFORMATION:  
; APPLICANT: Chen, Francis W.  
; APPLICANT: Dittlow, Charles C.  
; APPLICANT: Calenoff, Emanuel  
; TITLE OF INVENTION: ATHEROSCLEROTIC PLAQUE SPECIFIC  
; TITLE OF INVENTION: ANTIGENS, ANTIBODIES THERETO, AND USES THEREOF  
; NUMBER OF SEQUENCES: 176  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/053,451B  
; FILING DATE: 26-APR-1993

;; CLASSIFICATION: 424  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Halluin, Albert P.  
;; REGISTRATION NUMBER: 25,227  
;; REFERENCE/DOCKET NUMBER: 7606-033-999  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 415-854-3660  
;; TELEFAX: 415-854-3694  
;; TELEX: 66141 PENNIE  
;; INFORMATION FOR SEQ ID NO: 74:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 107 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: unknown  
;; TOPOLOGY: unknown  
;; MOLECULE TYPE: DNA  
;; HYPOTHETICAL: N  
;; ANTI-SENSE: N  
US-08-053-451B-74

Query Match 92.6%; Score 50; DB 1; Length 107;  
Best Local Similarity 100.0%; Pred. No. 0.12;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ASQDISNYLN 11  
Db 25 ASQDISNYLN 34

RESULT 33  
US-08-053-451B-176  
; Sequence 176, Application US/08053451B  
; Patent No. 5955584  
; GENERAL INFORMATION:  
; APPLICANT: Chen, Francis W.  
; APPLICANT: Ditlow, Charles C.  
; APPLICANT: Calenoff, Emanuel  
; TITLE OF INVENTION: ATHEROSCLEROTIC PLAQUE SPECIFIC  
; TITLE OF INVENTION: ANTIGENS, ANTIBODIES THERETO, AND USES THEREOF  
; NUMBER OF SEQUENCES: 176  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/053,451B  
; FILING DATE: 26-APR-1993  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Halluin, Albert P.  
; REGISTRATION NUMBER: 25,227  
; REFERENCE/DOCKET NUMBER: 7606-033-999  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-854-3660  
; TELEFAX: 415-854-3694  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 176:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 107 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; MOLECULE TYPE: protein  
US-08-053-451B-176

Query Match 92.6%; Score 50; DB 1; Length 107;  
Best Local Similarity 100.0%; Pred. No. 0.12;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ASQDISNYLN 11  
Db 25 ASQDISNYLN 34

RESULT 34  
US-09-065-059-3  
; Sequence 3, Application US/09065059  
; Patent No. 6068841  
; GENERAL INFORMATION:  
; APPLICANT: SEINO, Ken-ichiro  
; APPLICANT: KAYAGAKI, No. 6068841uhiko  
; APPLICANT: YAGITA, Hideo  
; APPLICANT: OKUMURA, Ko  
; APPLICANT: NAKATA, Motomi  
; TITLE OF INVENTION: THERAPEUTIC AGENT FOR HEPATITIS  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: McDermott, Will & Emery  
; STREET: 99 Canal Center Plaza  
; CITY: Alexandria  
; STATE: Virginia  
; COUNTRY: USA  
; ZIP: 22314  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/065,059  
; FILING DATE:  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Bucca Ph.D., Daniel  
; REGISTRATION NUMBER: P-42,368  
; REFERENCE/DOCKET NUMBER: 50356-151  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703-518-5100  
; TELEFAX: 703-684-1124  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 108 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-09-065-059-3

Query Match 92.6%; Score 50; DB 2; Length 108;  
Best Local Similarity 100.0%; Pred. No. 0.12;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ASQDISNYLN 11  
Db 25 ASQDISNYLN 34

RESULT 35  
US-09-232-290-21  
; Sequence 21, Application US/09232290A  
; Patent No. 6815540  
; GENERAL INFORMATION:  
; APPLICANT: PLUCKTHUN, ANDREAS  
; APPLICANT: NIEBA, LARS  
; APPLICANT: HONEGGER, ANNEMARIE  
; TITLE OF INVENTION: IMMUNOGLOBULIN SUPER FAMILY DOMAINS AND FRAGMENTS WITH  
; TITLE OF INVENTION: INCREASED SOLUBILITY  
; FILE REFERENCE: MORPHO/7

```
/ CURRENT APPLICATION NUMBER: US/09/232,290A
/ CURRENT FILING DATE: 1999-01-15
/ EARLIER APPLICATION NUMBER: PCT/EP96/02230
/ EARLIER FILING DATE: 1996-05-23
/ NUMBER OF SEQ ID NOS: 60
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 21
/ LENGTH: 108
/ TYPE: PRT
/ ORGANISM: Murine
/ US-09-232-290-21

Query Match          92.6%; Score 50; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 ASQDISNYLN 11
DB      25 ASQDISNYLN 34

RESULT 36
US-08-913-555-3
/ Sequence 3, Application US/08913555
/ Patent No. 6946255
/ GENERAL INFORMATION:
/ APPLICANT: KAYAGAKI, No. 6946255uhiko
/ APPLICANT: YAGITA, Kideo
/ APPLICANT: OKUMURA, KO
/ APPLICANT: NAKATA, Motomi
/ TITLE OF INVENTION: MONOCLONAL ANTIBODY SPECIFICALLY
/ TITLE OF INVENTION: REACTING WITH Fas LIGAND AND PRODUCTION PROCESS THEREOF
/ NUMBER OF SEQUENCES: 31
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: McDermott, Will & Emery
/ STREET: 99 Canal Center Plaza, Suite 300
/ CITY: Alexandria
/ STATE: Virginia
/ COUNTRY: USA
/ ZIP: 22314
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC Compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/913,555
/ FILING DATE: 19-SEP-1997
/ CLASSIFICATION: 530
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Bucca Ph.D., Daniel
/ REGISTRATION NUMBER: 42,368
/ REFERENCE/DOCKET NUMBER: 50356-150
/ TELEPHONE: 202-756-8600
/ TELEFAX: 202-756-8699
/ INFORMATION FOR SEQ ID NO: 21:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 108 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ US-08-913-555-21

Query Match          92.6%; Score 50; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 ASQDISNYLN 11
DB      25 ASQDISNYLN 34

RESULT 37
US-08-913-555-21
/ Sequence 21, Application US/08913555
/ Patent No. 6946255
/ GENERAL INFORMATION:
/ APPLICANT: KAYAGAKI, No. 6946255uhiko
/ APPLICANT: YAGITA, Kideo
/ APPLICANT: OKUMURA, KO
/ APPLICANT: NAKATA, Motomi
/ TITLE OF INVENTION: MONOCLONAL ANTIBODY SPECIFICALLY
/ TITLE OF INVENTION: REACTING WITH Fas LIGAND AND PRODUCTION PROCESS THEREOF
/ NUMBER OF SEQUENCES: 31
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: McDermott, Will & Emery
/ STREET: 99 Canal Center Plaza, Suite 300
/ CITY: Alexandria
/ STATE: Virginia
/ COUNTRY: USA
/ ZIP: 22314
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC Compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/913,555
/ FILING DATE: 19-SEP-1997
/ CLASSIFICATION: 530
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Bucca Ph.D., Daniel
/ REGISTRATION NUMBER: 42,368
/ REFERENCE/DOCKET NUMBER: 50356-150
/ TELEPHONE: 202-756-8600
/ TELEFAX: 202-756-8699
/ INFORMATION FOR SEQ ID NO: 21:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 108 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ US-08-913-555-21

Query Match          92.6%; Score 50; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 ASQDISNYLN 11
DB      25 ASQDISNYLN 34

RESULT 38
US-07-942-245-10
/ Sequence 10, Application US/07942245
/ Patent No. 5639641
/ GENERAL INFORMATION:
/ APPLICANT: PEDERSEN, Jan T.
/ APPLICANT: SEARLE, Stephen M.J.
/ APPLICANT: REES, Anthony R.
/ APPLICANT: ROGUSKA, Michael A.
/ APPLICANT: GUILD, Braydon C.
/ TITLE OF INVENTION: SURFACE RESIDUE VENEERING OF RODENT
/ TITLE OF INVENTION: ANTIBODIES
/ NUMBER OF SEQUENCES: 522
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Sughrue, Mion, Zinn, Macpeak & Seas
/ STREET: 2100 Pennsylvania Avenue, N.W.
/ CITY: Washington
/ STATE: D.C.
/ COUNTRY: United States
```

;; ZIP: 20037-3202  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: HP 9000/700 Workstation  
;; OPERATING SYSTEM: UNIX  
;; SOFTWARE: In house  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/07/942,245  
;; FILING DATE: 09-SEP-1992  
;; CLASSIFICATION: 530  
;; TELEPHONE: (202) 293-7060  
;; TELEX: 6491103  
;; INFORMATION FOR SEQ ID NO: 10:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 109 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
US-07-942-245-10

Query Match 92.6%; Score 50; DB 1; Length 109;  
Best Local Similarity 100.0%; Pred. No. 0.12;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ASQDISNYLN 11  
Db 25 ASQDISNYLN 34

RESULT 39  
US-08-137-117D-37  
; Sequence 37, Application US/08137117D  
; Patent No. 5795965  
; GENERAL INFORMATION:  
; APPLICANT: TSUCHIYA, Masayuki  
; APPLICANT: SATO, Koh  
; APPLICANT: BENDIG, Mary  
; APPLICANT: JONES, Steven  
; APPLICANT: SALDANHA, Jose  
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN  
; TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR  
; NUMBER OF SEQUENCES: 158  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 3000 K Street, N.W., Suite 500  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20007-5109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/137,117D  
; FILING DATE: 20-DEC-1993  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/JP92/00544  
; FILING DATE: 24-APR-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 4-32084  
; FILING DATE: 19-FEB-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: WEGNER, Harold C.  
; REGISTRATION NUMBER: 25,258  
; REFERENCE/DOCKET NUMBER: 53466/126/AAOK

;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (202)672-5300  
;; TELEX: 904136  
;; INFORMATION FOR SEQ ID NO: 37:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 127 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
US-08-137-117D-37

Query Match 92.6%; Score 50; DB 1; Length 127;  
Best Local Similarity 100.0%; Pred. No. 0.14;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ASQDISNYLN 11  
Db 45 ASQDISNYLN 54

RESULT 40  
US-08-436-717-37  
; Sequence 37, Application US/08436717  
; Patent No. 5817790  
; GENERAL INFORMATION:  
; APPLICANT: TSUCHIYA, Masayuki  
; APPLICANT: SATO, Koh  
; APPLICANT: BENDIG, Mary  
; APPLICANT: JONES, Steven  
; APPLICANT: SALDANHA, Jose  
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN  
; TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR  
; NUMBER OF SEQUENCES: 158  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 3000 K Street, N.W., Suite 500  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20007-5109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/436,717  
; FILING DATE:  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/137,117  
; FILING DATE: 20-DEC-1993  
; APPLICATION NUMBER: WO PCT/JP92/00544  
; FILING DATE: 24-APR-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 4-32084  
; FILING DATE: 19-FEB-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 3-95476  
; FILING DATE: 25-APR-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: WEGNER, Harold C.  
; REGISTRATION NUMBER: 25,258  
; REFERENCE/DOCKET NUMBER: 53466/126/AAOK  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)672-5300  
; TELEX: 904136  
; INFORMATION FOR SEQ ID NO: 37:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 127 amino acids  
; TYPE: amino acid



;  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-436-717-37

Query Match 92.6%; Score 50; DB 1; Length 127;  
Best Local Similarity 100.0%; Pred. No. 0.14;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ASQDISNYLN 11  
| | | | | | | | | |  
Db 45 ASQDISNYLN 54

RESULT 41  
US-08-649-100-17  
; Sequence 17, Application US/08649100  
; Patent No. 6114507  
; GENERAL INFORMATION:  
; APPLICANT: SHIRAKAWA, KAMON  
; APPLICANT: MATSUE, TOMOKAZU  
; APPLICANT: NAGATA, SHIGEKAZU  
; APPLICANT: CO, MAN SUNG  
; APPLICANT: VASQUEZ, MAXIMILIANO  
; TITLE OF INVENTION: ANTI-FAS LIGAND ANTIBODY AND ASSAY  
; TITLE OF INVENTION: METHOD USING THE ANTI-FAS LIGAND ANTIBODY  
; NUMBER OF SEQUENCES: 41  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH  
; STREET: PO BOX 747  
; CITY: FALLS CHURCH  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22040-0747  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MURPHY JR, GERALD M  
; REGISTRATION NUMBER: 28,977  
; REFERENCE/DOCKET NUMBER: 1110-160  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 205-8000  
; TELEFAX: (703) 205-8050  
; INFORMATION FOR SEQ ID NO: 17:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 127 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-649-100-17

Query Match 92.6%; Score 50; DB 2; Length 127;  
Best Local Similarity 100.0%; Pred. No. 0.14;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ASQDISNYLN 11  
| | | | | | | | | |  
Db 45 ASQDISNYLN 54

RESULT 42  
US-08-649-100-33  
; Sequence 33, Application US/08649100  
; Patent No. 6114507  
; GENERAL INFORMATION:  
; APPLICANT: SHIRAKAWA, KAMON

;  
; APPLICANT: MATSUE, TOMOKAZU  
; APPLICANT: NAGATA, SHIGEKAZU  
; APPLICANT: CO, MAN SUNG  
; APPLICANT: VASQUEZ, MAXIMILIANO  
; TITLE OF INVENTION: ANTI-FAS LIGAND ANTIBODY AND ASSAY  
; TITLE OF INVENTION: METHOD USING THE ANTI-FAS LIGAND ANTIBODY  
; NUMBER OF SEQUENCES: 41  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH  
; STREET: PO BOX 747  
; CITY: FALLS CHURCH  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22040-0747  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MURPHY JR, GERALD M  
; REGISTRATION NUMBER: 28,977  
; REFERENCE/DOCKET NUMBER: 1110-160  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 205-8000  
; TELEFAX: (703) 205-8050  
; INFORMATION FOR SEQ ID NO: 33:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 127 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-649-100-33

Query Match 92.6%; Score 50; DB 2; Length 127;  
Best Local Similarity 100.0%; Pred. No. 0.14;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ASQDISNYLN 11  
| | | | | | | | | |  
Db 45 ASQDISNYLN 54

RESULT 43  
US-08-236-520-2  
; Sequence 2, Application US/08236520  
; Patent No. 5591629  
; GENERAL INFORMATION:  
; APPLICANT: Rodriguez, Moses  
; APPLICANT: Miller, David J.  
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES WHICH PROMOTE  
; TITLE OF INVENTION: CENTRAL NERVOUS SYSTEM REMYELINATION  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hamilton, Brook, Smithy & Reynolds, P.C.  
; STREET: Two Militia Drive  
; CITY: Lexington  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02173  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/236,520  
; FILING DATE: 29-APR-1994

;; CLASSIFICATION: 424  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Granahan, Patricia  
;; REGISTRATION NUMBER: 27,227  
;; REFERENCE/DOCKET NUMBER: MMV92-01  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 617-861-6240  
;; TELEFAX: 617-861-9540  
;; INFORMATION FOR SEQ ID NO: 2:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 131 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
US-08-236-520-2  
  
Query Match 92.6%; Score 50; DB 1; Length 131;  
Best Local Similarity 100.0%; Pred. No. 0.15;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 2 ASQDISNYLN 11  
Db 45 ASQDISNYLN 54

RESULT 44  
PCT-US95-05262-2  
;; Sequence 2, Application PC/TUS9505262  
;; GENERAL INFORMATION:  
;; APPLICANT: Mayo Foundation for Medical Education Research  
;; TITLE OF INVENTION: MONOCLONAL ANTIBODIES WHICH PROMOTE  
;; TITLE OF INVENTION: CENTRAL NERVOUS SYSTEM REMYELINATION  
;; NUMBER OF SEQUENCES: 11  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Hamilton, Brook, Smithy & Reynolds, P.C.  
;; STREET: Two Militia Drive  
;; CITY: Lexington  
;; STATE: Massachusetts  
;; COUNTRY: USA  
;; ZIP: 02173  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patent In Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: PCT/US95/05262  
;; FILING DATE:  
;; CLASSIFICATION:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: U.S. 08/236,520  
;; FILING DATE: April 29, 1994  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Granahan, Patricia  
;; REGISTRATION NUMBER: 27,227  
;; REFERENCE/DOCKET NUMBER: MMV92-01 PCT  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 617-861-6240  
;; TELEFAX: 617-861-9540  
;; INFORMATION FOR SEQ ID NO: 2:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 131 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
PCT-US95-05262-2  
  
Query Match 92.6%; Score 50; DB 4; Length 131;  
Best Local Similarity 100.0%; Pred. No. 0.15;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 2 ASQDISNYLN 11  
Db 45 ASQDISNYLN 54

Db 45 ASQDISNYLN 54  
  
RESULT 45  
US-08-403-853-18  
;; Sequence 18, Application US/08403853  
;; Patent No. 5844094  
;; GENERAL INFORMATION:  
;; APPLICANT: HUDSON, Peter J.  
;; APPLICANT: LAH, Maria  
;; APPLICANT: KORRT, Alex A.  
;; APPLICANT: IRVING, Robert A.  
;; APPLICANT: ATWELL, John L.  
;; APPLICANT: MALBY, Robyn L.  
;; APPLICANT: POWER, Barbara E.  
;; APPLICANT: COLMAN, Peter M.  
;; TITLE OF INVENTION: TARGET BINDING POLYPEPTIDE  
;; NUMBER OF SEQUENCES: 25  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Foley & Lardner  
;; STREET: 3000 K Street, N.W., Suite 500  
;; CITY: Washington  
;; STATE: D.C.  
;; COUNTRY: USA  
;; ZIP: 20007-5109  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patent In Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA: US/08/403,853  
;; APPLICATION NUMBER: US/08/403,853  
;; FILING DATE: 30-MAY-1995  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: WO PCT/AU93/00491  
;; FILING DATE: 24-SEP-1993  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: AU PL 4973  
;; FILING DATE: 25-SEP-1992  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: BENT, Stephen A.  
;; REGISTRATION NUMBER: 29,768  
;; REFERENCE/DOCKET NUMBER: 16786/189/CHAC  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (202)672-5300  
;; TELEFAX: (202)672-5399  
;; TELEX: 904136  
;; INFORMATION FOR SEQ ID NO: 18:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 273 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
US-08-403-853-18

Query Match 92.6%; Score 50; DB 1; Length 273;  
Best Local Similarity 100.0%; Pred. No. 0.34;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 2 ASQDISNYLN 11  
Db 183 ASQDISNYLN 192

RESULT 46  
US-08-487-761-13  
;; Sequence 13, Application US/08487761  
;; Patent No. 6217866  
;; GENERAL INFORMATION:  
;; APPLICANT: Schlensing, Joseph  
;; APPLICANT: Givol, David  
;; APPLICANT: Bellot, Francoise

```
; APPLICANT: Kris, Richard
; APPLICANT: Ricca, George A.
; APPLICANT: Cheadle, Christopher
; APPLICANT: South, Victoria J.
; TITLE OF INVENTION: Monoclonal Antibodies Specific to Human
; TITLE OF INVENTION: Epidermal Growth Factor Receptor and Therapeutic Methods
; TITLE OF INVENTION: Employing Same
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Road, 3C43
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: System 7.1
; SOFTWARE: Word 5.0 (Patentin)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,761
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/086,411
; FILING DATE: 29-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Goodman, Rosanne
; REGISTRATION NUMBER: 32,534
; REFERENCE/DOCKET NUMBER: A0207C-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 454-3817
; TELEFAX: (215) 454-3808
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-487-761-13

Query Match 90.7%; Score 49; DB 2; Length 112;
Best Local Similarity 90.9%; Pred. No. 0.19;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SASQDISNYLN 11
    |||||
Db 24 SASQDIRNYLN 34

RESULT 47
US-08-851-362D-24
; Sequence 24, Application US/08851362D
; Patent No. 6235883
; GENERAL INFORMATION:
; APPLICANT: Jakobovits, Aya
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Gallo, Michael
; APPLICANT: Jia, Xiao-Chi
; TITLE OF INVENTION: Human Monoclonal Antibodies to Epidermal
; TITLE OF INVENTION: Growth Factor Receptor
; FILE REFERENCE: Cell 4.20
; CURRENT APPLICATION NUMBER: US/08/851,362D
; CURRENT FILING DATE: 1997-05-05
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 105
; TYPE: PRT
; ORGANISM: human
US-08-851-362D-24
```

```
Query Match 87.0%; Score 47; DB 2; Length 105;
Best Local Similarity 90.0%; Pred. No. 0.39;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ASQDISNYLN 11
    |||||
Db 6 ASQDINNYLN 15

RESULT 48
US-08-458-516-8
; Sequence 8, Application US/08458516
; Patent No. 577085
; GENERAL INFORMATION:
; APPLICANT: Co, Man Sung
; APPLICANT: Tso, J. Yun
; TITLE OF INVENTION: Humanized Antibodies Reactive with
; TITLE OF INVENTION: GPIIB/IIIA
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: William M. Smith
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/458,516
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/059,159
; FILING DATE: 03-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-37-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-458-516-8

Query Match 87.0%; Score 47; DB 1; Length 107;
Best Local Similarity 90.0%; Pred. No. 0.4;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ASQDISNYLN 11
    |||||
Db 25 ASQDINNYLN 34

RESULT 49
US-08-458-516-9
; Sequence 9, Application US/08458516
; Patent No. 577085
; GENERAL INFORMATION:
; APPLICANT: Co, Man Sung
; APPLICANT: Tso, J. Yun
; TITLE OF INVENTION: Humanized Antibodies Reactive with
; TITLE OF INVENTION: GPIIB/IIIA
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
```

ADDRESSEE: William M. Smith  
STREET: One Market Plaza, Steuart Tower, Suite 2000  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/458,516  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/059,159  
FILING DATE: 03-MAY-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M.  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 11823-37-3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-326-2400  
TELEFAX: 415-326-2422  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 107 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-458-516-9

Query Match 87.0%; Score 47; DB 1; Length 107;  
Best Local Similarity 90.0%; Pred. No. 0.4;  
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 2 ASQDISNYLN 11  
Db 25 ASQDINNYLN 34

RESULT 50  
US-08-652-558-2  
Sequence 2, Application US/08652558  
Patent No. 5861155  
GENERAL INFORMATION:  
APPLICANT: LIN, AUGUSTINE YEE-THARN  
TITLE OF INVENTION: HUMANIZED ANTIBODIES AND USES  
TITLE OF INVENTION: THEREOF  
NUMBER OF SEQUENCES: 52  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BANNER & WITCOFF  
STREET: 75 STATE STREET, 23RD FLOOR  
CITY: BOSTON  
STATE: MASSACHUSETTS  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WordPerfect 6.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/652,558  
FILING DATE: JUNE 6, 1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/IB94/00387  
FILING DATE: NOVEMBER 21, 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: YANKWICH, LEON R.  
REGISTRATION NUMBER: 30,237  
REFERENCE/DOCKET NUMBER: 95,497-L

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-345-9100  
TELEFAX: 617-345-9111  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 107 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-652-558-2

Query Match 87.0%; Score 47; DB 1; Length 107;  
Best Local Similarity 90.9%; Pred. No. 0.4;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SASQDISNYLN 11  
Db 24 SASQGISNYLN 34

Search completed: April 6, 2006, 09:00:59  
Job time : 17.7288 secs

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: April 6, 2006, 09:13:24 ; Search time 88.9322 Seconds  
(without alignments)  
51.681 Million cell updates/sec

Title: US-10-089-500-6

Perfect score: 54

Sequence: 1 SASQDISNYLN 11

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Published Applications AA Main:

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*
- 6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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3	54	100.0	11	5	US-10-974-591-4
4	54	100.0	103	4	US-10-379-392-100
5	54	100.0	103	4	US-10-379-392-121
6	54	100.0	103	4	US-10-379-392-123
7	54	100.0	103	4	US-10-379-392-129
8	54	100.0	103	4	US-10-379-392-131
9	54	100.0	107	3	US-09-056-160B-13
10	54	100.0	107	3	US-09-056-160B-15
11	54	100.0	107	4	US-10-234-671-13
12	54	100.0	107	4	US-10-234-671-15
13	54	100.0	107	4	US-10-723-434-1
14	54	100.0	107	4	US-10-723-434-2
15	54	100.0	107	4	US-10-723-434-3
16	54	100.0	107	4	US-10-723-434-4
17	54	100.0	107	4	US-10-723-434-5
18	54	100.0	107	4	US-10-723-434-6
19	54	100.0	107	4	US-10-723-434-7
20	54	100.0	107	4	US-10-723-434-8
21	54	100.0	107	4	US-10-723-434-9
22	54	100.0	107	4	US-10-723-434-10
23	54	100.0	107	4	US-10-723-434-11
24	54	100.0	107	4	US-10-723-434-12
25	54	100.0	107	4	US-10-723-434-13
26	54	100.0	107	4	US-10-723-434-14
27	54	100.0	107	5	US-10-974-591-13

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102	50	92.6	75	4	US-10-078-958-25	Sequence 25, Appl	175	47	87.0	107	4	US-10-410-997-52	Sequence 52, Appl
103	50	92.6	76	3	US-09-187-693-36	Sequence 36, Appl	176	47	87.0	107	4	US-10-411-012-51	Sequence 51, Appl
104	50	92.6	76	4	US-10-078-958-10	Sequence 10, Appl	177	47	87.0	107	4	US-10-411-012-52	Sequence 52, Appl
105	50	92.6	76	3	US-11-021-795-36	Sequence 36, Appl	178	47	87.0	107	4	US-10-287-994-51	Sequence 51, Appl
106	50	92.6	90	3	US-09-864-761-34739	Sequence 34739, A	179	47	87.0	107	4	US-10-287-994-52	Sequence 52, Appl
107	50	92.6	95	4	US-10-194-975-56	Sequence 56, Appl	180	47	87.0	107	4	US-10-410-913-51	Sequence 51, Appl
108	50	92.6	95	4	US-10-194-975-57	Sequence 57, Appl	181	47	87.0	107	4	US-10-410-913-52	Sequence 52, Appl
109	50	92.6	95	4	US-10-308-817-3	Sequence 3, Appl	182	47	87.0	107	5	US-10-410-980-51	Sequence 51, Appl
110	50	92.6	95	4	US-10-308-817-4	Sequence 4, Appl	183	47	87.0	107	5	US-10-410-980-52	Sequence 52, Appl
111	50	92.6	95	4	US-10-453-698-3	Sequence 3, Appl	184	47	87.0	107	5	US-10-410-897-51	Sequence 51, Appl
112	50	92.6	95	4	US-10-453-698-4	Sequence 4, Appl	185	47	87.0	107	5	US-10-410-897-52	Sequence 52, Appl
113	50	92.6	95	4	US-10-379-392-73	Sequence 73, Appl	186	47	87.0	107	5	US-10-492-261-51	Sequence 51, Appl
114	50	92.6	95	4	US-10-379-392-74	Sequence 74, Appl	187	47	87.0	107	5	US-10-492-261-52	Sequence 52, Appl
115	50	92.6	104	4	US-10-078-958-28	Sequence 28, Appl	188	47	87.0	108	4	US-10-683-815-19	Sequence 19, Appl
116	50	92.6	104	4	US-10-078-958-29	Sequence 29, Appl	189	47	87.0	112	4	US-10-364-743-51	Sequence 51, Appl
117	50	92.6	105	3	US-09-187-693-44	Sequence 44, Appl	190	47	87.0	112	5	US-10-452-593-51	Sequence 51, Appl
118	50	92.6	105	3	US-09-187-693-50	Sequence 50, Appl	191	47	87.0	115	4	US-10-364-743-50	Sequence 50, Appl
119	50	92.6	105	3	US-09-187-693-54	Sequence 54, Appl	192	47	87.0	115	5	US-10-452-593-50	Sequence 50, Appl
120	50	92.6	105	4	US-10-078-958-12	Sequence 12, Appl	193	47	87.0	166	4	US-10-364-743-22	Sequence 22, Appl
121	50	92.6	105	6	US-11-021-795-44	Sequence 44, Appl	194	47	87.0	166	5	US-10-452-593-22	Sequence 22, Appl
122	50	92.6	105	6	US-11-021-795-50	Sequence 50, Appl	195	47	87.0	212	4	US-10-011-125-5	Sequence 5, Appl
123	50	92.6	105	6	US-11-021-795-54	Sequence 54, Appl	196	47	87.0	214	3	US-09-754-998-1	Sequence 1, Appl
124	50	92.6	106	5	US-10-727-155-130	Sequence 130, App	197	47	87.0	214	3	US-09-940-166A-2	Sequence 2, Appl
125	50	92.6	107	3	US-09-892-613C-10	Sequence 10, Appl	198	47	87.0	214	3	US-09-811-384-11	Sequence 11, Appl
126	50	92.6	107	4	US-10-741-657A-16	Sequence 16, Appl	199	47	87.0	214	4	US-10-411-037-55	Sequence 55, Appl
127	50	92.6	107	5	US-10-473-977-69	Sequence 69, Appl	200	47	87.0	214	4	US-10-404-286-11	Sequence 11, Appl
128	50	92.6	107	5	US-10-482-759-10	Sequence 10, Appl	201	47	87.0	214	4	US-10-411-026-55	Sequence 55, Appl
129	50	92.6	107	5	US-10-727-155-318	Sequence 318, App	202	47	87.0	214	4	US-10-410-962-55	Sequence 55, Appl
130	50	92.6	107	5	US-10-490-535-4	Sequence 4, Appl	203	47	87.0	214	4	US-10-411-049-55	Sequence 55, Appl
131	50	92.6	107	5	US-10-938-982-17	Sequence 17, Appl	204	47	87.0	214	4	US-10-410-930-55	Sequence 55, Appl
132	50	92.6	107	6	US-10-084-139-2	Sequence 2, Appl	205	47	87.0	214	4	US-10-410-997-55	Sequence 55, Appl
133	50	92.6	108	4	US-10-140-555-4	Sequence 4, Appl	206	47	87.0	214	4	US-10-411-012-55	Sequence 55, Appl
134	50	92.6	111	4	US-10-203-754A-17	Sequence 17, Appl	207	47	87.0	214	4	US-10-287-994-55	Sequence 55, Appl
135	50	92.6	113	4	US-10-364-743-49	Sequence 49, Appl	208	47	87.0	214	4	US-10-762-967-2	Sequence 2, Appl
136	50	92.6	113	5	US-10-452-593-49	Sequence 49, Appl	209	47	87.0	214	4	US-10-410-913-55	Sequence 55, Appl
137	50	92.6	120	5	US-10-450-763-42267	Sequence 42267, A	210	47	87.0	214	4	US-10-683-815-6	Sequence 6, Appl
138	50	92.6	127	4	US-10-084-139-2	Sequence 2, Appl	211	47	87.0	214	5	US-10-835-641-24	Sequence 24, Appl
139	50	92.6	127	4	US-10-084-139-6	Sequence 6, Appl	212	47	87.0	214	5	US-10-835-641-25	Sequence 25, Appl
140	50	92.6	127	5	US-10-837-904-37	Sequence 37, Appl	213	47	87.0	214	5	US-10-410-980-55	Sequence 55, Appl
141	50	92.6	129	5	US-10-893-576-30	Sequence 30, Appl	214	47	87.0	214	5	US-10-410-897-55	Sequence 55, Appl
142	50	92.6	131	2	US-08-779-784-21	Sequence 21, Appl	215	47	87.0	214	6	US-10-492-261-55	Sequence 55, Appl
143	50	92.6	131	4	US-10-010-729-64	Sequence 64, Appl	216	47	87.0	214	6	US-11-077-717-2	Sequence 2, Appl
144	50	92.6	164	4	US-10-364-743-21	Sequence 21, Appl	217	47	87.0	233	5	US-10-835-641-25	Sequence 25, Appl
145	50	92.6	164	5	US-10-452-593-21	Sequence 21, Appl	218	47	87.0	234	3	US-09-800-729-150	Sequence 150, App
146	50	92.6	214	5	US-10-644-277-64	Sequence 64, Appl	219	47	87.0	237	3	US-09-833-245-2210	Sequence 210, Ap
147	50	92.6	233	4	US-10-660-128-9	Sequence 9, Appl	220	47	87.0	237	3	US-09-940-166A-6	Sequence 6, Appl
148	50	92.6	236	6	US-11-131-648-20	Sequence 20, Appl	221	47	87.0	237	4	US-10-762-967-6	Sequence 6, Appl
149	50	92.6	236	6	US-11-131-648-49	Sequence 49, Appl	222	47	87.0	237	5	US-10-754-212-2	Sequence 2, Appl
150	50	92.6	236	6	US-11-031-485-48	Sequence 48, Appl	223	47	87.0	237	6	US-11-077-717-10	Sequence 10, Appl
151	50	92.6	286	4	US-10-406-830-8	Sequence 8, Appl	224	46	85.2	11	4	US-10-697-399-9	Sequence 9, Appl
152	50	92.6	479	5	US-10-485-466-29	Sequence 29, Appl	225	46	85.2	103	4	US-10-379-392-125	Sequence 125, App
153	50	92.6	502	4	US-10-679-620-88	Sequence 88, Appl	226	46	85.2	106	4	US-10-466-242-20	Sequence 20, Appl
154	50	92.6	502	6	US-11-132-143-88	Sequence 88, Appl	227	46	85.2	107	4	US-10-310-674A-34	Sequence 34, Appl
155	50	92.6	551	5	US-10-485-466-31	Sequence 31, Appl	228	46	85.2	107	4	US-10-460-595-7	Sequence 7, Appl
156	50	92.6	731	6	US-11-035-599-51	Sequence 51, Appl	229	46	85.2	107	4	US-10-389-679-10	Sequence 10, Appl
157	47	87.0	11	4	US-10-279-633-53	Sequence 53, Appl	230	46	85.2	103	4	US-10-379-392-147	Sequence 147, App
158	47	87.0	103	4	US-10-078-958-26	Sequence 26, Appl	231	45	83.3	11	5	US-10-745-775-12	Sequence 12, Appl
159	47	87.0	105	3	US-09-187-693-40	Sequence 40, Appl	232	45	83.3	99	4	US-10-697-399-6	Sequence 6, Appl
160	47	87.0	105	6	US-11-021-795-40	Sequence 40, Appl	233	45	83.3	104	4	US-10-016-986-112	Sequence 112, App
161	47	87.0	107	4	US-10-330-613-26	Sequence 26, Appl	234	45	83.3	107	4	US-10-011-931-4	Sequence 4, Appl
162	47	87.0	107	4	US-10-330-530-26	Sequence 26, Appl	235	45	83.3	107	4	US-10-016-986-107	Sequence 107, App
163	47	87.0	107	4	US-10-411-037-51	Sequence 51, Appl	236	45	83.3	107	5	US-10-016-986-108	Sequence 108, App
164	47	87.0	107	4	US-10-411-037-52	Sequence 52, Appl	237	45	83.3	107	5	US-10-835-641-16	Sequence 16, Appl
165	47	87.0	107	4	US-10-411-026-51	Sequence 51, Appl	238	45	83.3	107	5	US-10-835-641-17	Sequence 17, Appl
166	47	87.0	107	4	US-10-411-026-52	Sequence 52, Appl	239	45	83.3	107	5	US-10-985-299-4	Sequence 4, Appl
167	47	87.0	107	4	US-10-410-962-51	Sequence 51, Appl	240	45	83.3	107	5	US-10-837-904-115	Sequence 115, App
168	47	87.0	107	4	US-10-410-962-52	Sequence 52, Appl	241	45	83.3	113	4	US-10-364-743-58	Sequence 58, Appl
169	47	87.0	107	4	US-10-411-049-51	Sequence 51, Appl	242	45	83.3	113	5	US-10-452-593-58	Sequence 58, Appl
170	47	87.0	107	4	US-10-411-049-52	Sequence 52, Appl	243	45	83.3	126	5	US-10-837-904-64	Sequence 64, Appl
171	47	87.0	107	4	US-10-410-930-51	Sequence 51, Appl	244	45	83.3	126	5	US-10-837-904-68	Sequence 68, Appl
172	47	87.0	107	4	US-10-410-930-52	Sequence 52, Appl	245	45	83.3	127	5	US-10-837-904-29	Sequence 29, Appl
173	47	87.0	107	4	US-10-660-337-26	Sequence 26, Appl	246	45	83.3	247	4	US-10-620-278-21	Sequence 21, Appl

247	45	83.3	247	4	US-10-620-278-23	Sequence 23, Appl	320	43	79.6	113	5	US-10-452-593-57	Sequence 57, Appl
248	45	83.3	247	4	US-10-620-278-25	Sequence 25, Appl	321	42	77.8	11	4	US-10-091-300-57	Sequence 57, Appl
249	45	83.3	247	5	US-10-620-043-21	Sequence 21, Appl	322	42	77.8	11	4	US-10-203-754A-51	Sequence 51, Appl
250	45	83.3	247	5	US-10-620-049-23	Sequence 23, Appl	323	42	77.8	11	4	US-10-436-782-34	Sequence 34, Appl
251	45	83.3	247	5	US-10-620-049-25	Sequence 25, Appl	324	42	77.8	11	4	US-10-436-783-2	Sequence 2, Appl
252	45	83.3	274	3	US-09-813-659-30	Sequence 30, Appl	325	42	77.8	11	5	US-10-482-630-109	Sequence 109, Appl
253	45	83.3	274	4	US-10-283-610A-30	Sequence 30, Appl	326	42	77.8	11	5	US-10-994-129-2	Sequence 2, Appl
254	45	83.3	302	3	US-09-813-659-18	Sequence 18, Appl	327	42	77.8	11	5	US-10-506-997-57	Sequence 57, Appl
255	45	83.3	302	3	US-09-813-659-32	Sequence 32, Appl	328	42	77.8	11	5	US-10-506-997-57	Sequence 57, Appl
256	45	83.3	302	4	US-10-283-610A-18	Sequence 18, Appl	329	42	77.8	11	6	US-11-004-795A-34	Sequence 34, Appl
257	45	83.3	302	4	US-10-283-610A-32	Sequence 32, Appl	330	42	77.8	11	6	US-11-004-795A-34	Sequence 34, Appl
258	45	83.3	504	4	US-10-207-655-348	Sequence 348, Appl	331	42	77.8	106	6	US-11-004-054-16	Sequence 5, Appl
259	45	83.3	504	5	US-10-627-556-113	Sequence 113, Appl	332	42	77.8	107	4	US-10-091-300-37	Sequence 37, Appl
260	45	83.3	555	4	US-10-107-991B-3	Sequence 3, Appl	333	42	77.8	107	4	US-10-016-986-103	Sequence 103, Appl
261	45	83.3	555	5	US-10-627-556-444	Sequence 444, Appl	334	42	77.8	107	4	US-10-436-782-33	Sequence 33, Appl
262	45	83.3	555	5	US-10-627-556-512	Sequence 512, Appl	335	42	77.8	107	4	US-10-436-783-1	Sequence 1, Appl
263	45	83.3	601	3	US-09-480-236-1	Sequence 1, Appl	336	42	77.8	107	5	US-10-482-630-89	Sequence 89, Appl
264	45	83.3	637	4	US-10-296-085A-16	Sequence 16, Appl	337	42	77.8	107	5	US-10-994-129-1	Sequence 1, Appl
265	45	83.3	638	4	US-10-296-085A-21	Sequence 21, Appl	338	42	77.8	107	5	US-10-506-997-37	Sequence 37, Appl
266	45	83.3	642	4	US-10-296-085A-18	Sequence 18, Appl	339	42	77.8	107	6	US-11-004-795A-33	Sequence 33, Appl
267	45	83.3	642	5	US-10-496-179-6	Sequence 6, Appl	340	42	77.8	107	6	US-11-004-794A-33	Sequence 33, Appl
268	45	83.3	643	4	US-10-296-085A-69	Sequence 69, Appl	341	42	77.8	111	4	US-10-203-754A-57	Sequence 57, Appl
269	45	83.3	643	5	US-10-496-179-1	Sequence 1, Appl	342	42	77.8	113	4	US-10-364-743-52	Sequence 52, Appl
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271	45	83.3	656	4	US-10-296-085A-39	Sequence 39, Appl	344	42	77.8	238	6	US-11-031-485-28	Sequence 28, Appl
272	45	83.3	657	4	US-10-296-085A-58	Sequence 58, Appl	345	41	75.9	11	3	US-03-861-234-22	Sequence 22, Appl
273	45	83.3	895	4	US-10-296-085A-19	Sequence 19, Appl	346	41	75.9	11	4	US-10-367-506-22	Sequence 22, Appl
274	45	83.3	895	4	US-10-296-085A-20	Sequence 20, Appl	347	41	75.9	11	4	US-10-203-754A-45	Sequence 45, Appl
275	45	83.3	895	4	US-10-296-085A-27	Sequence 27, Appl	348	41	75.9	105	3	US-09-187-693-46	Sequence 46, Appl
276	45	83.3	895	5	US-10-496-179-4	Sequence 4, Appl	349	41	75.9	105	6	US-11-021-795-46	Sequence 46, Appl
277	45	83.3	896	4	US-10-296-085A-17	Sequence 17, Appl	350	41	75.9	107	3	US-09-158-120A-20	Sequence 20, Appl
278	45	83.3	896	4	US-10-296-085A-18	Sequence 18, Appl	351	41	75.9	107	3	US-09-158-120A-21	Sequence 21, Appl
279	45	83.3	896	4	US-10-296-085A-26	Sequence 26, Appl	352	41	75.9	107	4	US-10-268-883-6	Sequence 6, Appl
280	45	83.3	896	5	US-10-496-179-2	Sequence 2, Appl	353	41	75.9	107	4	US-10-268-883-6	Sequence 6, Appl
281	45	83.3	896	5	US-10-496-179-3	Sequence 3, Appl	354	41	75.9	107	4	US-10-309-762-66	Sequence 66, Appl
282	45	83.3	896	5	US-10-496-179-7	Sequence 7, Appl	355	41	75.9	107	4	US-10-309-762-69	Sequence 69, Appl
283	45	83.3	899	4	US-10-296-085A-28	Sequence 28, Appl	356	41	75.9	108	3	US-09-229-200A-11	Sequence 11, Appl
284	45	83.3	899	5	US-10-496-179-5	Sequence 5, Appl	357	41	75.9	108	3	US-09-229-200A-15	Sequence 15, Appl
285	44	81.5	11	4	US-10-401-344-14	Sequence 14, Appl	358	41	75.9	112	4	US-10-203-754A-55	Sequence 55, Appl
286	44	81.5	11	5	US-10-783-633-61	Sequence 61, Appl	359	41	75.9	127	4	US-10-268-883-5	Sequence 5, Appl
287	44	81.5	11	5	US-10-783-311-152	Sequence 152, Appl	360	41	75.9	139	6	US-11-131-648-16	Sequence 16, Appl
288	44	81.5	11	5	US-10-725-962-102	Sequence 102, Appl	361	41	75.9	139	6	US-11-131-648-41	Sequence 41, Appl
289	44	81.5	102	4	US-10-078-958-14	Sequence 14, Appl	362	41	75.9	142	3	US-09-797-481-2	Sequence 2, Appl
290	44	81.5	102	4	US-10-803-622-173	Sequence 173, Appl	363	41	75.9	142	3	US-09-844-736-4	Sequence 4, Appl
291	44	81.5	102	4	US-10-803-653-173	Sequence 173, Appl	364	41	75.9	142	4	US-10-162-396-4	Sequence 4, Appl
292	44	81.5	106	4	US-10-466-242-4	Sequence 4, Appl	365	41	75.9	142	5	US-10-819-493-4	Sequence 4, Appl
293	44	81.5	107	3	US-09-848-798-173	Sequence 173, Appl	366	41	75.9	152	5	US-10-644-277-56	Sequence 56, Appl
294	44	81.5	107	4	US-10-251-085B-145	Sequence 145, Appl	367	41	75.9	234	5	US-10-938-353-8	Sequence 8, Appl
295	44	81.5	107	4	US-10-737-252-145	Sequence 145, Appl	368	40	74.1	11	3	US-09-155-106-4	Sequence 4, Appl
296	44	81.5	107	5	US-10-994-091A-28	Sequence 28, Appl	369	40	74.1	11	5	US-10-808-538-4	Sequence 4, Appl
297	44	81.5	108	4	US-10-016-986-102	Sequence 102, Appl	370	40	74.1	88	3	US-09-905-243-62	Sequence 62, Appl
298	44	81.5	108	5	US-10-726-332-22	Sequence 22, Appl	371	40	74.1	88	6	US-11-099-331-62	Sequence 62, Appl
299	44	81.5	109	4	US-10-330-613-10	Sequence 10, Appl	372	40	74.1	107	5	US-10-938-992-13	Sequence 13, Appl
300	44	81.5	109	4	US-10-330-530-10	Sequence 10, Appl	373	40	74.1	108	3	US-09-848-798-41	Sequence 41, Appl
301	44	81.5	109	4	US-10-660-357-10	Sequence 10, Appl	374	40	74.1	108	3	US-09-155-106-22	Sequence 22, Appl
302	44	81.5	113	4	US-10-364-743-55	Sequence 55, Appl	375	40	74.1	108	3	US-09-155-106-23	Sequence 23, Appl
303	44	81.5	113	5	US-10-452-593-55	Sequence 55, Appl	376	40	74.1	108	3	US-09-155-106-24	Sequence 24, Appl
304	44	81.5	116	5	US-10-783-311-150	Sequence 150, Appl	377	40	74.1	108	3	US-09-155-106-28	Sequence 28, Appl
305	44	81.5	236	4	US-10-401-344-4	Sequence 4, Appl	378	40	74.1	108	3	US-09-155-106-30	Sequence 30, Appl
306	44	81.5	243	4	US-10-689-921-2	Sequence 2, Appl	379	40	74.1	108	4	US-10-016-986-109	Sequence 109, Appl
307	44	81.5	260	4	US-10-264-049-2296	Sequence 2296, Appl	380	40	74.1	108	5	US-10-808-538-22	Sequence 22, Appl
308	44	81.5	634	4	US-10-416-011-2	Sequence 2, Appl	381	40	74.1	108	5	US-10-808-538-23	Sequence 23, Appl
309	43	79.6	11	4	US-10-279-633-52	Sequence 52, Appl	382	40	74.1	108	5	US-10-808-538-24	Sequence 24, Appl
310	43	79.6	30	3	US-09-956-206A-7	Sequence 7, Appl	383	40	74.1	108	5	US-10-808-538-28	Sequence 28, Appl
311	43	79.6	30	5	US-10-965-616-7	Sequence 7, Appl	384	40	74.1	108	5	US-10-808-538-30	Sequence 30, Appl
312	43	79.6	102	4	US-10-141-908-10	Sequence 10, Appl	385	40	74.1	108	5	US-10-726-332-26	Sequence 26, Appl
313	43	79.6	102	4	US-10-141-908-29	Sequence 29, Appl	386	40	74.1	111	4	US-10-203-754A-19	Sequence 19, Appl
314	43	79.6	105	4	US-10-141-908-31	Sequence 31, Appl	387	40	74.1	236	6	US-11-031-485-20	Sequence 20, Appl
315	43	79.6	108	3	US-09-905-243-73	Sequence 73, Appl	388	40	74.1	7201	6	US-11-097-143-40200	Sequence 40200, A
316	43	79.6	108	4	US-10-141-908-7	Sequence 7, Appl	389	39.5	73.1	12	3	US-09-563-222-38	Sequence 38, Appl
317	43	79.6	108	4	US-10-141-908-14	Sequence 14, Appl	390	39.5	73.1	12	4	US-10-783-950-38	Sequence 38, Appl
318	43	79.6	108	6	US-11-099-331-73	Sequence 73, Appl	391	39.5	73.1	109	3	US-09-929-665-21	Sequence 21, Appl
319	43	79.6	113	4	US-10-364-743-57	Sequence 57, Appl	392	39.5	73.1	109	3	US-09-929-546-21	Sequence 21, Appl

393	39.5	73.1	109	5	US-10-763-424-68	Sequence 68, Appl	466	39	72.2	11	3	US-09-968-561A-106	Sequence 106, App
394	39.5	73.1	109	5	US-10-763-539-68	Sequence 68, Appl	467	39	72.2	11	3	US-09-968-561A-112	Sequence 112, App
395	39	72.2	11	3	US-09-192-854-6	Sequence 6, Appl	468	39	72.2	11	3	US-09-968-561A-118	Sequence 118, App
396	39	72.2	11	3	US-09-968-561A-10	Sequence 10, Appl	469	39	72.2	11	3	US-09-968-561A-124	Sequence 124, App
397	39	72.2	11	3	US-09-968-561A-16	Sequence 16, Appl	470	39	72.2	11	3	US-09-968-561A-136	Sequence 136, App
398	39	72.2	11	3	US-09-968-561A-22	Sequence 22, Appl	471	39	72.2	11	3	US-09-968-561A-154	Sequence 154, App
399	39	72.2	11	3	US-09-968-561A-28	Sequence 28, Appl	472	39	72.2	11	3	US-09-968-561A-160	Sequence 160, App
400	39	72.2	11	3	US-09-968-561A-34	Sequence 34, Appl	473	39	72.2	11	3	US-09-968-561A-166	Sequence 166, App
401	39	72.2	11	3	US-09-968-561A-40	Sequence 40, Appl	474	39	72.2	11	3	US-09-968-561A-172	Sequence 172, App
402	39	72.2	11	3	US-09-968-561A-46	Sequence 46, Appl	475	39	72.2	11	3	US-09-968-561A-178	Sequence 178, App
403	39	72.2	11	3	US-09-968-561A-52	Sequence 52, Appl	476	39	72.2	11	3	US-09-968-561A-202	Sequence 202, App
404	39	72.2	11	3	US-09-968-561A-64	Sequence 64, Appl	477	39	72.2	11	3	US-09-968-561A-208	Sequence 208, App
405	39	72.2	11	3	US-09-968-561A-100	Sequence 100, App	478	39	72.2	11	3	US-09-968-561A-226	Sequence 226, App
406	39	72.2	11	3	US-09-968-561A-106	Sequence 106, App	479	39	72.2	11	3	US-09-968-561A-232	Sequence 232, App
407	39	72.2	11	3	US-09-968-561A-112	Sequence 112, App	480	39	72.2	11	3	US-09-968-561A-244	Sequence 244, App
408	39	72.2	11	3	US-09-968-561A-118	Sequence 118, App	481	39	72.2	11	3	US-09-968-561A-250	Sequence 250, App
409	39	72.2	11	3	US-09-968-561A-124	Sequence 124, App	482	39	72.2	11	3	US-09-968-561A-256	Sequence 256, App
410	39	72.2	11	3	US-09-968-561A-136	Sequence 136, App	483	39	72.2	11	3	US-09-968-561A-280	Sequence 280, App
411	39	72.2	11	3	US-09-968-561A-154	Sequence 154, App	484	39	72.2	11	3	US-09-968-561A-292	Sequence 292, App
412	39	72.2	11	3	US-09-968-561A-160	Sequence 160, App	485	39	72.2	11	3	US-09-968-561A-304	Sequence 304, App
413	39	72.2	11	3	US-09-968-561A-166	Sequence 166, App	486	39	72.2	11	4	US-10-161-445-6	Sequence 6, Appl
414	39	72.2	11	3	US-09-968-561A-172	Sequence 172, App	487	39	72.2	11	4	US-10-203-754A-48	Sequence 48, Appl
415	39	72.2	11	3	US-09-968-561A-178	Sequence 178, App	488	39	72.2	11	4	US-10-279-633-46	Sequence 46, Appl
416	39	72.2	11	3	US-09-968-561A-202	Sequence 202, App	489	39	72.2	11	4	US-10-279-633-51	Sequence 51, Appl
417	39	72.2	11	3	US-09-968-561A-208	Sequence 208, App	490	39	72.2	11	4	US-10-632-706-245	Sequence 245, App
418	39	72.2	11	3	US-09-968-561A-226	Sequence 226, App	491	39	72.2	11	4	US-10-386-578-89	Sequence 89, Appl
419	39	72.2	11	3	US-09-968-561A-232	Sequence 232, App	492	39	72.2	11	5	US-10-783-311-176	Sequence 176, App
420	39	72.2	11	3	US-09-968-561A-244	Sequence 244, App	493	39	72.2	11	5	US-10-783-311-200	Sequence 200, App
421	39	72.2	11	3	US-09-968-561A-250	Sequence 250, App	494	39	72.2	11	6	US-11-074-803-89	Sequence 89, Appl
422	39	72.2	11	3	US-09-968-561A-256	Sequence 256, App	495	39	72.2	11	6	US-11-115-682-10	Sequence 10, Appl
423	39	72.2	11	3	US-09-968-561A-280	Sequence 280, App	496	39	72.2	11	6	US-11-115-682-16	Sequence 16, Appl
424	39	72.2	11	3	US-09-968-561A-292	Sequence 292, App	497	39	72.2	11	6	US-11-115-682-22	Sequence 22, Appl
425	39	72.2	11	3	US-09-968-561A-304	Sequence 304, App	498	39	72.2	11	6	US-11-115-682-28	Sequence 28, Appl
426	39	72.2	11	3	US-09-968-744A-10	Sequence 10, Appl	499	39	72.2	11	6	US-11-115-682-34	Sequence 34, Appl
427	39	72.2	11	3	US-09-968-744A-16	Sequence 16, Appl	500	39	72.2	11	6	US-11-115-682-40	Sequence 40, Appl
428	39	72.2	11	3	US-09-968-744A-22	Sequence 22, Appl	501	39	72.2	11	6	US-11-115-682-46	Sequence 46, Appl
429	39	72.2	11	3	US-09-968-744A-28	Sequence 28, Appl	502	39	72.2	11	6	US-11-115-682-52	Sequence 52, Appl
430	39	72.2	11	3	US-09-968-744A-34	Sequence 34, Appl	503	39	72.2	11	6	US-11-115-682-64	Sequence 64, Appl
431	39	72.2	11	3	US-09-968-744A-40	Sequence 40, Appl	504	39	72.2	11	6	US-11-115-682-100	Sequence 100, App
432	39	72.2	11	3	US-09-968-744A-46	Sequence 46, Appl	505	39	72.2	11	6	US-11-115-682-106	Sequence 106, App
433	39	72.2	11	3	US-09-968-744A-52	Sequence 52, Appl	506	39	72.2	11	6	US-11-115-682-112	Sequence 112, App
434	39	72.2	11	3	US-09-968-744A-64	Sequence 64, Appl	507	39	72.2	11	6	US-11-115-682-118	Sequence 118, App
435	39	72.2	11	3	US-09-968-744A-100	Sequence 100, App	508	39	72.2	11	6	US-11-115-682-124	Sequence 124, App
436	39	72.2	11	3	US-09-968-744A-106	Sequence 106, App	509	39	72.2	11	6	US-11-115-682-136	Sequence 136, App
437	39	72.2	11	3	US-09-968-744A-112	Sequence 112, App	510	39	72.2	11	6	US-11-115-682-154	Sequence 154, App
438	39	72.2	11	3	US-09-968-744A-118	Sequence 118, App	511	39	72.2	11	6	US-11-115-682-160	Sequence 160, App
439	39	72.2	11	3	US-09-968-744A-124	Sequence 124, App	512	39	72.2	11	6	US-11-115-682-166	Sequence 166, App
440	39	72.2	11	3	US-09-968-744A-136	Sequence 136, App	513	39	72.2	11	6	US-11-115-682-172	Sequence 172, App
441	39	72.2	11	3	US-09-968-744A-154	Sequence 154, App	514	39	72.2	11	6	US-11-115-682-178	Sequence 178, App
442	39	72.2	11	3	US-09-968-744A-160	Sequence 160, App	515	39	72.2	11	6	US-11-115-682-202	Sequence 202, App
443	39	72.2	11	3	US-09-968-744A-166	Sequence 166, App	516	39	72.2	11	6	US-11-115-682-208	Sequence 208, App
444	39	72.2	11	3	US-09-968-744A-172	Sequence 172, App	517	39	72.2	11	6	US-11-115-682-226	Sequence 226, App
445	39	72.2	11	3	US-09-968-744A-178	Sequence 178, App	518	39	72.2	11	6	US-11-115-682-232	Sequence 232, App
446	39	72.2	11	3	US-09-968-744A-202	Sequence 202, App	519	39	72.2	11	6	US-11-115-682-244	Sequence 244, App
447	39	72.2	11	3	US-09-968-744A-208	Sequence 208, App	520	39	72.2	11	6	US-11-115-682-250	Sequence 250, App
448	39	72.2	11	3	US-09-968-744A-226	Sequence 226, App	521	39	72.2	11	6	US-11-115-682-256	Sequence 256, App
449	39	72.2	11	3	US-09-968-744A-232	Sequence 232, App	522	39	72.2	11	6	US-11-115-682-280	Sequence 280, App
450	39	72.2	11	3	US-09-968-744A-244	Sequence 244, App	523	39	72.2	11	6	US-11-115-682-292	Sequence 292, App
451	39	72.2	11	3	US-09-968-744A-250	Sequence 250, App	524	39	72.2	11	6	US-11-115-682-304	Sequence 304, App
452	39	72.2	11	3	US-09-968-744A-256	Sequence 256, App	525	39	72.2	11	6	US-11-010-797-10	Sequence 10, Appl
453	39	72.2	11	3	US-09-968-744A-280	Sequence 280, App	526	39	72.2	13	5	US-10-496-869-15	Sequence 15, Appl
454	39	72.2	11	3	US-09-968-744A-292	Sequence 292, App	527	39	72.2	73	4	US-10-078-958-13	Sequence 13, Appl
455	39	72.2	11	3	US-09-968-744A-304	Sequence 304, App	528	39	72.2	76	3	US-09-187-693-37	Sequence 37, Appl
456	39	72.2	11	3	US-09-968-561A-10	Sequence 10, Appl	529	39	72.2	76	6	US-11-021-795-37	Sequence 37, Appl
457	39	72.2	11	3	US-09-968-561A-16	Sequence 16, Appl	530	39	72.2	88	3	US-09-905-243-31	Sequence 31, Appl
458	39	72.2	11	3	US-09-968-561A-22	Sequence 22, Appl	531	39	72.2	88	3	US-09-905-243-36	Sequence 36, Appl
459	39	72.2	11	3	US-09-968-561A-28	Sequence 28, Appl	532	39	72.2	88	4	US-10-066-895-9	Sequence 9, Appl
460	39	72.2	11	3	US-09-968-561A-34	Sequence 34, Appl	533	39	72.2	88	5	US-10-887-954-9	Sequence 9, Appl
461	39	72.2	11	3	US-09-968-561A-40	Sequence 40, Appl	534	39	72.2	88	6	US-11-099-331-31	Sequence 31, Appl
462	39	72.2	11	3	US-09-968-561A-46	Sequence 46, Appl	535	39	72.2	88	6	US-11-099-331-36	Sequence 36, Appl
463	39	72.2	11	3	US-09-968-561A-52	Sequence 52, Appl	536	39	72.2	95	4	US-10-194-975-54	Sequence 54, Appl
464	39	72.2	11	3	US-09-968-561A-64	Sequence 64, Appl	537	39	72.2	95	4	US-10-194-975-55	Sequence 55, Appl
465	39	72.2	11	3	US-09-968-561A-100	Sequence 100, App	538	39	72.2	95	4	US-10-125-687-22	Sequence 22, Appl



539	39	72.2	95	4	US-10-153-382-29	Sequence 29, Appl	612	39	72.2	114	4	US-10-364-743-54	Sequence 54, Appl
540	39	72.2	95	4	US-10-308-817-1	Sequence 1, Appl	613	39	72.2	114	5	US-10-452-593-54	Sequence 54, Appl
541	39	72.2	95	4	US-10-308-817-2	Sequence 2, Appl	614	39	72.2	116	5	US-10-783-311-174	Sequence 174, Appl
542	39	72.2	95	4	US-10-309-762-65	Sequence 65, Appl	615	39	72.2	116	5	US-10-783-311-198	Sequence 198, Appl
543	39	72.2	95	4	US-10-453-698-1	Sequence 1, Appl	616	39	72.2	116	5	US-10-916-758-38	Sequence 38, Appl
544	39	72.2	95	4	US-10-453-698-2	Sequence 2, Appl	617	39	72.2	118	3	US-09-811-737-4	Sequence 4, Appl
545	39	72.2	95	4	US-10-379-397-77	Sequence 77, Appl	618	39	72.2	118	3	US-09-811-737-11	Sequence 11, Appl
546	39	72.2	95	4	US-10-379-397-78	Sequence 78, Appl	619	39	72.2	127	4	US-10-309-762-101	Sequence 101, Appl
547	39	72.2	95	5	US-10-612-497-94	Sequence 94, Appl	620	39	72.2	134	4	US-10-153-382-32	Sequence 32, Appl
548	39	72.2	95	5	US-10-776-649-94	Sequence 94, Appl	621	39	72.2	134	5	US-10-612-497-23	Sequence 23, Appl
549	39	72.2	95	5	US-10-869-355-19	Sequence 19, Appl	622	39	72.2	134	5	US-10-612-497-97	Sequence 97, Appl
550	39	72.2	95	5	US-10-996-191-22	Sequence 22, Appl	623	39	72.2	134	5	US-10-776-649-23	Sequence 23, Appl
551	39	72.2	95	6	US-11-085-368-29	Sequence 29, Appl	624	39	72.2	134	5	US-10-776-649-97	Sequence 97, Appl
552	39	72.2	96	4	US-10-038-591-42	Sequence 42, Appl	625	39	72.2	134	6	US-11-085-368-32	Sequence 32, Appl
553	39	72.2	96	4	US-10-775-444A-42	Sequence 42, Appl	626	39	72.2	134	6	US-11-085-368-75	Sequence 75, Appl
554	39	72.2	102	5	US-10-916-840-42	Sequence 42, Appl	627	39	72.2	137	4	US-10-390-986-24	Sequence 24, Appl
555	39	72.2	103	3	US-09-848-798-42	Sequence 42, Appl	628	39	72.2	150	5	US-10-153-382-33	Sequence 33, Appl
556	39	72.2	105	4	US-10-309-762-155	Sequence 155, Appl	629	39	72.2	150	5	US-10-612-497-24	Sequence 24, Appl
557	39	72.2	105	4	US-10-466-242-42	Sequence 42, Appl	630	39	72.2	150	5	US-10-612-497-98	Sequence 98, Appl
558	39	72.2	106	4	US-10-377-121-5	Sequence 5, Appl	631	39	72.2	150	5	US-10-776-649-24	Sequence 24, Appl
559	39	72.2	106	6	US-11-031-485-128	Sequence 128, Appl	632	39	72.2	150	5	US-10-776-649-98	Sequence 98, Appl
560	39	72.2	107	3	US-09-187-693-48	Sequence 48, Appl	633	39	72.2	150	6	US-11-085-368-33	Sequence 33, Appl
561	39	72.2	107	3	US-09-848-798-33	Sequence 33, Appl	634	39	72.2	150	6	US-11-085-368-79	Sequence 79, Appl
562	39	72.2	107	3	US-09-848-798-37	Sequence 37, Appl	635	39	72.2	157	6	US-11-131-648-27	Sequence 27, Appl
563	39	72.2	107	3	US-09-848-798-38	Sequence 38, Appl	636	39	72.2	157	6	US-11-131-648-63	Sequence 63, Appl
564	39	72.2	107	3	US-09-848-798-39	Sequence 39, Appl	637	39	72.2	164	4	US-10-364-743-24	Sequence 24, Appl
565	39	72.2	107	3	US-09-848-798-40	Sequence 40, Appl	638	39	72.2	164	5	US-10-452-593-24	Sequence 24, Appl
566	39	72.2	107	3	US-09-848-798-156	Sequence 156, Appl	639	39	72.2	214	5	US-10-916-758-20	Sequence 20, Appl
567	39	72.2	107	3	US-09-848-798-158	Sequence 158, Appl	640	39	72.2	214	6	US-11-010-797-4	Sequence 4, Appl
568	39	72.2	107	3	US-09-848-798-168	Sequence 168, Appl	641	39	72.2	224	3	US-09-453-234-48	Sequence 48, Appl
569	39	72.2	107	3	US-09-848-798-175	Sequence 175, Appl	642	39	72.2	236	6	US-11-031-485-58	Sequence 58, Appl
570	39	72.2	107	3	US-09-848-798-176	Sequence 176, Appl	643	39	72.2	240	3	US-09-192-854-2	Sequence 2, Appl
571	39	72.2	107	3	US-09-791-153A-67	Sequence 67, Appl	644	39	72.2	240	3	US-09-968-561A-2	Sequence 2, Appl
572	39	72.2	107	4	US-10-325-694-148	Sequence 148, Appl	645	39	72.2	240	3	US-09-968-744A-2	Sequence 2, Appl
573	39	72.2	107	4	US-10-325-694-152	Sequence 152, Appl	646	39	72.2	240	3	US-09-968-561A-2	Sequence 2, Appl
574	39	72.2	107	4	US-10-016-986-104	Sequence 104, Appl	647	39	72.2	240	5	US-10-744-774-1	Sequence 1, Appl
575	39	72.2	107	4	US-10-016-986-105	Sequence 105, Appl	648	39	72.2	240	6	US-11-115-682-2	Sequence 2, Appl
576	39	72.2	107	4	US-10-309-762-67	Sequence 67, Appl	649	39	72.2	250	3	US-09-880-748-1174	Sequence 1174, Appl
577	39	72.2	107	4	US-10-309-762-68	Sequence 68, Appl	650	39	72.2	250	4	US-10-293-418-1174	Sequence 1174, Appl
578	39	72.2	107	4	US-10-309-762-88	Sequence 88, Appl	651	39	72.2	253	3	US-09-811-737-18	Sequence 18, Appl
579	39	72.2	107	4	US-10-309-762-89	Sequence 89, Appl	652	39	72.2	255	3	US-09-811-737-15	Sequence 15, Appl
580	39	72.2	107	4	US-10-363-349-4	Sequence 4, Appl	653	39	72.2	255	3	US-09-811-737-16	Sequence 16, Appl
581	39	72.2	107	4	US-10-460-595-9	Sequence 9, Appl	654	39	72.2	260	3	US-09-811-737-17	Sequence 17, Appl
582	39	72.2	107	5	US-10-744-774-18	Sequence 18, Appl	655	39	72.2	262	3	US-09-811-737-19	Sequence 19, Appl
583	39	72.2	107	5	US-10-461-885-14	Sequence 14, Appl	656	39	72.2	288	4	US-10-363-349-7	Sequence 7, Appl
584	39	72.2	107	5	US-10-727-155-308	Sequence 308, Appl	657	39	72.2	291	4	US-10-406-830-9	Sequence 9, Appl
585	39	72.2	107	5	US-10-938-353-103	Sequence 103, Appl	658	39	72.2	291	4	US-10-406-830-10	Sequence 10, Appl
586	39	72.2	107	5	US-10-893-576-180	Sequence 180, Appl	659	39	72.2	581	4	US-10-282-122A-48395	Sequence 48395, A
587	39	72.2	107	6	US-11-021-795-48	Sequence 48, Appl	660	38	70.4	11	3	US-09-791-153A-1	Sequence 1, Appl
588	39	72.2	107	6	US-11-031-485-124	Sequence 124, Appl	661	38	70.4	49	3	US-09-850-185-95	Sequence 95, Appl
589	39	72.2	108	3	US-09-848-798-32	Sequence 32, Appl	662	38	70.4	78	4	US-10-424-599-254977	Sequence 254977, A
590	39	72.2	108	3	US-09-848-798-43	Sequence 43, Appl	663	38	70.4	85	3	US-09-795-515-8	Sequence 8, Appl
591	39	72.2	108	3	US-09-848-798-163	Sequence 163, Appl	664	38	70.4	85	4	US-10-704-352-8	Sequence 8, Appl
592	39	72.2	108	4	US-09-848-798-167	Sequence 167, Appl	665	38	70.4	85	4	US-10-704-071-8	Sequence 8, Appl
593	39	72.2	108	4	US-10-409-814A-4	Sequence 4, Appl	666	38	70.4	85	4	US-10-703-963-8	Sequence 8, Appl
594	39	72.2	108	5	US-10-744-774-15	Sequence 15, Appl	667	38	70.4	85	5	US-10-937-971-8	Sequence 8, Appl
595	39	72.2	108	5	US-10-744-774-16	Sequence 16, Appl	668	38	70.4	85	5	US-10-937-949-8	Sequence 8, Appl
596	39	72.2	108	5	US-10-726-332-28	Sequence 28, Appl	669	38	70.4	85	5	US-10-703-344-8	Sequence 8, Appl
597	39	72.2	108	5	US-10-726-332-209	Sequence 209, Appl	670	38	70.4	88	4	US-10-105-545-27	Sequence 27, Appl
598	39	72.2	108	5	US-10-726-332-214	Sequence 214, Appl	671	38	70.4	90	4	US-10-141-908-15	Sequence 15, Appl
599	39	72.2	108	5	US-10-805-177-64	Sequence 64, Appl	672	38	70.4	103	3	US-09-791-153A-68	Sequence 68, Appl
600	39	72.2	108	5	US-10-477-830-90	Sequence 90, Appl	673	38	70.4	104	4	US-10-078-958-27	Sequence 27, Appl
601	39	72.2	108	5	US-10-496-869-33	Sequence 33, Appl	674	38	70.4	104	4	US-10-016-986-106	Sequence 106, Appl
602	39	72.2	108	6	US-11-010-797-6	Sequence 6, Appl	675	38	70.4	105	3	US-09-187-693-42	Sequence 42, Appl
603	39	72.2	108	6	US-11-031-485-126	Sequence 126, Appl	676	38	70.4	105	6	US-11-021-795-42	Sequence 42, Appl
604	39	72.2	109	3	US-09-229-200A-7	Sequence 7, Appl	677	38	70.4	106	4	US-10-466-242-44	Sequence 44, Appl
605	39	72.2	111	4	US-10-203-754A-56	Sequence 56, Appl	678	38	70.4	107	3	US-09-253-794-6	Sequence 6, Appl
606	39	72.2	111	5	US-10-726-332-216	Sequence 216, Appl	679	38	70.4	107	3	US-09-999-025-15	Sequence 15, Appl
607	39	72.2	111	5	US-10-726-332-220	Sequence 220, Appl	680	38	70.4	107	3	US-09-999-040-15	Sequence 15, Appl
608	39	72.2	111	5	US-10-726-332-221	Sequence 221, Appl	681	38	70.4	107	3	US-09-998-817-15	Sequence 15, Appl
609	39	72.2	113	4	US-10-364-743-53	Sequence 53, Appl	682	38	70.4	107	3	US-09-999-021-15	Sequence 15, Appl
610	39	72.2	113	5	US-10-452-593-53	Sequence 53, Appl	683	38	70.4	107	3	US-09-848-798-44	Sequence 44, Appl
611	39	72.2	113	5	US-10-916-758-78	Sequence 78, Appl	684	38	70.4	107	3	US-09-848-798-162	Sequence 162, Appl

685	38	70.4	107	4	US-10-040-997-15	Sequence 15, Appl	758	37	68.5	95	4	US-10-379-392-72	Sequence 72, Appl
686	38	70.4	107	4	US-10-268-501-5	Sequence 5, Appl	759	37	68.5	95	5	US-10-986-089A-42	Sequence 42, Appl
687	38	70.4	107	4	US-10-223-880-15	Sequence 44, Appl	760	37	68.5	96	4	US-10-041-860-327	Sequence 327, App
688	38	70.4	107	4	US-10-366-709-44	Sequence 15, Appl	761	37	68.5	96	4	US-10-041-860-329	Sequence 329, App
689	38	70.4	107	4	US-10-608-626-5	Sequence 5, Appl	762	37	68.5	102	4	US-10-010-729-35	Sequence 35, Appl
690	38	70.4	107	4	US-10-600-152-14	Sequence 14, Appl	763	37	68.5	102	5	US-10-502-307-8	Sequence 8, Appl
691	38	70.4	107	4	US-10-619-754-5	Sequence 5, Appl	764	37	68.5	102	5	US-10-916-840-22	Sequence 22, Appl
692	38	70.4	107	4	US-10-680-734-6	Sequence 6, Appl	765	37	68.5	103	4	US-10-379-392-101	Sequence 101, App
693	38	70.4	107	5	US-10-835-641-18	Sequence 18, Appl	766	37	68.5	103	4	US-10-379-392-173	Sequence 173, App
694	38	70.4	107	5	US-10-719-310-5	Sequence 5, Appl	767	37	68.5	103	4	US-10-379-392-176	Sequence 176, App
695	38	70.4	107	5	US-10-763-424-56	Sequence 56, Appl	768	37	68.5	103	5	US-10-473-977-66	Sequence 66, Appl
696	38	70.4	107	5	US-10-755-382-6	Sequence 6, Appl	769	37	68.5	105	3	US-09-187-693-52	Sequence 52, Appl
697	38	70.4	107	5	US-10-763-539-56	Sequence 56, Appl	770	37	68.5	105	4	US-10-466-242-22	Sequence 22, Appl
698	38	70.4	107	6	US-11-044-749-5	Sequence 5, Appl	771	37	68.5	105	6	US-11-021-795-52	Sequence 52, Appl
699	38	70.4	107	6	US-11-154-465-5	Sequence 5, Appl	772	37	68.5	107	4	US-10-041-860-32	Sequence 32, Appl
700	38	70.4	108	3	US-09-056-160B-12	Sequence 12, Appl	773	37	68.5	107	4	US-10-041-860-34	Sequence 34, Appl
701	38	70.4	108	3	US-09-229-200A-14	Sequence 14, Appl	774	37	68.5	107	4	US-10-041-860-223	Sequence 223, App
702	38	70.4	108	3	US-09-848-798-181	Sequence 181, App	775	37	68.5	107	4	US-10-041-860-224	Sequence 224, App
703	38	70.4	108	3	US-09-795-798-3	Sequence 3, Appl	776	37	68.5	107	4	US-10-041-860-257	Sequence 257, App
704	38	70.4	108	4	US-10-267-286A-7	Sequence 7, Appl	777	37	68.5	107	4	US-10-041-860-258	Sequence 258, App
705	38	70.4	108	4	US-10-428-662-100	Sequence 100, App	778	37	68.5	107	4	US-10-041-860-334	Sequence 334, App
706	38	70.4	108	4	US-10-234-671-12	Sequence 12, Appl	779	37	68.5	107	4	US-10-127-890-123	Sequence 123, App
707	38	70.4	108	4	US-10-422-049-7	Sequence 7, Appl	780	37	68.5	107	4	US-10-127-890-125	Sequence 125, App
708	38	70.4	108	4	US-10-371-942-8	Sequence 8, Appl	781	37	68.5	107	4	US-10-016-986-82	Sequence 82, Appl
709	38	70.4	108	4	US-10-371-942-20	Sequence 20, Appl	782	37	68.5	107	4	US-10-016-986-84	Sequence 84, Appl
710	38	70.4	108	4	US-10-307-276B-13	Sequence 13, Appl	783	37	68.5	107	4	US-10-340-189-26	Sequence 26, Appl
711	38	70.4	108	4	US-10-727-737-3	Sequence 3, Appl	784	37	68.5	107	4	US-10-340-189-27	Sequence 27, Appl
712	38	70.4	108	5	US-10-744-774-17	Sequence 17, Appl	785	37	68.5	107	4	US-10-340-189-87	Sequence 87, Appl
713	38	70.4	108	5	US-10-631-722-43	Sequence 43, Appl	786	37	68.5	107	4	US-10-325-696-26	Sequence 26, Appl
714	38	70.4	108	5	US-10-726-332-18	Sequence 18, Appl	787	37	68.5	107	4	US-10-325-696-27	Sequence 27, Appl
715	38	70.4	108	5	US-10-903-858-5	Sequence 5, Appl	788	37	68.5	107	4	US-10-325-696-65	Sequence 65, Appl
716	38	70.4	108	5	US-10-861-049-38	Sequence 38, Appl	789	37	68.5	107	4	US-10-309-762-86	Sequence 86, Appl
717	38	70.4	108	5	US-10-861-049-38	Sequence 38, Appl	790	37	68.5	107	4	US-10-665-383-44	Sequence 44, Appl
718	38	70.4	108	6	US-11-061-956-13	Sequence 13, Appl	791	37	68.5	107	4	US-10-665-383-48	Sequence 48, Appl
719	38	70.4	108	6	US-11-021-874-38	Sequence 38, Appl	792	37	68.5	107	4	US-10-774-076-3	Sequence 3, Appl
720	38	70.4	109	3	US-09-811-123-6	Sequence 6, Appl	793	37	68.5	107	4	US-10-774-076-14	Sequence 14, Appl
721	38	70.4	109	5	US-10-835-641-3	Sequence 3, Appl	794	37	68.5	107	5	US-10-727-155-264	Sequence 264, App
722	38	70.4	110	4	US-10-044-896-4	Sequence 4, Appl	795	37	68.5	107	5	US-10-727-155-306	Sequence 306, App
723	38	70.4	111	4	US-10-251-215-42	Sequence 42, Appl	796	37	68.5	107	5	US-10-717-243-123	Sequence 123, App
724	38	70.4	111	5	US-10-916-840-100	Sequence 100, App	797	37	68.5	107	5	US-10-717-243-125	Sequence 125, App
725	38	70.4	112	5	US-10-916-758-66	Sequence 66, Appl	798	37	68.5	107	5	US-10-959-326-23	Sequence 23, Appl
726	38	70.4	126	4	US-10-469-125-8	Sequence 8, Appl	799	37	68.5	107	5	US-10-959-326-25	Sequence 25, Appl
727	38	70.4	128	5	US-10-473-287-35	Sequence 35, Appl	800	37	68.5	107	5	US-10-959-326-29	Sequence 29, Appl
728	38	70.4	128	5	US-10-473-287-50	Sequence 50, Appl	801	37	68.5	107	5	US-10-959-326-30	Sequence 30, Appl
729	38	70.4	182	4	US-10-424-599-246625	Sequence 246625,	802	37	68.5	107	5	US-10-959-326-31	Sequence 31, Appl
730	38	70.4	215	3	US-09-791-153A-45	Sequence 45, Appl	803	37	68.5	107	5	US-10-959-326-32	Sequence 32, Appl
731	37	68.5	11	3	US-09-802-083-10	Sequence 10, Appl	804	37	68.5	107	6	US-11-021-715-97	Sequence 97, Appl
732	37	68.5	11	4	US-10-283-349-43	Sequence 43, Appl	805	37	68.5	107	6	US-11-133-775-26	Sequence 26, Appl
733	37	68.5	11	4	US-10-165-732A-10	Sequence 10, Appl	806	37	68.5	107	6	US-11-133-775-27	Sequence 27, Appl
734	37	68.5	11	4	US-10-172-785-10	Sequence 10, Appl	807	37	68.5	107	6	US-11-133-775-65	Sequence 65, Appl
735	37	68.5	11	4	US-10-364-953-7	Sequence 7, Appl	808	37	68.5	108	4	US-10-041-860-328	Sequence 328, App
736	37	68.5	11	4	US-10-279-633-57	Sequence 57, Appl	809	37	68.5	108	5	US-10-725-962-36	Sequence 36, Appl
737	37	68.5	11	4	US-10-745-455-10	Sequence 10, Appl	810	37	68.5	108	5	US-10-725-962-38	Sequence 38, Appl
738	37	68.5	11	5	US-10-725-962-107	Sequence 107, App	811	37	68.5	108	5	US-10-725-962-39	Sequence 39, Appl
739	37	68.5	11	5	US-10-813-977-21	Sequence 21, Appl	812	37	68.5	108	5	US-10-725-962-40	Sequence 40, Appl
740	37	68.5	11	5	US-10-959-326-17	Sequence 17, Appl	813	37	68.5	108	5	US-10-625-307A-39	Sequence 39, Appl
741	37	68.5	51	4	US-10-340-189-73	Sequence 73, Appl	814	37	68.5	108	5	US-10-625-307A-67	Sequence 67, Appl
742	37	68.5	51	4	US-10-340-189-74	Sequence 74, Appl	815	37	68.5	109	3	US-09-802-083-4	Sequence 4, Appl
743	37	68.5	88	3	US-09-905-243-29	Sequence 29, Appl	816	37	68.5	109	4	US-10-165-732A-4	Sequence 4, Appl
744	37	68.5	88	3	US-09-905-243-33	Sequence 33, Appl	817	37	68.5	109	4	US-10-172-785-4	Sequence 4, Appl
745	37	68.5	88	6	US-11-099-331-29	Sequence 29, Appl	818	37	68.5	109	4	US-10-745-455-4	Sequence 4, Appl
746	37	68.5	88	6	US-11-099-331-33	Sequence 33, Appl	819	37	68.5	110	4	US-10-251-215-41	Sequence 41, Appl
747	37	68.5	95	4	US-10-194-975-58	Sequence 58, Appl	820	37	68.5	110	5	US-10-251-215-43	Sequence 43, Appl
748	37	68.5	95	4	US-10-194-975-61	Sequence 61, Appl	821	37	68.5	110	5	US-10-996-316-209	Sequence 209, App
749	37	68.5	95	4	US-10-041-860-9	Sequence 9, Appl	822	37	68.5	112	5	US-10-355-780-1	Sequence 1, Appl
750	37	68.5	95	4	US-10-041-860-333	Sequence 333, App	823	37	68.5	115	5	US-10-916-758-30	Sequence 30, Appl
751	37	68.5	95	4	US-10-041-860-335	Sequence 335, App	824	37	68.5	125	5	US-10-473-287-48	Sequence 48, Appl
752	37	68.5	95	4	US-10-041-860-345	Sequence 345, App	825	37	68.5	127	4	US-10-283-349-29	Sequence 29, Appl
753	37	68.5	95	4	US-10-308-817-5	Sequence 5, Appl	826	37	68.5	127	4	US-10-283-349-71	Sequence 71, Appl
754	37	68.5	95	4	US-10-308-817-8	Sequence 8, Appl	827	37	68.5	127	4	US-10-283-349-88	Sequence 88, Appl
755	37	68.5	95	4	US-10-453-698-5	Sequence 5, Appl	828	37	68.5	127	4	US-10-283-349-92	Sequence 92, Appl
756	37	68.5	95	4	US-10-453-698-8	Sequence 8, Appl	829	37	68.5	127	4	US-10-283-349-98	Sequence 98, Appl
757	37	68.5	95	4	US-10-379-392-68	Sequence 68, Appl	830	37	68.5	127	4	US-10-283-349-103	Sequence 103, Appl

831	37	68.5	127	4	US-10-395-894-17	Sequence 17, Appl	904	36	66.7	239	4	US-10-719-642-11	Sequence 11, Appl
832	37	68.5	127	4	US-10-695-667-17	Sequence 17, Appl	905	36	66.7	251	4	US-10-239-656-65	Sequence 65, Appl
833	37	68.5	127	4	US-10-774-076-11	Sequence 11, Appl	906	36	66.7	649	4	US-10-437-963-179618	Sequence 179618,
834	37	68.5	127	5	US-10-976-352-17	Sequence 17, Appl	907	36	66.7	997	4	US-10-437-963-179614	Sequence 179614,
835	37	68.5	127	5	US-10-976-352-17	Sequence 17, Appl	908	35	64.8	11	3	US-09-192-854-105	Sequence 105, App
836	37	68.5	129	6	US-11-003-839-38	Sequence 38, Appl	909	35	64.8	11	3	US-09-968-561A-184	Sequence 184, App
837	37	68.5	130	4	US-10-424-599-175944	Sequence 175944,	910	35	64.8	11	3	US-09-977-797A-18	Sequence 18, Appl
838	37	68.5	130	5	US-10-763-424-69	Sequence 69, Appl	911	35	64.8	11	3	US-09-977-797A-22	Sequence 22, Appl
839	37	68.5	130	5	US-10-763-539-69	Sequence 69, Appl	912	35	64.8	11	3	US-09-968-744A-184	Sequence 184, App
840	37	68.5	136	5	US-10-473-287-49	Sequence 49, Appl	913	35	64.8	11	3	US-09-968-561A-184	Sequence 184, App
841	37	68.5	214	4	US-10-364-953-4	Sequence 4, Appl	914	35	64.8	11	4	US-10-305-231-110	Sequence 110, App
842	37	68.5	214	4	US-10-364-953-11	Sequence 11, Appl	915	35	64.8	11	4	US-10-279-633-55	Sequence 55, Appl
843	37	68.5	214	4	US-10-379-392-170	Sequence 170, App	916	35	64.8	11	4	US-10-279-633-58	Sequence 58, Appl
844	37	68.5	214	4	US-10-379-392-175	Sequence 175, App	917	35	64.8	11	5	US-10-745-775-6	Sequence 6, Appl
845	37	68.5	214	5	US-10-880-028-41	Sequence 41, Appl	918	35	64.8	11	5	US-10-745-775-18	Sequence 18, Appl
846	37	68.5	214	5	US-10-880-320-41	Sequence 41, Appl	919	35	64.8	11	5	US-10-503-504-2	Sequence 2, Appl
847	37	68.5	226	5	US-10-813-977-17	Sequence 17, Appl	920	35	64.8	11	5	US-10-894-672-4	Sequence 4, Appl
848	37	68.5	237	4	US-10-020-786-8	Sequence 8, Appl	921	35	64.8	11	5	US-10-484-280-5	Sequence 5, Appl
849	37	68.5	237	4	US-10-227-694-4	Sequence 4, Appl	922	35	64.8	11	5	US-10-996-316-4	Sequence 4, Appl
850	37	68.5	237	5	US-10-754-212-5	Sequence 5, Appl	923	35	64.8	11	6	US-11-036-098-2	Sequence 2, Appl
851	37	68.5	237	5	US-10-697-995-2	Sequence 2, Appl	924	35	64.8	11	6	US-11-115-682-184	Sequence 184, App
852	37	68.5	237	5	US-10-697-995-5	Sequence 5, Appl	925	35	64.8	11	6	US-09-900-590-82	Sequence 82, Appl
853	37	68.5	237	5	US-10-697-995-17	Sequence 17, Appl	926	35	64.8	13	3	US-10-305-231-82	Sequence 82, Appl
854	37	68.5	237	5	US-10-697-995-20	Sequence 20, Appl	927	35	64.8	13	4	US-10-463-847-82	Sequence 82, Appl
855	37	68.5	237	6	US-11-071-291-8	Sequence 8, Appl	928	35	64.8	61	4	US-10-379-151-18	Sequence 18, Appl
856	37	68.5	240	4	US-10-127-890-147	Sequence 147, App	929	35	64.8	61	4	US-10-736-188-18	Sequence 18, Appl
857	37	68.5	240	4	US-10-127-890-148	Sequence 148, App	930	35	64.8	84	5	US-10-926-683-816	Sequence 816, App
858	37	68.5	240	5	US-10-717-243-147	Sequence 147, App	931	35	64.8	103	4	US-10-379-392-99	Sequence 99, Appl
859	37	68.5	240	5	US-10-717-243-148	Sequence 148, App	932	35	64.8	103	4	US-10-379-392-111	Sequence 111, App
860	37	68.5	244	6	US-11-090-847-69	Sequence 69, Appl	933	35	64.8	106	4	US-10-466-242-38	Sequence 38, Appl
861	37	68.5	1091	6	US-11-097-143-6909	Sequence 6909, Ap	934	35	64.8	106	4	US-10-466-242-56	Sequence 56, Appl
862	37	68.5	4128	4	US-10-205-194-1	Sequence 1, Appl	935	35	64.8	107	4	US-10-325-694-142	Sequence 142, App
863	36	66.7	11	4	US-10-364-953-6	Sequence 6, Appl	936	35	64.8	107	4	US-10-325-694-149	Sequence 149, App
864	36	66.7	11	4	US-10-279-633-60	Sequence 60, Appl	937	35	64.8	107	4	US-10-663-244-79	Sequence 79, Appl
865	36	66.7	11	5	US-10-745-775-20	Sequence 20, Appl	938	35	64.8	107	5	US-10-727-155-142	Sequence 142, App
866	36	66.7	11	5	US-10-745-775-22	Sequence 22, Appl	939	35	64.8	107	5	US-10-727-155-150	Sequence 150, App
867	36	66.7	11	5	US-10-456-092A-4	Sequence 4, Appl	940	35	64.8	107	5	US-10-727-155-156	Sequence 156, App
868	36	66.7	11	5	US-10-687-035-18	Sequence 18, Appl	941	35	64.8	107	5	US-10-727-155-160	Sequence 160, App
869	36	66.7	40	4	US-10-724-972A-6031	Sequence 6031, Ap	942	35	64.8	107	5	US-10-503-504-7	Sequence 7, Appl
870	36	66.7	105	5	US-10-456-092A-12	Sequence 12, Appl	943	35	64.8	107	5	US-10-484-280-2	Sequence 2, Appl
871	36	66.7	106	5	US-10-456-092A-9	Sequence 9, Appl	944	35	64.8	107	5	US-10-484-280-12	Sequence 12, Appl
872	36	66.7	106	5	US-10-456-092A-10	Sequence 10, Appl	945	35	64.8	107	5	US-10-484-280-27	Sequence 27, Appl
873	36	66.7	106	5	US-10-456-092A-11	Sequence 11, Appl	946	35	64.8	107	5	US-10-977-369-2	Sequence 2, Appl
874	36	66.7	107	3	US-09-848-798-112	Sequence 172, App	947	35	64.8	107	5	US-10-977-369-8	Sequence 8, Appl
875	36	66.7	107	3	US-09-848-798-174	Sequence 174, App	948	35	64.8	107	5	US-10-977-369-9	Sequence 9, Appl
876	36	66.7	107	4	US-10-723-434-35	Sequence 35, Appl	949	35	64.8	107	5	US-10-977-369-10	Sequence 10, Appl
877	36	66.7	107	4	US-10-723-434-40	Sequence 40, Appl	950	35	64.8	107	5	US-10-977-369-11	Sequence 11, Appl
878	36	66.7	107	4	US-10-723-434-43	Sequence 43, Appl	951	35	64.8	107	5	US-10-977-369-12	Sequence 12, Appl
879	36	66.7	108	5	US-10-768-952-25	Sequence 25, Appl	952	35	64.8	107	5	US-10-977-369-41	Sequence 41, Appl
880	36	66.7	110	3	US-09-056-160B-109	Sequence 109, App	953	35	64.8	107	5	US-10-977-369-42	Sequence 42, Appl
881	36	66.7	110	3	US-09-056-160B-111	Sequence 111, App	954	35	64.8	107	5	US-10-977-369-43	Sequence 43, Appl
882	36	66.7	110	3	US-09-056-160B-113	Sequence 113, App	955	35	64.8	107	5	US-10-977-369-44	Sequence 44, Appl
883	36	66.7	110	3	US-09-056-160B-115	Sequence 115, App	956	35	64.8	107	5	US-10-977-369-45	Sequence 45, Appl
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885	36	66.7	110	4	US-10-234-671-109	Sequence 109, App	958	35	64.8	107	5	US-10-977-369-47	Sequence 47, Appl
886	36	66.7	110	4	US-10-234-671-111	Sequence 111, App	959	35	64.8	107	5	US-10-977-369-48	Sequence 48, Appl
887	36	66.7	110	4	US-10-234-671-113	Sequence 113, App	960	35	64.8	107	5	US-10-977-369-49	Sequence 49, Appl
888	36	66.7	110	4	US-10-624-153-95	Sequence 95, Appl	961	35	64.8	107	5	US-10-977-369-50	Sequence 50, Appl
889	36	66.7	110	5	US-10-683-043-2	Sequence 2, Appl	962	35	64.8	107	5	US-10-977-369-51	Sequence 51, Appl
890	36	66.7	110	5	US-10-683-043-3	Sequence 3, Appl	963	35	64.8	107	5	US-10-977-369-52	Sequence 52, Appl
891	36	66.7	110	5	US-10-683-043-4	Sequence 4, Appl	964	35	64.8	107	5	US-10-977-369-53	Sequence 53, Appl
892	36	66.7	110	5	US-10-683-043-6	Sequence 6, Appl	965	35	64.8	107	5	US-10-977-369-54	Sequence 54, Appl
893	36	66.7	110	5	US-10-683-043-7	Sequence 7, Appl	966	35	64.8	107	5	US-10-977-369-55	Sequence 55, Appl
894	36	66.7	110	5	US-10-683-043-8	Sequence 8, Appl	967	35	64.8	107	5	US-10-977-369-56	Sequence 56, Appl
895	36	66.7	110	5	US-10-974-591-107	Sequence 107, App	968	35	64.8	107	5	US-10-977-369-57	Sequence 57, Appl
896	36	66.7	110	5	US-10-974-591-109	Sequence 109, App	969	35	64.8	107	5	US-10-977-369-58	Sequence 58, Appl
897	36	66.7	110	5	US-10-974-591-111	Sequence 111, App	970	35	64.8	107	5	US-10-977-369-59	Sequence 59, Appl
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899	36	66.7	124	5	US-10-066-895-10	Sequence 10, Appl	972	35	64.8	107	5	US-10-977-369-61	Sequence 61, Appl
900	36	66.7	124	5	US-10-887-954-10	Sequence 10, Appl	973	35	64.8	107	5	US-10-977-369-62	Sequence 62, Appl
901	36	66.7	128	5	US-10-687-035-31	Sequence 31, Appl	974	35	64.8	107	5	US-10-977-369-63	Sequence 63, Appl
902	36	66.7	150	4	US-10-719-642-57	Sequence 57, Appl	975	35	64.8	107	5	US-10-977-369-64	Sequence 64, Appl
903	36	66.7	214	4	US-10-364-953-3	Sequence 3, Appl	976	35	64.8	107	5	US-10-977-369-65	Sequence 65, Appl

977 35 64.8 107 5 US-10-977-369-66  
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981 35 64.8 107 5 US-10-977-369-70  
982 35 64.8 107 6 US-11-036-098-16  
983 35 64.8 108 4 US-10-268-883-12  
984 35 64.8 109 5 US-10-745-775-2  
985 35 64.8 109 5 US-10-783-730-2  
986 35 64.8 111 5 US-10-726-332-20  
987 35 64.8 111 5 US-10-726-332-22  
988 35 64.8 113 4 US-10-364-743-44  
989 35 64.8 113 4 US-10-364-743-45  
990 35 64.8 113 4 US-10-364-743-46  
991 35 64.8 113 5 US-10-452-593-44  
992 35 64.8 113 5 US-10-452-593-45  
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995 35 64.8 127 4 US-10-351-748-37  
996 35 64.8 127 4 US-10-351-748-37  
997 35 64.8 129 4 US-10-351-748-39  
998 35 64.8 129 4 US-10-351-748-39  
999 35 64.8 130 4 US-10-268-883-11  
1000 35 64.8 156 4 US-10-437-963-146204

## ALIGNMENTS

RESULT 1  
US-09-056-160B-4  
; Sequence 4, Application US/09056160B  
; Patent No. US2002032315A1  
; GENERAL INFORMATION:  
; APPLICANT: Baca, Manuel  
; APPLICANT: Wells, James A.  
; APPLICANT: Presta, Leonard G.  
; APPLICANT: Lowman, Henry B.  
; APPLICANT: Chen, Yvonne M.  
; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES  
; NUMBER OF SEQUENCES: 131  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/056,160B  
; FILING DATE: 06-Apr-1998  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/054,856  
; FILING DATE: 06-AUG-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hasak, Janet E.  
; REGISTRATION NUMBER: 28,616  
; REFERENCE/DOCKET NUMBER: P1093R2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-1896  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
; US-09-056-160B-4

Sequence 66, Appl  
Sequence 67, Appl  
Sequence 68, Appl  
Sequence 69, Appl  
Sequence 70, Appl  
Sequence 16, Appl  
Sequence 12, Appl  
Sequence 2, Appl  
Sequence 2, Appl  
Sequence 20, Appl  
Sequence 22, App  
Sequence 44, Appl  
Sequence 45, Appl  
Sequence 46, Appl  
Sequence 44, Appl  
Sequence 45, Appl  
Sequence 46, Appl  
Sequence 38599, A  
Sequence 37, Appl  
Sequence 37, Appl  
Sequence 39, Appl  
Sequence 39, Appl  
Sequence 11, Appl  
Sequence 146204,

Query Match 100.0%; Score 54; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.013;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 1 SASQDISNYLN 11  
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Db 1 SASQDISNYLN 11  
| | | | | | | | | |

## RESULT 2

US-10-234-671-4  
; Sequence 4, Application US/10234671  
; Publication No. US20030190317A1  
; GENERAL INFORMATION:  
; APPLICANT: Baca, Manuel  
; APPLICANT: Wells, James A.  
; APPLICANT: Presta, Leonard G.  
; APPLICANT: Lowman, Henry B.  
; APPLICANT: Chen, Yvonne M.  
; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES  
; NUMBER OF SEQUENCES: 131  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/234,671  
; FILING DATE: 03-Sep-2002  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/056160  
; FILING DATE: 06-APR-1998  
; APPLICATION NUMBER: 60/126446  
; FILING DATE: 07-APR-1997  
; APPLICATION NUMBER: 60/054856  
; FILING DATE: 06-AUG-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Cui, Steven X.  
; REGISTRATION NUMBER: 44,637  
; REFERENCE/DOCKET NUMBER: P1093R2C1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-8674  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
US-10-234-671-4

Query Match 100.0%; Score 54; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.013;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 SASQDISNYLN 11  
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Db 1 SASQDISNYLN 11  
| | | | | | | | | |

## RESULT 3

US-10-974-591-4  
; Sequence 4, Application US/10974591  
; Publication No. US20050112126A1

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; GENERAL INFORMATION:
; APPLICANT: Baca, Manuel
;           Wells, James A.
;           Presta, Leonard G.
;           Lowman, Henry B.
;           Chen, Yvonne M.
; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
; NUMBER OF SEQUENCES: 131
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Genentech, Inc.
;   STREET: 1 DNA Way
;   CITY: South San Francisco
;   STATE: California
;   COUNTRY: USA
;   ZIP: 94080
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/10/974,591
;   FILING DATE: 26-Oct-2004
; CLASSIFICATION DATA:
;   PRIOR APPLICATION DATA: <Unknown>
;   APPLICATION NUMBER: 09/723752
;   FILING DATE: 27-NOV-2000
;   APPLICATION NUMBER: 08/908469
;   FILING DATE: 06-AUG-1997
;   APPLICATION NUMBER: 08/833504
;   FILING DATE: 07-APR-1997
; ATTORNEY/AGENT INFORMATION:
;   NAME: Cui, Steven X.
;   REGISTRATION NUMBER: 44,637
; REFERENCE/DOCKET NUMBER: P1093PID1C1
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 650/225-8674
;   TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 4:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 11 amino acids
;     TYPE: Amino Acid
;     TOPOLOGY: Linear
;   SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-974-591-4
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Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      1 SASQDISNYLN 11
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RESULT 4
US-10-379-392-100
; Sequence 100, Application US/10379392
; Publication No. US20040110226A1
; GENERAL INFORMATION:
; APPLICANT: Lazar, Gregory Alan
; APPLICANT: Desjarlais, John Rudolf
; APPLICANT: Marshall, Shannon Alicia
; APPLICANT: Dahiyat, Basil I.
; TITLE OF INVENTION: ANTIBODY OPTIMIZATION
; FILE REFERENCE: A-71386-3 463077-236
; CURRENT APPLICATION NUMBER: US/10/379,392
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/360,843
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 60/384,197
; PRIOR FILING DATE: 2002-05-29
; NUMBER OF SEQ ID NOS: 184
; SOFTWARE: PatentIn version 3.2

Query Match          100.0%; Score 54; DB 4; Length 103;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SASQDISNYLN 11
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Db      24 SASQDISNYLN 34
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RESULT 5
US-10-379-392-121
; Sequence 121, Application US/10379392
; Publication No. US20040110226A1
; GENERAL INFORMATION:
; APPLICANT: Lazar, Gregory Alan
; APPLICANT: Desjarlais, John Rudolf
; APPLICANT: Marshall, Shannon Alicia
; APPLICANT: Dahiyat, Basil I.
; TITLE OF INVENTION: ANTIBODY OPTIMIZATION
; FILE REFERENCE: A-71386-3 463077-236
; CURRENT APPLICATION NUMBER: US/10/379,392
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/360,843
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 60/384,197
; PRIOR FILING DATE: 2002-05-29
; NUMBER OF SEQ ID NOS: 184
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 121
; LENGTH: 103
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-379-392-121
Query Match          100.0%; Score 54; DB 4; Length 103;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SASQDISNYLN 11
      |||||
Db      24 SASQDISNYLN 34
      |||||

RESULT 6
US-10-379-392-123
; Sequence 123, Application US/10379392
; Publication No. US20040110226A1
; GENERAL INFORMATION:
; APPLICANT: Lazar, Gregory Alan
; APPLICANT: Desjarlais, John Rudolf
; APPLICANT: Marshall, Shannon Alicia
; APPLICANT: Dahiyat, Basil I.
; TITLE OF INVENTION: ANTIBODY OPTIMIZATION
; FILE REFERENCE: A-71386-3 463077-236
; CURRENT APPLICATION NUMBER: US/10/379,392
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/360,843
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 60/384,197
; PRIOR FILING DATE: 2002-05-29
; NUMBER OF SEQ ID NOS: 184
; SOFTWARE: PatentIn version 3.2
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SEQ ID NO 123
LENGTH: 103
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Synthetic
US-10-379-392-123

Query Match          100.0%; Score 54; DB 4; Length 103;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches    11; Conservative   0; Mismatches     0; Indels      0; Gaps       0;

QY      1 SASQDISNYLN 11
         |||||
Db       24 SASQDISNYLN 34

RESULT 7
US-10-379-392-129
Sequence 129, Application US/10379392
Publication No. US20040110226A1
GENERAL INFORMATION:
APPLICANT: Lazar, Gregory Alan
APPLICANT: Desjarlais, John Rudolf
APPLICANT: Marshall, Shannon Alicia
APPLICANT: Dahiyat, Bassil I.
TITLE OF INVENTION: ANTIBODY OPTIMIZATION
FILE REFERENCE: A-71386-3 463077-236
CURRENT APPLICATION NUMBER: US/10/379,392
PRIORITY FILING DATE: 2003-03-03
PRIOR APPLICATION NUMBER: US 60/360,843
PRIOR FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: US 60/384,197
NUMBER OF SEQ ID NOS: 184
SOFTWARE: PatentIn version 3.2
SEQ ID NO 129
LENGTH: 103
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Synthetic
US-10-379-392-123

Query Match          100.0%; Score 54; DB 4; Length 103;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches    11; Conservative   0; Mismatches     0; Indels      0; Gaps       0;

QY      1 SASQDISNYLN 11
         |||||
Db       24 SASQDISNYLN 34

RESULT 8
US-10-379-392-131
Sequence 131, Application US/10379392
Publication No. US20040110226A1
GENERAL INFORMATION:
APPLICANT: Lazar, Gregory Alan
APPLICANT: Desjarlais, John Rudolf
APPLICANT: Marshall, Shannon Alicia
APPLICANT: Dahiyat, Bassil I.
TITLE OF INVENTION: ANTIBODY OPTIMIZATION
FILE REFERENCE: A-71386-3 463077-236
CURRENT APPLICATION NUMBER: US/10/379,392
PRIORITY FILING DATE: 2003-03-03
PRIOR APPLICATION NUMBER: US 60/360,843
PRIOR FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: US 60/384,197
NUMBER OF SEQ ID NOS: 184
SOFTWARE: PatentIn version 3.2
SEQ ID NO 131
LENGTH: 103
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Synthetic
US-10-379-392-131

Query Match          100.0%; Score 54; DB 4; Length 103;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches    11; Conservative   0; Mismatches     0; Indels      0; Gaps       0;

QY      1 SASQDISNYLN 11
         |||||
Db       24 SASQDISNYLN 34

RESULT 9
US-09-056-160B-13
Sequence 13, Application US/09056160B
Patent No. US20020032315A1
GENERAL INFORMATION:
APPLICANT: Baca, Manuel
APPLICANT: Wells, James A.
APPLICANT: Presta, Leonard G.
APPLICANT: Lowman, Henry B.
APPLICANT: Chen, Yvonne M.
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056.160B
FILING DATE: 06-Apr-1998
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/054,856
FILING DATE: 06-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: PI093R2
TELECOMMUNICATION INFORMATION:

```

TELEPHONE: 650/225-1896  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 107 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-09-056-160B-13

Query Match 100.0%; Score 54; DB 3; Length 107;  
Best Local Similarity 100.0%; Pred. No. 0.14;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SASQDISNYLN 11  
Db 24 SASQDISNYLN 34

## RESULT 10

US-09-056-160B-15  
Sequence 15, Application US/09056160B  
Patent No. US20020032315A1  
GENERAL INFORMATION:  
APPLICANT: Baca, Manuel  
APPLICANT: Wells, James A.  
APPLICANT: Presta, Leonard G.  
APPLICANT: Lowman, Henry B.  
APPLICANT: Chen, Yvonne M.  
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES  
NUMBER OF SEQUENCES: 131  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/056,160B  
FILING DATE: 06-Apr-1998  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/054,856  
FILING DATE: 06-Aug-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Hasak, Janet E.  
REGISTRATION NUMBER: 28,616  
REFERENCE/DOCKET NUMBER: P1093R2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-1896  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 107 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-09-056-160B-15

Query Match 100.0%; Score 54; DB 3; Length 107;  
Best Local Similarity 100.0%; Pred. No. 0.14;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SASQDISNYLN 11  
Db 24 SASQDISNYLN 34

## RESULT 11

US-10-234-671-13  
Sequence 13, Application US/10234671  
Publication No. US20030190317A1  
GENERAL INFORMATION:  
APPLICANT: Baca, Manuel  
APPLICANT: Wells, James A.  
APPLICANT: Presta, Leonard G.  
APPLICANT: Lowman, Henry B.  
APPLICANT: Chen, Yvonne M.  
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES  
NUMBER OF SEQUENCES: 131  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/234,671  
FILING DATE: 03-Sep-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/056160  
FILING DATE: 06-APR-1998  
APPLICATION NUMBER: 60/126446  
FILING DATE: 07-APR-1997  
APPLICATION NUMBER: 60/054856  
FILING DATE: 06-AUG-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Cui, Steven X.  
REGISTRATION NUMBER: 44,637  
REFERENCE/DOCKET NUMBER: P1093R2C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-8674  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 107 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-10-234-671-13

Query Match 100.0%; Score 54; DB 4; Length 107;  
Best Local Similarity 100.0%; Pred. No. 0.14;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SASQDISNYLN 11  
Db 24 SASQDISNYLN 34

## RESULT 12

US-10-234-671-15  
Sequence 15, Application US/10234671  
Publication No. US20030190317A1  
GENERAL INFORMATION:  
APPLICANT: Baca, Manuel  
APPLICANT: Wells, James A.  
APPLICANT: Presta, Leonard G.  
APPLICANT: Lowman, Henry B.  
APPLICANT: Chen, Yvonne M.  
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES  
NUMBER OF SEQUENCES: 131  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way

;  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
;  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
;  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/234,671  
; FILING DATE: 03-Sep-2002  
; CLASSIFICATION: <Unknown>  
;  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/056160  
; FILING DATE: 06-APR-1998  
; APPLICATION NUMBER: 60/126446  
; FILING DATE: 07-APR-1997  
; APPLICATION NUMBER: 60/054856  
; FILING DATE: 06-AUG-1997  
;  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Cui, Steven X.  
; REGISTRATION NUMBER: 44,637  
; REFERENCE/DOCKET NUMBER: P1093R2C1  
;  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-8674  
; TELEFAX: 650/952-9881  
;  
; INFORMATION FOR SEQ ID NO: 15:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 107 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
;  
; SEQUENCE DESCRIPTION: SEQ ID NO: 15:  
US-10-234-671-15

Query Match 100.0%; Score 54; DB 4; Length 107;  
Best Local Similarity 100.0%; Pred. No. 0.14; Mismatches 0; Indels 0; Gaps 0;  
Matches 11; Conservative 0;

Qy 1 SASQDISNYLN 11  
| | | | | | | | | | | | |  
Db 24 SASQDISNYLN 34

RESULT 13  
US-10-723-434-1  
; Sequence 1, Application US/10723434  
; Publication No. US20040133357A1  
; GENERAL INFORMATION:  
; APPLICANT: Zhong, Pingyu  
; APPLICANT: Luo, Peizhi  
; APPLICANT: Wang, Kevin C.  
; APPLICANT: Hsieh, Mark  
; APPLICANT: Li, Yan  
; TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST VASCULAR ENDOTHELIAL GROWTH FACTOR  
; CURRENT APPLICATION NUMBER: US/10/723,434  
; CURRENT FILING DATE: 2003-11-26  
; PRIOR APPLICATION NUMBER: US 60/284,407  
; PRIOR FILING DATE: 2001-04-17  
; PRIOR APPLICATION NUMBER: US 10/125,687  
; PRIOR FILING DATE: 2002-04-17  
; PRIOR APPLICATION NUMBER: US 10/153,176  
; PRIOR FILING DATE: 2002-05-20  
; PRIOR APPLICATION NUMBER: US 10/443,134  
; PRIOR FILING DATE: 2003-05-20  
; NUMBER OF SEQ ID NOS: 156  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 107  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: VL  
US-10-723-434-2

Query Match 100.0%; Score 54; DB 4; Length 107;  
Best Local Similarity 100.0%; Pred. No. 0.14; Mismatches 0; Indels 0; Gaps 0;  
Matches 11; Conservative 0;

Qy 1 SASQDISNYLN 11  
| | | | | | | | | | | | |  
Db 24 SASQDISNYLN 34

RESULT 15  
US-10-723-434-3  
; Sequence 3, Application US/10723434  
; Publication No. US20040133357A1  
; GENERAL INFORMATION:  
; APPLICANT: Zhong, Pingyu  
; APPLICANT: Luo, Peizhi  
; APPLICANT: Wang, Kevin C.  
; APPLICANT: Hsieh, Mark  
; APPLICANT: Li, Yan  
; TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST VASCULAR ENDOTHELIAL GROWTH FACTOR  
; FILE REFERENCE: 26050-709.501  
; CURRENT APPLICATION NUMBER: US/10/723,434  
; CURRENT FILING DATE: 2003-11-26  
; PRIOR APPLICATION NUMBER: US 60/284,407  
; PRIOR FILING DATE: 2001-04-17  
; PRIOR APPLICATION NUMBER: US 10/125,687  
; PRIOR FILING DATE: 2002-04-17  
; PRIOR APPLICATION NUMBER: US 10/153,176  
; PRIOR FILING DATE: 2002-05-20  
; NUMBER OF SEQ ID NOS: 156  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 107  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: VL  
US-10-723-434-2

Query Match 100.0%; Score 54; DB 4; Length 107;  
Best Local Similarity 100.0%; Pred. No. 0.14; Mismatches 0; Indels 0; Gaps 0;  
Matches 11; Conservative 0;

Qy 1 SASQDISNYLN 11  
| | | | | | | | | | | | |  
Db 24 SASQDISNYLN 34



; PRIOR APPLICATION NUMBER: US 10/443,134  
; PRIOR FILING DATE: 2003-05-20  
; NUMBER OF SEQ ID NOS: 156  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 3  
; LENGTH: 107  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: VL  
US-10-723-434-3

Query Match 100.0%; Score 54; DB 4; Length 107;  
Best Local Similarity 100.0%; Pred. No. 0.14; Mismatches 0; Indels 0; Gaps 0;  
Matches 11; Conservative 0;

Qy 1 SASQDISNYLN 11  
Db 24 SASQDISNYLN 34

RESULT 16  
US-10-723-434-4  
; Sequence 4, Application US/10723434  
; Publication No. US20040133357A1  
; GENERAL INFORMATION:  
; APPLICANT: Zhong, Pingyu  
; APPLICANT: Luo, Peizhi  
; APPLICANT: Wang, Kevin C.  
; APPLICANT: Hsieh, Mark  
; APPLICANT: Li, Yan  
; TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST VASCULAR ENDOTHELIAL GROWTH FACTOR  
; FILE REFERENCE: 26050-709.501  
; CURRENT APPLICATION NUMBER: US/10/723,434  
; CURRENT FILING DATE: 2003-11-26  
; PRIOR APPLICATION NUMBER: US 60/284,407  
; PRIOR FILING DATE: 2001-04-17  
; PRIOR APPLICATION NUMBER: US 10/125,687  
; PRIOR FILING DATE: 2002-04-17  
; PRIOR APPLICATION NUMBER: US 10/153,176  
; PRIOR FILING DATE: 2002-05-20  
; PRIOR APPLICATION NUMBER: US 10/443,134  
; PRIOR FILING DATE: 2003-05-20  
; NUMBER OF SEQ ID NOS: 156  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 4  
; LENGTH: 107  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: VL  
US-10-723-434-4

Query Match 100.0%; Score 54; DB 4; Length 107;  
Best Local Similarity 100.0%; Pred. No. 0.14; Mismatches 0; Indels 0; Gaps 0;  
Matches 11; Conservative 0;

Qy 1 SASQDISNYLN 11  
Db 24 SASQDISNYLN 34

RESULT 17  
US-10-723-434-5  
; Sequence 5, Application US/10723434  
; Publication No. US20040133357A1  
; GENERAL INFORMATION:  
; APPLICANT: Zhong, Pingyu  
; APPLICANT: Luo, Peizhi  
; APPLICANT: Wang, Kevin C.  
; APPLICANT: Hsieh, Mark  
; APPLICANT: Li, Yan  
; TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST VASCULAR ENDOTHELIAL GROWTH FACTOR

; FILE REFERENCE: 26050-709.501  
; CURRENT APPLICATION NUMBER: US/10/723,434  
; CURRENT FILING DATE: 2003-11-26  
; PRIOR APPLICATION NUMBER: US 60/284,407  
; PRIOR FILING DATE: 2001-04-17  
; PRIOR APPLICATION NUMBER: US 10/125,687  
; PRIOR FILING DATE: 2002-04-17  
; PRIOR APPLICATION NUMBER: US 10/153,176  
; PRIOR FILING DATE: 2002-05-20  
; PRIOR APPLICATION NUMBER: US 10/443,134  
; PRIOR FILING DATE: 2003-05-20  
; NUMBER OF SEQ ID NOS: 156  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 5  
; LENGTH: 107  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: VL  
US-10-723-434-5

Query Match 100.0%; Score 54; DB 4; Length 107;  
Best Local Similarity 100.0%; Pred. No. 0.14; Mismatches 0; Indels 0; Gaps 0;  
Matches 11; Conservative 0;

Qy 1 SASQDISNYLN 11  
Db 24 SASQDISNYLN 34

RESULT 18  
US-10-723-434-6  
; Sequence 6, Application US/10723434  
; Publication No. US20040133357A1  
; GENERAL INFORMATION:  
; APPLICANT: Zhong, Pingyu  
; APPLICANT: Luo, Peizhi  
; APPLICANT: Wang, Kevin C.  
; APPLICANT: Hsieh, Mark  
; APPLICANT: Li, Yan  
; TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST VASCULAR ENDOTHELIAL GROWTH FACTOR  
; FILE REFERENCE: 26050-709.501  
; CURRENT APPLICATION NUMBER: US/10/723,434  
; CURRENT FILING DATE: 2003-11-26  
; PRIOR APPLICATION NUMBER: US 60/284,407  
; PRIOR FILING DATE: 2001-04-17  
; PRIOR APPLICATION NUMBER: US 10/125,687  
; PRIOR FILING DATE: 2002-04-17  
; PRIOR APPLICATION NUMBER: US 10/153,176  
; PRIOR FILING DATE: 2002-05-20  
; PRIOR APPLICATION NUMBER: US 10/443,134  
; PRIOR FILING DATE: 2003-05-20  
; NUMBER OF SEQ ID NOS: 156  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 6  
; LENGTH: 107  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: VL  
US-10-723-434-6

Query Match 100.0%; Score 54; DB 4; Length 107;  
Best Local Similarity 100.0%; Pred. No. 0.14; Mismatches 0; Indels 0; Gaps 0;  
Matches 11; Conservative 0;

Qy 1 SASQDISNYLN 11  
Db 24 SASQDISNYLN 34

RESULT 19  
US-10-723-434-7

```

; Sequence 7, Application US/10723434
; Publication No. US20040133357A1
; GENERAL INFORMATION:
; APPLICANT: Zhong, Pingyu
; APPLICANT: Luo, Peizhi
; APPLICANT: Wang, Kevin C.
; APPLICANT: Hsieh, Mark
; APPLICANT: Li, Yan
; TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST VASCULAR ENDOTHELIAL GROWTH FACTOR
; FILE REFERENCE: 26050-709.501
; CURRENT APPLICATION NUMBER: US/10/723,434
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 60/284,407
; PRIOR FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: US 10/125,687
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: US 10/153,176
; PRIOR FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: US 10/443,134
; PRIOR FILING DATE: 2003-05-20
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VL
US-10-723-434-7

Query Match          100.0%; Score 54; DB 4; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SASQDISNYLN 11
Db      24 SASQDISNYLN 34

; Sequence 8, Application US/10723434
; Publication No. US20040133357A1
; GENERAL INFORMATION:
; APPLICANT: Zhong, Pingyu
; APPLICANT: Luo, Peizhi
; APPLICANT: Wang, Kevin C.
; APPLICANT: Hsieh, Mark
; APPLICANT: Li, Yan
; TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST VASCULAR ENDOTHELIAL GROWTH FACTOR
; FILE REFERENCE: 26050-709.501
; CURRENT APPLICATION NUMBER: US/10/723,434
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 60/284,407
; PRIOR FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: US 10/125,687
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: US 10/153,176
; PRIOR FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: US 10/443,134
; PRIOR FILING DATE: 2003-05-20
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VL
US-10-723-434-8

Query Match          100.0%; Score 54; DB 4; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SASQDISNYLN 11
Db      24 SASQDISNYLN 34

; Sequence 9, Application US/10723434
; Publication No. US20040133357A1
; GENERAL INFORMATION:
; APPLICANT: Zhong, Pingyu
; APPLICANT: Luo, Peizhi
; APPLICANT: Wang, Kevin C.
; APPLICANT: Hsieh, Mark
; APPLICANT: Li, Yan
; TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST VASCULAR ENDOTHELIAL GROWTH FACTOR
; FILE REFERENCE: 26050-709.501
; CURRENT APPLICATION NUMBER: US/10/723,434
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 60/284,407
; PRIOR FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: US 10/125,687
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: US 10/153,176
; PRIOR FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: US 10/443,134
; PRIOR FILING DATE: 2003-05-20
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VL
US-10-723-434-9

Query Match          100.0%; Score 54; DB 4; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SASQDISNYLN 11
Db      24 SASQDISNYLN 34

; Sequence 10, Application US/10723434
; Publication No. US20040133357A1
; GENERAL INFORMATION:
; APPLICANT: Zhong, Pingyu
; APPLICANT: Luo, Peizhi
; APPLICANT: Wang, Kevin C.
; APPLICANT: Hsieh, Mark
; APPLICANT: Li, Yan
; TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST VASCULAR ENDOTHELIAL GROWTH FACTOR
; FILE REFERENCE: 26050-709.501
; CURRENT APPLICATION NUMBER: US/10/723,434
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 60/284,407
; PRIOR FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: US 10/125,687
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: US 10/153,176
; PRIOR FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: US 10/443,134
; PRIOR FILING DATE: 2003-05-20
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VL
US-10-723-434-10

Query Match          100.0%; Score 54; DB 4; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SASQDISNYLN 11
Db      24 SASQDISNYLN 34

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Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SASQDISNYLN 11
Db      24 SASQDISNYLN 34

RESULT 21
US-10-723-434-9
; Sequence 9, Application US/10723434
; Publication No. US20040133357A1
; GENERAL INFORMATION:
; APPLICANT: Zhong, Pingyu
; APPLICANT: Luo, Peizhi
; APPLICANT: Wang, Kevin C.
; APPLICANT: Hsieh, Mark
; APPLICANT: Li, Yan
; TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST VASCULAR ENDOTHELIAL GROWTH FACTOR
; FILE REFERENCE: 26050-709.501
; CURRENT APPLICATION NUMBER: US/10/723,434
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 60/284,407
; PRIOR FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: US 10/125,687
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: US 10/153,176
; PRIOR FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: US 10/443,134
; PRIOR FILING DATE: 2003-05-20
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VL
US-10-723-434-9

Query Match          100.0%; Score 54; DB 4; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SASQDISNYLN 11
Db      24 SASQDISNYLN 34

RESULT 22
US-10-723-434-10
; Sequence 10, Application US/10723434
; Publication No. US20040133357A1
; GENERAL INFORMATION:
; APPLICANT: Zhong, Pingyu
; APPLICANT: Luo, Peizhi
; APPLICANT: Wang, Kevin C.
; APPLICANT: Hsieh, Mark
; APPLICANT: Li, Yan
; TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST VASCULAR ENDOTHELIAL GROWTH FACTOR
; FILE REFERENCE: 26050-709.501
; CURRENT APPLICATION NUMBER: US/10/723,434
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 60/284,407
; PRIOR FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: US 10/125,687
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: US 10/153,176
; PRIOR FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: US 10/443,134
; PRIOR FILING DATE: 2003-05-20
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10

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; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VL
US-10-723-434-10

Query Match      100.0%; Score 54; DB 4; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SASQDISNYLN 11
Db      24 SASQDISNYLN 34

RESULT 23
US-10-723-434-11
; Sequence 11, Application US/10723434
; Publication No. US20040133357A1
; GENERAL INFORMATION:
; APPLICANT: Zhong, Pingyu
; APPLICANT: Luo, Peizhi
; APPLICANT: Wang, Kevin C.
; APPLICANT: Hsieh, Mark
; APPLICANT: Li, Yan
; TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST VASCULAR ENDOTHELIAL GROWTH FACTOR
; FILE REFERENCE: 26050-709.501
; CURRENT APPLICATION NUMBER: US/10/723,434
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 60/284,407
; PRIOR FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: US 10/125,687
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: US 10/153,176
; PRIOR FILING DATE: 2003-05-20
; PRIOR APPLICATION NUMBER: US 10/443,134
; PRIOR FILING DATE: 2003-05-20
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VL
US-10-723-434-11

Query Match      100.0%; Score 54; DB 4; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SASQDISNYLN 11
Db      24 SASQDISNYLN 34

RESULT 24
US-10-723-434-12
; Sequence 12, Application US/10723434
; Publication No. US20040133357A1
; GENERAL INFORMATION:
; APPLICANT: Zhong, Pingyu
; APPLICANT: Luo, Peizhi
; APPLICANT: Wang, Kevin C.
; APPLICANT: Hsieh, Mark
; APPLICANT: Li, Yan
; TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST VASCULAR ENDOTHELIAL GROWTH FACTOR
; FILE REFERENCE: 26050-709.501
; CURRENT APPLICATION NUMBER: US/10/723,434
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 60/284,407
; PRIOR FILING DATE: 2001-04-17
```

```
; PRIOR APPLICATION NUMBER: US 10/125,687
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: US 10/153,176
; PRIOR FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: US 10/443,134
; PRIOR FILING DATE: 2003-05-20
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VL
US-10-723-434-12

Query Match      100.0%; Score 54; DB 4; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SASQDISNYLN 11
Db      24 SASQDISNYLN 34

RESULT 25
US-10-723-434-13
; Sequence 13, Application US/10723434
; Publication No. US20040133357A1
; GENERAL INFORMATION:
; APPLICANT: Zhong, Pingyu
; APPLICANT: Luo, Peizhi
; APPLICANT: Wang, Kevin C.
; APPLICANT: Hsieh, Mark
; APPLICANT: Li, Yan
; TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST VASCULAR ENDOTHELIAL GROWTH FACTOR
; FILE REFERENCE: 26050-709.501
; CURRENT APPLICATION NUMBER: US/10/723,434
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 60/284,407
; PRIOR FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: US 10/125,687
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: US 10/153,176
; PRIOR FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: US 10/443,134
; PRIOR FILING DATE: 2003-05-20
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VL
US-10-723-434-13

Query Match      100.0%; Score 54; DB 4; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SASQDISNYLN 11
Db      24 SASQDISNYLN 34

RESULT 26
US-10-723-434-14
; Sequence 14, Application US/10723434
; Publication No. US20040133357A1
; GENERAL INFORMATION:
; APPLICANT: Zhong, Pingyu
; APPLICANT: Luo, Peizhi
```

```

; APPLICANT: Wang, Kevin C.
; APPLICANT: Heich, Mark
; APPLICANT: Li, Yan
; TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST VASCULAR ENDOTHELIAL GROWTH FACTOR
; FILE REFERENCE: 26050-709.501
; CURRENT APPLICATION NUMBER: US 10/723,434
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 60/284,407
; PRIOR FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: US 10/125,687
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: US 10/153,176
; PRIOR FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: US 10/443,134
; PRIOR FILING DATE: 2003-05-20
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VL
US-10-723-434-14

Query Match          100.0%; Score 54; DB 4; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SASQDISNYLN 11
Db      24 SASQDISNYLN 34

RESULT 27
US-10-974-591-13
; Sequence 13, Application US/10974591
; Publication No. US20050112126A1
; GENERAL INFORMATION:
; APPLICANT: Baca, Manuel
;           Wells, James A.
;           Presta, Leonard G.
;           Lowman, Henry B.
;           Chen, Yvonne M.
; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
; NUMBER OF SEQUENCES: 131
; CORRESPONDENCE ADDRESS:
; ADDRESS: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/974,591
; FILING DATE: 26-Oct-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/723752
; FILING DATE: 27-NOV-2000
; APPLICATION NUMBER: 08/908469
; FILING DATE: 06-AUG-1997
; APPLICATION NUMBER: 08/833504
; FILING DATE: 07-APR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Cui, Steven X.
; REGISTRATION NUMBER: 44,637
; REFERENCE/DOCKET NUMBER: P1093PID1C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-8674
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-10-974-591-15

Query Match          100.0%; Score 54; DB 5; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-8674
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-10-974-591-13

Query Match          100.0%; Score 54; DB 5; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SASQDISNYLN 11
Db      24 SASQDISNYLN 34

RESULT 28
US-10-974-591-15
; Sequence 15, Application US/10974591
; Publication No. US20050112126A1
; GENERAL INFORMATION:
; APPLICANT: Baca, Manuel
;           Wells, James A.
;           Presta, Leonard G.
;           Lowman, Henry B.
;           Chen, Yvonne M.
; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
; NUMBER OF SEQUENCES: 131
; CORRESPONDENCE ADDRESS:
; ADDRESS: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/974,591
; FILING DATE: 26-Oct-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/723752
; FILING DATE: 27-NOV-2000
; APPLICATION NUMBER: 08/908469
; FILING DATE: 06-AUG-1997
; APPLICATION NUMBER: 08/833504
; FILING DATE: 07-APR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Cui, Steven X.
; REGISTRATION NUMBER: 44,637
; REFERENCE/DOCKET NUMBER: P1093PID1C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-8674
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-10-974-591-15

Query Match          100.0%; Score 54; DB 5; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy 1 SASQDISNYLN 11  
 |||||  
 Db 24 SASQDISNYLN 34

## RESULT 29

US-09-056-160B-8  
 ; Sequence 8, Application US/09056160B  
 ; Patent No. US20020032315A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Baca, Manuel  
 ; APPLICANT: Wells, James A.  
 ; APPLICANT: Presta, Leonard G.  
 ; APPLICANT: Lowman, Henry B.  
 ; APPLICANT: Chen, Yvonne M.  
 ; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES  
 ; NUMBER OF SEQUENCES: 131  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Genentech, Inc.  
 ; STREET: 1 DNA Way  
 ; CITY: South San Francisco  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 94080

; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: WinPatIn (Genentech)  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/056,160B  
 ; FILING DATE: 06-Apr-1998  
 ; CLASSIFICATION: 424  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 60/054,856  
 ; FILING DATE: 06-AUG-1997  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Hasak, Janet E.  
 ; REFERENCE/DOCKET NUMBER: P1093R2  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 650/225-1896  
 ; TELEFAX: 650/952-9881  
 ; INFORMATION FOR SEQ ID NO: 8:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 108 amino acids  
 ; TYPE: Amino Acid  
 ; TOPOLOGY: Linear

## US-09-056-160B-8

Query Match 100.0%; Score 54; DB 3; Length 108;  
 Best Local Similarity 100.0%; Pred. No. 0.14;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SASQDISNYLN 11  
 |||||  
 Db 24 SASQDISNYLN 34

## RESULT 30

US-09-056-160B-10  
 ; Sequence 10, Application US/09056160B  
 ; Patent No. US20020032315A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Baca, Manuel  
 ; APPLICANT: Wells, James A.  
 ; APPLICANT: Presta, Leonard G.  
 ; APPLICANT: Lowman, Henry B.  
 ; APPLICANT: Chen, Yvonne M.  
 ; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES  
 ; NUMBER OF SEQUENCES: 131  
 ; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.  
 ; STREET: 1 DNA Way  
 ; CITY: South San Francisco  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 94080  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: WinPatIn (Genentech)  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/056,160B  
 ; FILING DATE: 06-Apr-1998  
 ; CLASSIFICATION: 424

; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 60/054,856  
 ; FILING DATE: 06-AUG-1997  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Hasak, Janet E.  
 ; REGISTRATION NUMBER: 28,616  
 ; REFERENCE/DOCKET NUMBER: P1093R2  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 650/225-1896  
 ; TELEFAX: 650/952-9881  
 ; INFORMATION FOR SEQ ID NO: 10:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 108 amino acids  
 ; TYPE: Amino Acid  
 ; TOPOLOGY: Linear

## US-09-056-160B-10

Query Match 100.0%; Score 54; DB 3; Length 108;  
 Best Local Similarity 100.0%; Pred. No. 0.14;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SASQDISNYLN 11  
 |||||  
 Db 24 SASQDISNYLN 34

## RESULT 31

US-09-056-160B-126  
 ; Sequence 126, Application US/09056160B  
 ; Patent No. US20020032315A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Baca, Manuel  
 ; APPLICANT: Wells, James A.  
 ; APPLICANT: Presta, Leonard G.  
 ; APPLICANT: Lowman, Henry B.  
 ; APPLICANT: Chen, Yvonne M.  
 ; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES  
 ; NUMBER OF SEQUENCES: 131  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Genentech, Inc.  
 ; STREET: 1 DNA Way  
 ; CITY: South San Francisco  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 94080

; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: WinPatIn (Genentech)  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/056,160B  
 ; FILING DATE: 06-Apr-1998  
 ; CLASSIFICATION: 424  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 60/054,856  
 ; FILING DATE: 06-AUG-1997  
 ; ATTORNEY/AGENT INFORMATION:

; NAME: Hsiek, Janet E.  
; REGISTRATION NUMBER: 28,616  
; REFERENCE/DOCKET NUMBER: P1093R2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-1896  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 126:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 108 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
US-09-056-160B-126

Query Match 100.0%; Score 54; DB 3; Length 108;  
Best Local Similarity 100.0%; Pred. No. 0.14;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SASQDISNYLN 11  
| | | | | | | | | |  
Db 24 SASQDISNYLN 34

## RESULT 32

US-10-153-159-2  
; Sequence 2, Application US/10153159  
; Publication No. US20020177170A1  
; GENERAL INFORMATION:  
; APPLICANT: Luo, Peter  
; APPLICANT: Hsieh, Mark  
; APPLICANT: Zhong, Pingyu  
; APPLICANT: Wang, Caili  
; TITLE OF INVENTION: STRUCTURE-BASED SELECTION AND AFFINITY MATURATION OF ANTIBODY LIB  
; TITLE OF INVENTION: SILICO  
; FILE REFERENCE: 26050-704  
; CURRENT APPLICATION NUMBER: US/10/153,159  
; CURRENT FILING DATE: 2002-05-20  
; PRIOR APPLICATION NUMBER: US 10/125,687  
; PRIOR FILING DATE: 2002-04-17  
; PRIOR APPLICATION NUMBER: US 60/284,407  
; PRIOR FILING DATE: 2001-04-17  
; NUMBER OF SEQ ID NOS: 125  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 108  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: VL of parental anti-VEGF antibody  
US-10-153-159-2

Query Match 100.0%; Score 54; DB 4; Length 108;  
Best Local Similarity 100.0%; Pred. No. 0.14;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SASQDISNYLN 11  
| | | | | | | | | |  
Db 24 SASQDISNYLN 34

## RESULT 33

US-10-153-159-4  
; Sequence 4, Application US/10153159  
; Publication No. US20020177170A1  
; GENERAL INFORMATION:  
; APPLICANT: Luo, Peter  
; APPLICANT: Hsieh, Mark  
; APPLICANT: Zhong, Pingyu  
; APPLICANT: Wang, Caili  
; TITLE OF INVENTION: STRUCTURE-BASED SELECTION AND AFFINITY MATURATION OF ANTIBODY LIB  
; TITLE OF INVENTION: SILICO  
; FILE REFERENCE: 26050-704  
; CURRENT APPLICATION NUMBER: US/10/153,159  
; CURRENT FILING DATE: 2002-05-20

; PRIOR APPLICATION NUMBER: US 10/125,687  
; PRIOR FILING DATE: 2002-04-17  
; PRIOR APPLICATION NUMBER: US 60/284,407  
; PRIOR FILING DATE: 2001-04-17  
; NUMBER OF SEQ ID NOS: 125  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 4  
; LENGTH: 108  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: VL of matured anti-VEGF antibody  
US-10-153-159-4

Query Match 100.0%; Score 54; DB 4; Length 108;  
Best Local Similarity 100.0%; Pred. No. 0.14;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SASQDISNYLN 11  
| | | | | | | | | |  
Db 24 SASQDISNYLN 34

## RESULT 34

US-10-153-159-16  
; Sequence 16, Application US/10153159  
; Publication No. US20020177170A1  
; GENERAL INFORMATION:  
; APPLICANT: Luo, Peter  
; APPLICANT: Hsieh, Mark  
; APPLICANT: Zhong, Pingyu  
; APPLICANT: Wang, Caili  
; TITLE OF INVENTION: STRUCTURE-BASED SELECTION AND AFFINITY MATURATION OF ANTIBODY LIB  
; TITLE OF INVENTION: SILICO  
; FILE REFERENCE: 26050-704  
; CURRENT APPLICATION NUMBER: US/10/153,159  
; CURRENT FILING DATE: 2002-05-20  
; PRIOR APPLICATION NUMBER: US 10/125,687  
; PRIOR FILING DATE: 2002-04-17  
; PRIOR APPLICATION NUMBER: US 60/284,407  
; PRIOR FILING DATE: 2001-04-17  
; NUMBER OF SEQ ID NOS: 125  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 16  
; LENGTH: 108  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: VL of AM2-ccFv  
US-10-153-159-16

Query Match 100.0%; Score 54; DB 4; Length 108;  
Best Local Similarity 100.0%; Pred. No. 0.14;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SASQDISNYLN 11  
| | | | | | | | | |  
Db 24 SASQDISNYLN 34

## RESULT 35

US-10-153-176-2  
; Sequence 2, Application US/10153176  
; Publication No. US20030022240A1  
; GENERAL INFORMATION:  
; APPLICANT: Luo, Peter  
; APPLICANT: Hsieh, Mark  
; APPLICANT: Zhong, Pingyu  
; APPLICANT: Wang, Caili  
; APPLICANT: Cao, Yicheng  
; APPLICANT: Li, Shengfeng  
; APPLICANT: Liu, Shengjiang  
; TITLE OF INVENTION: GENERATION AND AFFINITY MATURATION OF ANTIBODY LIBRARY IN SILICO

; FILE REFERENCE: 26050-701  
; CURRENT APPLICATION NUMBER: US/10/153,176  
; CURRENT FILING DATE: 2002-05-20  
; PRIOR APPLICATION NUMBER: US 10/125,687  
; PRIOR FILING DATE: 2002-04-17  
; PRIOR APPLICATION NUMBER: US 60/284,407  
; PRIOR FILING DATE: 2001-04-17  
; NUMBER OF SEQ ID NOS: 125  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 108  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: VL of parental anti-VEGF antibody  
US-10-153-176-2

Query Match 100.0%; Score 54; DB 4; Length 108;  
Best Local Similarity 100.0%; Pred. No. 0.14;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASQDISNYLN 11  
Db 24 SASQDISNYLN 34

RESULT 36  
US-10-153-176-4  
; Sequence 4, Application US/10153176  
; Publication No. US2003002240A1  
; GENERAL INFORMATION:  
; APPLICANT: Luo, Peter  
; APPLICANT: Hsieh, Mark  
; APPLICANT: Zhong, Pingyu  
; APPLICANT: Wang, Cailli  
; APPLICANT: Cao, Yicheng  
; APPLICANT: Li, Shengfeng  
; APPLICANT: Liu, Shengjiang  
; TITLE OF INVENTION: GENERATION AND AFFINITY MATURATION OF ANTIBODY LIBRARY IN SILICO  
; FILE REFERENCE: 26050-701  
; CURRENT APPLICATION NUMBER: US/10/153,176  
; CURRENT FILING DATE: 2002-05-20  
; PRIOR APPLICATION NUMBER: US 10/125,687  
; PRIOR FILING DATE: 2002-04-17  
; PRIOR APPLICATION NUMBER: US 60/284,407  
; PRIOR FILING DATE: 2001-04-17  
; NUMBER OF SEQ ID NOS: 125  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 4  
; LENGTH: 108  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: VL of matured anti-VEGF antibody  
US-10-153-176-4

Query Match 100.0%; Score 54; DB 4; Length 108;  
Best Local Similarity 100.0%; Pred. No. 0.14;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASQDISNYLN 11  
Db 24 SASQDISNYLN 34

RESULT 37  
US-10-153-176-16  
; Sequence 16, Application US/10153176  
; Publication No. US2003002240A1  
; GENERAL INFORMATION:  
; APPLICANT: Luo, Peter  
; APPLICANT: Hsieh, Mark  
; APPLICANT: Zhong, Pingyu

; APPLICANT: Wang, Cailli  
; APPLICANT: Cao, Yicheng  
; APPLICANT: Li, Shengfeng  
; APPLICANT: Liu, Shengjiang  
; TITLE OF INVENTION: GENERATION AND AFFINITY MATURATION OF ANTIBODY LIBRARY IN SILICO  
; FILE REFERENCE: 26050-701  
; CURRENT APPLICATION NUMBER: US/10/153,176  
; CURRENT FILING DATE: 2002-05-20  
; PRIOR APPLICATION NUMBER: US 10/125,687  
; PRIOR FILING DATE: 2002-04-17  
; PRIOR APPLICATION NUMBER: US 60/284,407  
; PRIOR FILING DATE: 2001-04-17  
; NUMBER OF SEQ ID NOS: 125  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 16  
; LENGTH: 108  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: VL of AM2-ccFv  
US-10-153-176-16

Query Match 100.0%; Score 54; DB 4; Length 108;  
Best Local Similarity 100.0%; Pred. No. 0.14;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASQDISNYLN 11  
Db 24 SASQDISNYLN 34

RESULT 38  
US-10-234-671-10  
; Sequence 10, Application US/10234671  
; Publication No. US20030190317A1  
; GENERAL INFORMATION:  
; APPLICANT: Baca, Manuel  
; APPLICANT: Wells, James A.  
; APPLICANT: Presta, Leonard G.  
; APPLICANT: Lowman, Henry B.  
; APPLICANT: Chen, Yvonne M.  
; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES  
; NUMBER OF SEQUENCES: 131  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/234,671  
; FILING DATE: 03-Sep-2002  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/056160  
; FILING DATE: 06-APR-1998  
; APPLICATION NUMBER: 60/126446  
; FILING DATE: 07-APR-1997  
; APPLICATION NUMBER: 60/054856  
; FILING DATE: 06-AUG-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Cui, Steven X.  
; REGISTRATION NUMBER: 44,637  
; REFERENCE/DOCKET NUMBER: P1093R2C1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-8674  
; TELEFAX: 650/952-9881

```
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 108 amino acids
;   TYPE: Amino Acid
;   TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-234-671-10

Query Match      100.0%; Score 54; DB 4; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SASQDISNYLN 11
      |||||
Db      24 SASQDISNYLN 34

RESULT 39
US-10-234-671-124
; Sequence 124, Application US/10234671
; Publication No. US20030190317A1
; GENERAL INFORMATION:
; APPLICANT: Baca, Manuel
;           Wells, James A.
;           Presta, Leonard G.
;           Lowman, Henry B.
;           Chen, Yvonne M.
; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
; NUMBER OF SEQUENCES: 131
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/10/234,671
;   FILING DATE: 03-Sep-2002
;   CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 09/056160
;   FILING DATE: 06-APR-1998
;   APPLICATION NUMBER: 60/126446
;   FILING DATE: 07-APR-1997
;   APPLICATION NUMBER: 60/054856
;   FILING DATE: 06-AUG-1997
; ATTORNEY/AGENT INFORMATION:
;   NAME: Cui, Steven X.
;   REGISTRATION NUMBER: 44,637
; REFERENCE/DOCKET NUMBER: P1093R2C1
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 650/225-8674
;   TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 124:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 108 amino acids
;   TYPE: Amino Acid
;   TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 124:
US-10-234-671-124

Query Match      100.0%; Score 54; DB 4; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SASQDISNYLN 11
      |||||
Db      24 SASQDISNYLN 34

INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 108 amino acids
;   TYPE: Amino Acid
;   TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-443-134A-2
; Sequence 2, Application US/10443134A
; Publication No. US20040010376A1
; GENERAL INFORMATION:
; APPLICANT: Luo, Peizhi
; APPLICANT: Hsieh, Mark
; APPLICANT: Zhong, Pingyu
; APPLICANT: Wang, Caili
; APPLICANT: Cao, Yicheng
; APPLICANT: Liu, Shengjiang
; TITLE OF INVENTION: GENERATION AND SELECTION OF PROTEIN LIBRARY IN SILICO
; FILE REFERENCE: 26050-709
; CURRENT APPLICATION NUMBER: US/10/443,134A
; CURRENT FILING DATE: 2003-05-20
; PRIOR APPLICATION NUMBER: US 10/125,687
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: US 60/284,407
; PRIOR FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: US 10/153,176
; PRIOR FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: US 10/153,159
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 2
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VL of parental anti-VEGF antibody
US-10-443-134A-2

Query Match      100.0%; Score 54; DB 4; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SASQDISNYLN 11
      |||||
Db      24 SASQDISNYLN 34

RESULT 41
US-10-443-134A-4
; Sequence 4, Application US/10443134A
; Publication No. US20040010376A1
; GENERAL INFORMATION:
; APPLICANT: Luo, Peizhi
; APPLICANT: Hsieh, Mark
; APPLICANT: Zhong, Pingyu
; APPLICANT: Wang, Caili
; APPLICANT: Cao, Yicheng
; APPLICANT: Liu, Shengjiang
; TITLE OF INVENTION: GENERATION AND SELECTION OF PROTEIN LIBRARY IN SILICO
; FILE REFERENCE: 26050-709
; CURRENT APPLICATION NUMBER: US/10/443,134A
; CURRENT FILING DATE: 2003-05-20
; PRIOR APPLICATION NUMBER: US 10/125,687
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: US 60/284,407
; PRIOR FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: US 10/153,176
; PRIOR FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: US 10/153,159
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 4
; LENGTH: 108
; TYPE: PRT
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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VL of matured anti-VEGF antibody
US-10-443-134A-4

Query Match      100.0%; Score 54; DB 4; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASQDISNYLN 11
   |||||
Db 24 SASQDISNYLN 34

RESULT 42
US-10-443-134A-16
; Sequence 16, Application US/10443134A
; Publication No. US20040010376A1
; GENERAL INFORMATION:
; APPLICANT: Luo, Peizhi
; APPLICANT: Hsieh, Mark
; APPLICANT: Zhong, Pingyu
; APPLICANT: Wang, Caili
; APPLICANT: Cao, Yicheng
; APPLICANT: Liu, Shengjiang
; TITLE OF INVENTION: GENERATION AND SELECTION OF PROTEIN LIBRARY IN SILICO
; FILE REFERENCE: 26050-709
; CURRENT APPLICATION NUMBER: US/10/443,134A
; CURRENT FILING DATE: 2003-05-20
; PRIOR APPLICATION NUMBER: US 10/125,687
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: US 60/284,407
; PRIOR FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: US 10/153,176
; PRIOR FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: US 10/153,159
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 16
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VL of AM2-ccFv
US-10-443-134A-16

Query Match      100.0%; Score 54; DB 4; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASQDISNYLN 11
   |||||
Db 24 SASQDISNYLN 34

RESULT 43
US-10-443-134A-127
; Sequence 127, Application US/10443134A
; Publication No. US20040010376A1
; GENERAL INFORMATION:
; APPLICANT: Luo, Peizhi
; APPLICANT: Hsieh, Mark
; APPLICANT: Zhong, Pingyu
; APPLICANT: Wang, Caili
; APPLICANT: Cao, Yicheng
; APPLICANT: Liu, Shengjiang
; TITLE OF INVENTION: GENERATION AND SELECTION OF PROTEIN LIBRARY IN SILICO
; FILE REFERENCE: 26050-709
; CURRENT APPLICATION NUMBER: US/10/443,134A
; CURRENT FILING DATE: 2003-05-20
; PRIOR APPLICATION NUMBER: US 10/125,687
; PRIOR FILING DATE: 2002-04-17
```

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; PRIOR APPLICATION NUMBER: US 60/284,407
; PRIOR FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: US 10/153,176
; PRIOR FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: US 10/153,159
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 127
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VL of antibody X64, X65, D36, D40 and D42
US-10-443-134A-127

Query Match      100.0%; Score 54; DB 4; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASQDISNYLN 11
   |||||
Db 24 SASQDISNYLN 34

RESULT 44
US-10-877-532-7
; Sequence 7, Application US/10877532
; Publication No. US20050038231A1
; GENERAL INFORMATION:
; APPLICANT: FAHRNER, ROBERT L.
; APPLICANT: LAVERDIERE, AMY
; APPLICANT: MCDONALD, PAUL J.
; APPLICANT: O'LEARY, RHONA M.
; TITLE OF INVENTION: REDUCING PROTEIN A LEACHING DURING PROTEIN A AFFINITY CHROMATOGR
; FILE REFERENCE: P2015R1
; CURRENT APPLICATION NUMBER: US/10/877,532
; CURRENT FILING DATE: 2004-06-24
; PRIOR APPLICATION NUMBER: US 60/490,500
; PRIOR FILING DATE: 2003-07-28
; NUMBER OF SEQ ID NOS: 8
; SEQ ID NO 7
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-10-877-532-7

Query Match      100.0%; Score 54; DB 5; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASQDISNYLN 11
   |||||
Db 24 SASQDISNYLN 34

RESULT 45
US-10-974-591-10
; Sequence 10, Application US/10974591
; Publication No. US20050112126A1
; GENERAL INFORMATION:
; APPLICANT: Baca, Manuel
; APPLICANT: Wells, James A.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Lowman, Henry B.
; APPLICANT: Chen, Yvonne M.
; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
; NUMBER OF SEQUENCES: 131
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
```

;  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
;  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
;  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/974,591  
; FILING DATE: 26-Oct-2004  
; CLASSIFICATION: <Unknown>  
;  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/723752  
; FILING DATE: 27-NOV-2000  
; APPLICATION NUMBER: 08/908469  
; FILING DATE: 06-AUG-1997  
; APPLICATION NUMBER: 08/833504  
; FILING DATE: 07-APR-1997  
;  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Cui, Steven X.  
; REGISTRATION NUMBER: 44,637  
; REFERENCE/DOCKET NUMBER: P1093PID1C1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-8674  
; TELEFAX: 650/952-9881  
;  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 108 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
;  
; SEQUENCE DESCRIPTION: SEQ ID NO: 10:  
US-10-974-591-10  
  
Query Match 100.0%; Score 54; DB 5; Length 108;  
Best Local Similarity 100.0%; Pred. No. 0.14;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 SASQDISNYLN 11  
Db 24 SASQDISNYLN 34  
  
RESULT 46  
US-10-974-591-124  
; Sequence 124, Application US/10974591  
; Publication No. US20050112126A1  
; GENERAL INFORMATION:  
; APPLICANT: Baca, Manuel  
; APPLICANT: Wells, James A.  
; APPLICANT: Presta, Leonard G.  
; APPLICANT: Lowman, Henry B.  
; APPLICANT: Chen, Yvonne M.  
; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES  
; NUMBER OF SEQUENCES: 131  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
;  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
;  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/974,591  
; FILING DATE: 26-Oct-2004  
; CLASSIFICATION: <Unknown>  
;  
; PRIOR APPLICATION DATA:

;  
; APPLICATION NUMBER: 09/723752  
; FILING DATE: 27-NOV-2000  
; APPLICATION NUMBER: 08/908469  
; FILING DATE: 06-AUG-1997  
; APPLICATION NUMBER: 08/833504  
; FILING DATE: 07-APR-1997  
;  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Cui, Steven X.  
; REGISTRATION NUMBER: 44,637  
; REFERENCE/DOCKET NUMBER: P1093PID1C1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-8674  
; TELEFAX: 650/952-9881  
;  
; INFORMATION FOR SEQ ID NO: 124:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 108 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
;  
; SEQUENCE DESCRIPTION: SEQ ID NO: 124:  
US-10-974-591-124  
  
Query Match 100.0%; Score 54; DB 5; Length 108;  
Best Local Similarity 100.0%; Pred. No. 0.14;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 SASQDISNYLN 11  
Db 24 SASQDISNYLN 34  
  
RESULT 47  
US-09-056-1608-103  
; Sequence 103, Application US/09056160B  
; Patent No. US20020032315A1  
; GENERAL INFORMATION:  
; APPLICANT: Baca, Manuel  
; APPLICANT: Wells, James A.  
; APPLICANT: Presta, Leonard G.  
; APPLICANT: Lowman, Henry B.  
; APPLICANT: Chen, Yvonne M.  
; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES  
; NUMBER OF SEQUENCES: 131  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
;  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
;  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/056,160B  
; FILING DATE: 06-Apr-1998  
; CLASSIFICATION: 424  
;  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/054,856  
; FILING DATE: 06-AUG-1997  
;  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hasak, Janet E.  
; REGISTRATION NUMBER: 28,616  
; REFERENCE/DOCKET NUMBER: P1093R2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-1896  
; TELEFAX: 650/952-9881  
;  
; INFORMATION FOR SEQ ID NO: 103:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 110 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear

## US-09-056-160B-103

Query Match 100.0%; Score 54; DB 3; Length 110;  
 Best Local Similarity 100.0%; Pred. No. 0.14;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASQDISNYLN 11  
 |||||  
 Db 24 SASQDISNYLN 34

## RESULT 48

US-09-056-160B-105  
 ; Sequence 105, Application US/09056160B

; Patent No. US20020032315A1  
 ; GENERAL INFORMATION:

; APPLICANT: Baca, Manuel  
 ; APPLICANT: Wells, James A.  
 ; APPLICANT: Presta, Leonard G.  
 ; APPLICANT: Lowman, Henry B.

; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES  
 ; NUMBER OF SEQUENCES: 131  
 ; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.  
 ; STREET: 1 DNA Way  
 ; CITY: South San Francisco  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 94080

; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: WinPatIn (Genentech)  
 ; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/056,160B  
 ; FILING DATE: 06-Apr-1998

; CLASSIFICATION: 424  
 ; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 60/054,856  
 ; FILING DATE: 06-AUG-1997

; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Hasak, Janet E.

; REGISTRATION NUMBER: 28,616  
 ; REFERENCE/DOCKET NUMBER: P1093R2  
 ; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 650/225-1896  
 ; TELEFAX: 650/952-9881

; INFORMATION FOR SEQ ID NO: 105:  
 ; SEQUENCE CHARACTERISTICS:

; LENGTH: 110 amino acids  
 ; TYPE: Amino Acid  
 ; TOPOLOGY: Linear

## US-09-056-160B-105

Query Match 100.0%; Score 54; DB 3; Length 110;  
 Best Local Similarity 100.0%; Pred. No. 0.14;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASQDISNYLN 11  
 |||||  
 Db 24 SASQDISNYLN 34

## RESULT 49

US-09-056-160B-107

; Sequence 107, Application US/09056160B  
 ; Patent No. US20020032315A1

; GENERAL INFORMATION:

; APPLICANT: Baca, Manuel  
 ; APPLICANT: Wells, James A.

; APPLICANT: Presta, Leonard G.

; APPLICANT: Lowman, Henry B.  
 ; APPLICANT: Chen, Yvonne M.  
 ; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES  
 ; NUMBER OF SEQUENCES: 131  
 ; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.  
 ; STREET: 1 DNA Way  
 ; CITY: South San Francisco  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 94080

; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: WinPatIn (Genentech)  
 ; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/056,160B  
 ; FILING DATE: 06-Apr-1998

; CLASSIFICATION: 424  
 ; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 60/054,856  
 ; FILING DATE: 06-AUG-1997

; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Hasak, Janet E.

; REGISTRATION NUMBER: 28,616  
 ; REFERENCE/DOCKET NUMBER: P1093R2  
 ; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 650/225-1896  
 ; TELEFAX: 650/952-9881

; INFORMATION FOR SEQ ID NO: 107:  
 ; SEQUENCE CHARACTERISTICS:

; LENGTH: 110 amino acids  
 ; TYPE: Amino Acid  
 ; TOPOLOGY: Linear

## US-09-056-160B-107

Query Match 100.0%; Score 54; DB 3; Length 110;  
 Best Local Similarity 100.0%; Pred. No. 0.14;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SASQDISNYLN 11  
 |||||  
 Db 24 SASQDISNYLN 34

## RESULT 50

US-09-056-160B-117

; Sequence 117, Application US/09056160B  
 ; Patent No. US20020032315A1

; GENERAL INFORMATION:

; APPLICANT: Baca, Manuel  
 ; APPLICANT: Wells, James A.

; APPLICANT: Presta, Leonard G.  
 ; APPLICANT: Lowman, Henry B.

; APPLICANT: Chen, Yvonne M.  
 ; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES

; NUMBER OF SEQUENCES: 131  
 ; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.  
 ; STREET: 1 DNA Way

; CITY: South San Francisco  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 94080

; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: WinPatIn (Genentech)  
 ; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/056,160B  
 ; FILING DATE: 06-Apr-1998

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; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/054,856
; FILING DATE: 06-AUG-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hasak, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: P1093R2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1896
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 117:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 110 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-09-056-160B-117

Query Match      100.0%; Score 54; DB 3; Length 110;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SASQDISNYLN 11
      |||||
Db      24 SASQDISNYLN 34

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Search completed: April 6, 2006, 09:22:27  
Job time : 91.9322 secs

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: April 6, 2006, 09:13:32 ; Search time 11.1864 Seconds  
(without alignments)  
30.672 Million cell updates/sec

Title: US-10-089-500-6

Perfect score: 54

Sequence: 1 SASQDISNYLN 11

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 184161 seqs, 31191982 residues

Total number of hits satisfying chosen parameters: 184161

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

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- 3: /SIDSS/prodata/2/pubpaa/US07\_NEW\_PUB.pep.\*
- 4: /SIDSS/prodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*
- 5: /SIDSS/prodata/2/pubpaa/US09\_NEW\_PUB.pep.\*
- 6: /SIDSS/prodata/2/pubpaa/US10\_NEW\_PUB.pep.\*
- 7: /SIDSS/prodata/2/pubpaa/US11\_NEW\_PUB.pep.\*
- 8: /SIDSS/prodata/2/pubpaa/US60\_NEW\_PUB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	54	100.0	11	6	US-10-473-037-6
2	54	100.0	108	6	US-10-473-037-10
3	54	100.0	108	6	US-10-473-037-50
4	54	100.0	108	7	US-11-208-422-7
5	54	100.0	108	7	US-11-208-422-9
6	54	100.0	108	7	US-11-208-422-11
7	54	100.0	110	6	US-10-648-816-1
8	54	100.0	110	6	US-10-648-816-5
9	54	100.0	128	6	US-11-228-293-2
10	54	100.0	128	7	US-11-228-293-10
11	54	100.0	128	7	US-11-228-293-19
12	54	100.0	128	7	US-11-228-319-10
13	54	100.0	128	7	US-11-228-319-19
14	50	92.6	95	7	US-11-054-669-56
15	50	92.6	95	7	US-11-054-669-57
16	50	92.6	95	7	US-11-084-554-145
17	50	92.6	95	7	US-11-084-554-148
18	50	92.6	95	7	US-11-061-848-33
19	50	92.6	95	7	US-11-061-848-62
20	50	92.6	95	7	US-11-061-848-68
21	50	92.6	95	7	US-11-004-590-68
22	50	92.6	95	7	US-11-004-590-69
23	50	92.6	95	7	US-11-136-250-145
24	50	92.6	95	7	US-11-136-250-148
25	50	92.6	108	6	US-10-771-257-38

26	50	92.6	108	7	US-11-127-677-38	Sequence 38, Appl
27	50	92.6	108	7	US-11-049-536-184	Sequence 184, App
28	50	92.6	108	7	US-11-199-739-184	Sequence 184, App
29	50	92.6	127	7	US-11-089-872-5	Sequence 5, Appl
30	47	87.0	11	6	US-10-999-866-55	Sequence 55, Appl
31	47	87.0	11	7	US-11-009-939-38	Sequence 38, Appl
32	47	87.0	107	6	US-10-999-866-43	Sequence 43, Appl
33	47	87.0	107	7	US-11-183-205-51	Sequence 51, Appl
34	47	87.0	107	7	US-11-183-205-52	Sequence 52, Appl
35	47	87.0	108	7	US-11-009-939-37	Sequence 37, Appl
36	47	87.0	108	7	US-11-061-848-2	Sequence 2, Appl
37	47	87.0	108	7	US-11-061-848-10	Sequence 10, Appl
38	47	87.0	108	7	US-11-061-848-11	Sequence 11, Appl
39	47	87.0	108	7	US-11-061-848-12	Sequence 12, Appl
40	47	87.0	108	7	US-11-061-848-13	Sequence 13, Appl
41	47	87.0	108	7	US-11-061-848-14	Sequence 14, Appl
42	47	87.0	108	7	US-11-061-848-15	Sequence 15, Appl
43	47	87.0	214	7	US-11-025-712-11	Sequence 11, Appl
44	47	87.0	214	7	US-11-173-564-1	Sequence 1, Appl
45	47	87.0	214	7	US-11-183-205-55	Sequence 55, Appl
46	46	85.2	107	6	US-10-946-836A-10	Sequence 10, Appl
47	46	85.2	107	6	US-10-988-207-10	Sequence 10, Appl
48	45	83.3	247	7	US-11-084-717-21	Sequence 21, Appl
49	45	83.3	247	7	US-11-084-717-23	Sequence 23, Appl
50	45	83.3	247	7	US-11-084-717-25	Sequence 25, Appl
51	45	83.3	247	7	US-11-179-244-21	Sequence 21, Appl
52	45	83.3	247	7	US-11-179-244-23	Sequence 23, Appl
53	45	83.3	247	7	US-11-179-244-25	Sequence 25, Appl
54	45	83.3	247	7	US-11-084-055B-21	Sequence 21, Appl
55	45	83.3	247	7	US-11-084-055B-23	Sequence 23, Appl
56	45	83.3	247	7	US-11-084-055B-25	Sequence 25, Appl
57	45	83.3	277	7	US-11-126-817-52	Sequence 52, Appl
58	44	81.5	107	6	US-10-834-397-14	Sequence 14, Appl
59	44	81.5	108	6	US-10-993-543-126	Sequence 126, App
60	44	81.5	120	6	US-11-004-590-388	Sequence 388, App
61	42	77.8	106	7	US-11-004-590-392	Sequence 392, App
62	42	77.8	106	7	US-11-004-590-393	Sequence 393, App
63	42	77.8	106	7	US-11-004-590-394	Sequence 394, App
64	42	77.8	106	7	US-11-004-590-395	Sequence 395, App
65	42	77.8	106	7	US-11-004-590-396	Sequence 396, App
66	42	77.8	106	7	US-11-004-590-397	Sequence 397, App
67	42	77.8	106	7	US-11-004-590-398	Sequence 398, App
68	42	77.8	106	7	US-11-004-590-399	Sequence 399, App
69	42	77.8	106	7	US-11-004-590-400	Sequence 400, App
70	42	77.8	106	7	US-11-004-590-401	Sequence 401, App
71	42	77.8	106	7	US-11-004-590-402	Sequence 402, App
72	42	77.8	106	7	US-11-004-590-403	Sequence 403, App
73	42	77.8	106	7	US-11-004-590-404	Sequence 404, App
74	42	77.8	106	7	US-11-004-590-405	Sequence 405, App
75	42	77.8	106	7	US-11-004-590-406	Sequence 406, App
76	42	77.8	106	7	US-11-004-590-407	Sequence 407, App
77	42	77.8	106	7	US-11-004-590-408	Sequence 408, App
78	42	77.8	106	7	US-11-004-590-409	Sequence 409, App
79	42	77.8	106	7	US-11-004-590-410	Sequence 410, App
80	42	77.8	106	7	US-11-004-590-411	Sequence 411, App
81	42	77.8	106	7	US-11-004-590-456	Sequence 456, App
82	42	77.8	106	6	US-10-771-257-40	Sequence 40, Appl
83	42	77.8	108	6	US-11-127-677-40	Sequence 40, Appl
84	40	74.1	108	7	US-11-064-174-41	Sequence 41, Appl
85	40	74.1	109	7	US-11-096-074-52	Sequence 52, Appl
86	39.5	73.1	109	7	US-11-095-822-52	Sequence 52, Appl
87	39.5	73.1	109	7	US-10-993-543-274	Sequence 274, App
88	39	72.2	95	6	US-10-496-349B-54	Sequence 54, Appl
89	39	72.2	95	6	US-11-054-669-54	Sequence 54, Appl
90	39	72.2	95	7	US-11-054-669-55	Sequence 55, Appl
91	39	72.2	95	7	US-11-084-554-143	Sequence 143, App
92	39	72.2	95	7	US-11-084-554-146	Sequence 146, App
93	39	72.2	95	7	US-11-061-848-36	Sequence 36, Appl
94	39	72.2	95	7	US-11-061-848-37	Sequence 37, Appl
95	39	72.2	95	7	US-11-061-848-63	Sequence 63, Appl
96	39	72.2	95	7	US-11-138-900-94	Sequence 94, Appl
97	39	72.2	95	7	US-11-138-900-97	Sequence 97, Appl
98	39	72.2	95	7	US-11-004-590-72	Sequence 72, Appl

99	39	72.2	95	7	US-11-004-590-73	Sequence 73, Appl	172	38	70.4	108	7	US-11-127-932-12	Sequence 35, Appl
100	39	72.2	95	7	US-11-136-250-143	Sequence 143, App	173	38	70.4	108	7	US-11-127-932-12	Sequence 12, Appl
101	39	72.2	95	7	US-11-136-250-146	Sequence 146, App	174	38	70.4	108	7	US-11-127-932-13	Sequence 13, Appl
102	39	72.2	96	7	US-11-144-248-42	Sequence 42, Appl	175	38	70.4	108	7	US-11-064-174-181	Sequence 181, App
103	39	72.2	96	7	US-11-144-222-42	Sequence 42, Appl	176	38	70.4	108	7	US-11-127-903-12	Sequence 12, Appl
104	39	72.2	96	7	US-11-182-343-42	Sequence 42, Appl	177	38	70.4	108	7	US-11-127-903-13	Sequence 13, Appl
105	39	72.2	99	7	US-11-195-095-14	Sequence 14, Appl	178	38	70.4	108	7	US-11-106-820-3	Sequence 3, Appl
106	39	72.2	102	7	US-11-049-536-42	Sequence 42, Appl	179	38	70.4	108	7	US-11-221-900-7	Sequence 7, Appl
107	39	72.2	102	7	US-11-199-739-42	Sequence 42, Appl	180	38	70.4	108	7	US-11-143-077-3	Sequence 3, Appl
108	39	72.2	103	7	US-11-064-174-42	Sequence 42, Appl	181	38	70.4	108	7	US-11-190-364-3	Sequence 3, Appl
109	39	72.2	105	7	US-11-155-775-52	Sequence 52, Appl	182	38	70.4	108	7	US-11-147-780-3	Sequence 3, Appl
110	39	72.2	107	6	US-10-925-366A-234	Sequence 234, App	183	38	70.4	108	7	US-11-143-386-3	Sequence 3, Appl
111	39	72.2	107	6	US-11-064-174-33	Sequence 33, Appl	184	38	70.4	108	7	US-11-187-364-3	Sequence 3, Appl
112	39	72.2	107	7	US-11-064-174-37	Sequence 37, Appl	185	38	70.4	109	6	US-10-981-356A-5	Sequence 5, Appl
113	39	72.2	107	7	US-11-064-174-38	Sequence 38, Appl	186	38	70.4	109	7	US-11-040-159-7	Sequence 7, Appl
114	39	72.2	107	7	US-11-064-174-39	Sequence 39, Appl	187	38	70.4	109	7	US-11-040-159-9	Sequence 9, Appl
115	39	72.2	107	7	US-11-064-174-40	Sequence 40, Appl	188	38	70.4	109	7	US-11-040-159-11	Sequence 11, Appl
116	39	72.2	107	7	US-11-064-174-456	Sequence 156, App	189	38	70.4	109	7	US-11-040-159-13	Sequence 13, Appl
117	39	72.2	107	7	US-11-064-174-158	Sequence 158, App	190	38	70.4	109	7	US-11-096-046-5	Sequence 5, Appl
118	39	72.2	107	7	US-11-064-174-168	Sequence 168, App	191	38	70.4	109	7	US-11-127-932-16	Sequence 16, Appl
119	39	72.2	107	7	US-11-064-174-175	Sequence 175, App	192	38	70.4	109	7	US-11-127-932-17	Sequence 17, Appl
120	39	72.2	107	7	US-11-064-174-176	Sequence 176, App	193	38	70.4	109	7	US-11-127-932-20	Sequence 20, Appl
121	39	72.2	108	6	US-10-925-366A-3	Sequence 3, Appl	194	38	70.4	109	7	US-11-127-903-16	Sequence 16, Appl
122	39	72.2	108	6	US-10-925-366A-6	Sequence 6, Appl	195	38	70.4	109	7	US-11-127-903-17	Sequence 17, Appl
123	39	72.2	108	6	US-10-925-366A-232	Sequence 232, App	196	38	70.4	109	7	US-11-127-903-20	Sequence 20, Appl
124	39	72.2	108	6	US-10-771-257-28	Sequence 28, Appl	197	38	70.4	110	7	US-11-049-536-672	Sequence 672, App
125	39	72.2	108	6	US-10-771-257-36	Sequence 36, Appl	198	38	70.4	110	7	US-11-199-739-672	Sequence 672, App
126	39	72.2	108	6	US-10-771-257-63	Sequence 63, Appl	199	38	70.4	111	7	US-11-049-536-100	Sequence 100, App
127	39	72.2	108	6	US-10-515-241-9	Sequence 9, Appl	200	38	70.4	111	7	US-11-199-739-100	Sequence 100, App
128	39	72.2	108	7	US-11-127-677-28	Sequence 28, Appl	201	37	68.5	111	7	US-11-193-512-43	Sequence 43, Appl
129	39	72.2	108	7	US-11-127-677-36	Sequence 36, Appl	202	37	68.5	95	6	US-10-993-543-281	Sequence 281, App
130	39	72.2	108	7	US-11-127-677-61	Sequence 61, Appl	203	37	68.5	95	7	US-11-054-669-58	Sequence 58, Appl
131	39	72.2	108	7	US-11-127-932-19	Sequence 19, Appl	204	37	68.5	95	7	US-11-054-669-61	Sequence 61, Appl
132	39	72.2	108	7	US-11-064-174-32	Sequence 32, Appl	205	37	68.5	95	7	US-11-084-554-111	Sequence 111, App
133	39	72.2	108	7	US-11-064-174-43	Sequence 43, Appl	206	37	68.5	95	7	US-11-084-554-121	Sequence 121, App
134	39	72.2	108	7	US-11-064-174-163	Sequence 163, App	207	37	68.5	95	7	US-11-061-848-35	Sequence 35, Appl
135	39	72.2	108	7	US-11-064-174-167	Sequence 167, App	208	37	68.5	95	7	US-11-061-848-70	Sequence 70, Appl
136	39	72.2	108	7	US-11-127-903-19	Sequence 19, Appl	209	37	68.5	95	7	US-11-004-590-63	Sequence 63, Appl
137	39	72.2	108	7	US-11-049-536-172	Sequence 172, App	210	37	68.5	95	7	US-11-004-590-67	Sequence 67, Appl
138	39	72.2	108	7	US-11-199-739-172	Sequence 172, App	211	37	68.5	95	7	US-11-136-250-111	Sequence 111, App
139	39	72.2	108	7	US-11-102-512-3	Sequence 3, Appl	212	37	68.5	95	7	US-11-136-250-121	Sequence 121, App
140	39	72.2	108	7	US-11-102-512-6	Sequence 6, Appl	213	37	68.5	102	6	US-10-771-257-108	Sequence 108, App
141	39	72.2	109	7	US-11-127-932-14	Sequence 14, Appl	214	37	68.5	102	7	US-11-049-536-22	Sequence 22, Appl
142	39	72.2	109	7	US-11-127-932-18	Sequence 18, Appl	215	37	68.5	102	7	US-11-199-739-22	Sequence 22, Appl
143	39	72.2	109	7	US-11-127-903-14	Sequence 14, Appl	216	37	68.5	103	6	US-10-771-257-102	Sequence 102, App
144	39	72.2	109	7	US-11-127-903-18	Sequence 18, Appl	217	37	68.5	103	6	US-10-771-257-114	Sequence 114, App
145	39	72.2	119	6	US-11-127-903-18	Sequence 18, App	218	37	68.5	108	7	US-11-049-536-248	Sequence 248, App
146	39	72.2	121	6	US-10-993-543-30	Sequence 30, Appl	219	37	68.5	108	7	US-11-049-536-480	Sequence 480, App
147	39	72.2	134	7	US-11-128-900-23	Sequence 23, Appl	220	37	68.5	108	7	US-11-049-536-604	Sequence 604, App
148	39	72.2	134	7	US-11-128-900-97	Sequence 97, Appl	221	37	68.5	108	7	US-11-199-739-248	Sequence 248, App
149	39	72.2	150	7	US-11-128-900-24	Sequence 24, Appl	222	37	68.5	108	7	US-11-199-739-480	Sequence 480, App
150	39	72.2	150	7	US-11-128-900-98	Sequence 98, Appl	223	37	68.5	108	7	US-11-199-739-604	Sequence 604, App
151	39	72.2	236	7	US-11-086-289-8	Sequence 8, Appl	224	37	68.5	110	6	US-11-171-567-209	Sequence 209, App
152	39	72.2	240	6	US-10-925-366A-219	Sequence 219, App	225	37	68.5	119	6	US-10-993-543-122	Sequence 122, App
153	39	72.2	250	7	US-11-054-515-1174	Sequence 1174, Ap	226	37	68.5	127	7	US-11-193-512-29	Sequence 29, Appl
154	39	72.2	250	7	US-11-266-444-1174	Sequence 1174, Ap	227	37	68.5	127	7	US-11-193-512-71	Sequence 71, Appl
155	38	70.4	27	7	US-11-143-077-6	Sequence 6, Appl	228	37	68.5	127	7	US-11-193-512-88	Sequence 88, Appl
156	38	70.4	27	7	US-11-187-364-6	Sequence 6, Appl	229	37	68.5	127	7	US-11-193-512-92	Sequence 92, Appl
157	38	70.4	90	7	US-11-173-071-23	Sequence 23, Appl	230	37	68.5	127	7	US-11-193-512-98	Sequence 98, Appl
158	38	70.4	107	7	US-11-096-074-54	Sequence 54, Appl	231	37	68.5	127	7	US-11-193-512-103	Sequence 103, App
159	38	70.4	107	7	US-11-064-174-44	Sequence 44, Appl	232	37	68.5	213	7	US-11-158-505-34	Sequence 34, Appl
160	38	70.4	107	7	US-11-064-174-162	Sequence 162, App	233	36	66.7	11	7	US-11-223-834-4	Sequence 4, Appl
161	38	70.4	107	7	US-11-095-822-54	Sequence 54, Appl	234	36	66.7	105	7	US-11-155-775-40	Sequence 40, Appl
162	38	70.4	107	7	US-11-154-337-5	Sequence 5, Appl	235	36	66.7	106	7	US-11-223-834-12	Sequence 12, Appl
163	38	70.4	107	7	US-11-182-908-5	Sequence 5, Appl	236	36	66.7	106	7	US-11-004-590-390	Sequence 390, App
164	38	70.4	107	7	US-11-049-536-428	Sequence 428, App	237	36	66.7	106	7	US-11-223-834-9	Sequence 9, Appl
165	38	70.4	107	7	US-11-102-120-5	Sequence 5, Appl	238	36	66.7	106	7	US-11-223-834-10	Sequence 10, Appl
166	38	70.4	107	7	US-11-223-131-5	Sequence 5, Appl	239	36	66.7	106	7	US-11-223-834-11	Sequence 11, Appl
167	38	70.4	107	7	US-11-739-428	Sequence 428, App	240	36	66.7	107	7	US-11-064-174-172	Sequence 172, App
168	38	70.4	108	6	US-10-925-366A-233	Sequence 233, App	241	36	66.7	107	7	US-11-064-174-174	Sequence 174, App
169	38	70.4	108	6	US-10-665-658-3	Sequence 3, Appl	242	36	66.7	108	6	US-10-771-257-4	Sequence 4, Appl
170	38	70.4	108	6	US-10-771-257-35	Sequence 35, Appl	243	36	66.7	108	7	US-11-127-677-4	Sequence 4, Appl
171	38	70.4	108	7	US-11-120-338-3	Sequence 3, Appl	244	36	66.7	108	7	US-11-127-932-11	Sequence 11, Appl

245	36	66.7	108	7	US-11-127-903-11	Sequence 11, Appl	318	34	63.0	248	7	US-11-054-515-1446	Sequence 1446, Ap
246	36	66.7	108	7	US-11-049-536-452	Sequence 452, App	319	34	63.0	248	7	US-11-266-444-1360	Sequence 1360, Ap
247	36	66.7	108	7	US-11-199-739-452	Sequence 452, App	320	34	63.0	248	7	US-11-266-444-1446	Sequence 1446, Ap
248	36	66.7	110	6	US-10-648-816-2	Sequence 2, Appli	321	34	63.0	251	7	US-11-054-515-1921	Sequence 1921, Ap
249	36	66.7	110	6	US-10-648-816-3	Sequence 3, Appli	322	34	63.0	251	7	US-11-266-444-1921	Sequence 1921, Ap
250	36	66.7	110	6	US-10-648-816-4	Sequence 4, Appli	323	34	63.0	426	7	US-11-098-686-10340	Sequence 10340, A
251	36	66.7	110	6	US-10-648-816-6	Sequence 6, Appli	324	33	61.1	94	7	US-11-097-812-9	Sequence 9, Appli
252	36	66.7	110	6	US-10-648-816-7	Sequence 7, Appli	325	33	61.1	106	7	US-11-155-775-8	Sequence 8, Appli
253	36	66.7	110	6	US-10-648-816-8	Sequence 8, Appli	326	33	61.1	106	7	US-11-149-943-34	Sequence 34, Appli
254	36	66.7	257	6	US-10-496-349B-53	Sequence 53, Appl	327	33	61.1	107	7	US-11-064-174-36	Sequence 36, Appli
255	35	64.8	11	7	US-11-108-135-38	Sequence 38, Appl	328	33	61.1	107	7	US-11-064-174-169	Sequence 169, App
256	35	64.8	11	7	US-11-152-846-19	Sequence 19, Appl	329	33	61.1	107	7	US-11-049-536-158	Sequence 158, App
257	35	64.8	11	7	US-11-126-978-38	Sequence 38, Appl	330	33	61.1	108	7	US-11-049-536-288	Sequence 288, App
258	35	64.8	11	7	US-11-203-253A-73	Sequence 73, Appl	331	33	61.1	108	7	US-11-049-536-560	Sequence 560, App
259	35	64.8	11	7	US-11-171-567-4	Sequence 4, Appli	332	33	61.1	108	7	US-11-199-739-288	Sequence 288, App
260	35	64.8	107	6	US-10-507-662-40	Sequence 40, Appl	333	33	61.1	108	7	US-11-199-739-560	Sequence 560, App
261	35	64.8	107	6	US-10-507-662-41	Sequence 41, Appl	334	33	61.1	109	7	US-11-049-536-324	Sequence 324, App
262	35	64.8	107	7	US-11-108-135-46	Sequence 46, Appl	335	33	61.1	109	7	US-11-049-536-332	Sequence 332, App
263	35	64.8	107	7	US-11-126-978-46	Sequence 46, Appl	336	33	61.1	109	7	US-11-199-739-324	Sequence 324, App
264	35	64.8	107	7	US-11-165-023-7	Sequence 7, Appli	337	33	61.1	109	7	US-11-199-739-332	Sequence 332, App
265	35	64.8	107	7	US-11-203-253A-4	Sequence 4, Appli	338	33	61.1	111	7	US-11-049-536-86	Sequence 86, Appli
266	35	64.8	107	7	US-11-203-253A-4	Sequence 4, Appli	339	33	61.1	111	7	US-11-199-739-86	Sequence 86, Appli
267	35	64.8	108	6	US-10-925-366A-155	Sequence 155, App	340	33	61.1	173	7	US-11-206-587-35	Sequence 35, Appl
268	35	64.8	108	6	US-10-771-257-33	Sequence 33, Appl	341	33	61.1	170	7	US-11-100-183-50	Sequence 50, Appl
269	35	64.8	108	6	US-10-771-257-39	Sequence 39, Appl	342	33	61.1	228	7	US-11-100-183-42	Sequence 42, Appl
270	35	64.8	108	7	US-11-127-677-33	Sequence 33, Appl	343	33	61.1	234	7	US-11-100-183-41	Sequence 41, Appl
271	35	64.8	108	7	US-11-127-677-39	Sequence 39, Appl	344	33	61.1	248	6	US-10-793-626-464	Sequence 464, App
272	35	64.8	109	7	US-11-102-201-2	Sequence 2, Appli	345	33	61.1	265	7	US-11-096-568A-16031	Sequence 16031, A
273	35	64.8	109	7	US-11-049-536-372	Sequence 372, App	346	33	61.1	265	7	US-11-096-568A-22573	Sequence 22573, A
274	35	64.8	109	7	US-11-199-739-372	Sequence 372, App	347	33	61.1	285	7	US-11-096-568A-16030	Sequence 16030, A
275	35	64.8	110	7	US-11-049-536-468	Sequence 468, App	348	33	61.1	285	7	US-11-096-568A-22572	Sequence 22572, A
276	35	64.8	110	7	US-11-199-739-468	Sequence 468, App	349	33	61.1	345	7	US-11-100-352-4	Sequence 4, Appli
277	35	64.8	119	6	US-10-993-543-130	Sequence 130, App	350	33	61.1	364	7	US-11-096-568A-16029	Sequence 16029, A
278	34	63.0	11	7	US-11-203-253A-8	Sequence 8, Appli	351	33	61.1	364	7	US-11-096-568A-22571	Sequence 22571, A
279	34	63.0	92	7	US-11-144-248-18	Sequence 18, Appl	352	32	59.3	11	6	US-10-981-356A-7	Sequence 7, Appli
280	34	63.0	92	7	US-11-144-248-18	Sequence 18, Appl	353	32	59.3	11	7	US-11-093-274-10	Sequence 10, Appl
281	34	63.0	92	7	US-11-182-343-18	Sequence 18, Appl	354	32	59.3	11	7	US-11-093-274-11	Sequence 11, Appl
282	34	63.0	95	7	US-11-004-590-70	Sequence 70, Appl	355	32	59.3	11	7	US-11-096-046-7	Sequence 12, Appl
283	34	63.0	95	7	US-11-004-590-71	Sequence 71, Appl	356	32	59.3	11	7	US-11-051-453-19	Sequence 19, Appl
284	34	63.0	96	7	US-11-084-554-144	Sequence 144, App	357	32	59.3	11	7	US-11-104-117-7	Sequence 7, Appli
285	34	63.0	96	7	US-11-084-554-147	Sequence 147, App	358	32	59.3	11	7	US-11-233-252-7	Sequence 7, Appli
286	34	63.0	96	7	US-11-136-250-144	Sequence 144, App	359	32	59.3	11	7	US-11-171-567-7	Sequence 7, Appli
287	34	63.0	96	7	US-11-136-250-147	Sequence 147, App	360	32	59.3	11	7	US-11-171-567-16	Sequence 16, Appl
288	34	63.0	107	6	US-10-537-061-8	Sequence 8, Appli	361	32	59.3	11	7	US-11-093-274-33	Sequence 33, Appl
289	34	63.0	107	7	US-11-064-174-179	Sequence 179, App	362	32	59.3	94	7	US-10-993-543-273	Sequence 273, App
290	34	63.0	107	7	US-11-049-536-632	Sequence 632, App	363	32	59.3	95	6	US-10-993-543-283	Sequence 283, App
291	34	63.0	107	7	US-11-199-739-632	Sequence 632, App	364	32	59.3	95	6	US-10-993-543-283	Sequence 284, App
292	34	63.0	108	7	US-11-049-536-228	Sequence 228, App	365	32	59.3	95	7	US-11-054-669-60	Sequence 60, Appl
293	34	63.0	108	7	US-11-049-536-596	Sequence 596, App	366	32	59.3	95	7	US-11-054-669-67	Sequence 67, Appl
294	34	63.0	108	7	US-11-199-739-228	Sequence 228, App	367	32	59.3	95	7	US-11-054-669-68	Sequence 68, Appl
295	34	63.0	108	7	US-11-199-739-596	Sequence 596, App	368	32	59.3	95	7	US-11-054-669-69	Sequence 69, Appl
296	34	63.0	108	7	US-11-102-512-89	Sequence 89, Appl	369	32	59.3	95	7	US-11-054-669-86	Sequence 86, Appl
297	34	63.0	109	7	US-11-049-536-598	Sequence 598, App	370	32	59.3	95	7	US-11-084-554-125	Sequence 125, App
298	34	63.0	109	7	US-11-049-536-620	Sequence 620, App	371	32	59.3	95	7	US-11-084-554-133	Sequence 133, App
299	34	63.0	109	7	US-11-049-536-644	Sequence 644, App	372	32	59.3	95	7	US-11-084-554-138	Sequence 138, App
300	34	63.0	109	7	US-11-049-536-684	Sequence 684, App	373	32	59.3	95	7	US-11-084-554-139	Sequence 139, App
301	34	63.0	109	7	US-11-199-739-598	Sequence 598, App	374	32	59.3	95	7	US-11-084-554-140	Sequence 140, App
302	34	63.0	109	7	US-11-199-739-620	Sequence 620, App	375	32	59.3	95	7	US-11-061-848-34	Sequence 34, Appl
303	34	63.0	109	7	US-11-199-739-644	Sequence 644, App	376	32	59.3	95	7	US-11-061-848-44	Sequence 44, Appl
304	34	63.0	109	7	US-11-199-739-684	Sequence 684, App	377	32	59.3	95	7	US-11-061-848-45	Sequence 45, Appl
305	34	63.0	118	6	US-10-993-543-6	Sequence 6, Appli	378	32	59.3	95	7	US-11-061-848-46	Sequence 46, Appl
306	34	63.0	120	6	US-10-993-543-62	Sequence 62, Appl	379	32	59.3	95	7	US-11-061-848-52	Sequence 52, Appl
307	34	63.0	120	6	US-10-993-543-162	Sequence 162, App	380	32	59.3	95	7	US-11-061-848-57	Sequence 57, Appl
308	34	63.0	241	7	US-11-054-515-1577	Sequence 1577, Ap	381	32	59.3	95	7	US-11-061-848-64	Sequence 64, Appl
309	34	63.0	241	7	US-11-266-444-1577	Sequence 1577, Ap	382	32	59.3	95	7	US-11-061-848-65	Sequence 65, Appl
310	34	63.0	242	7	US-11-054-515-1915	Sequence 1915, Ap	383	32	59.3	95	7	US-11-061-848-66	Sequence 66, Appl
311	34	63.0	242	7	US-11-266-444-1915	Sequence 1915, Ap	384	32	59.3	95	7	US-11-061-848-72	Sequence 72, Appl
312	34	63.0	243	6	US-10-537-061-2	Sequence 2, Appli	385	32	59.3	95	7	US-11-004-590-56	Sequence 56, Appl
313	34	63.0	243	6	US-10-537-061-3	Sequence 3, Appli	386	32	59.3	95	7	US-11-004-590-58	Sequence 58, Appl
314	34	63.0	246	7	US-11-054-515-2075	Sequence 2075, Ap	387	32	59.3	95	7	US-11-004-590-56	Sequence 56, Appl
315	34	63.0	246	7	US-11-266-444-2075	Sequence 2075, Ap	388	32	59.3	95	7	US-11-004-590-56	Sequence 56, Appl
316	34	63.0	247	7	US-11-054-515-3240	Sequence 3240, Ap	389	32	59.3	95	7	US-11-004-590-56	Sequence 56, Appl
317	34	63.0	248	7	US-11-054-515-1360	Sequence 1360, Ap	390	32	59.3	95	7	US-11-004-590-75	Sequence 75, Appl

391	32	59.3	95	7	US-11-004-590-88	Sequence 88, Appl	464	32	59.3	115	7	US-11-009-873A-307	Sequence 307, App
392	32	59.3	95	7	US-11-136-250-125	Sequence 125, App	465	32	59.3	115	7	US-11-009-769A-307	Sequence 307, App
393	32	59.3	95	7	US-11-136-250-133	Sequence 133, App	466	32	59.3	119	6	US-10-993-543-26	Sequence 26, Appl
394	32	59.3	95	7	US-11-136-250-138	Sequence 138, App	467	32	59.3	119	6	US-10-993-543-82	Sequence 82, Appl
395	32	59.3	95	7	US-11-136-250-139	Sequence 139, App	468	32	59.3	120	6	US-10-993-543-78	Sequence 78, Appl
396	32	59.3	95	7	US-11-136-250-140	Sequence 140, App	469	32	59.3	128	6	US-10-721-763-31	Sequence 31, Appl
397	32	59.3	102	7	US-11-049-536-30	Sequence 30, Appl	470	32	59.3	128	7	US-11-051-453-50	Sequence 50, Appl
398	32	59.3	102	7	US-11-049-536-38	Sequence 38, Appl	471	32	59.3	139	7	US-11-128-900-16	Sequence 16, Appl
399	32	59.3	102	7	US-11-199-739-30	Sequence 30, Appl	472	32	59.3	139	7	US-11-128-900-90	Sequence 90, Appl
400	32	59.3	102	7	US-11-199-739-38	Sequence 38, Appl	473	32	59.3	142	7	US-11-128-900-91	Sequence 91, Appl
401	32	59.3	105	7	US-11-084-554-12	Sequence 12, Appl	474	32	59.3	146	7	US-11-128-900-21	Sequence 21, Appl
402	32	59.3	105	7	US-11-155-775-12	Sequence 12, Appl	475	32	59.3	146	7	US-11-128-900-93	Sequence 93, Appl
403	32	59.3	105	7	US-11-155-775-60	Sequence 60, Appl	476	32	59.3	196	7	US-11-098-686-10778	Sequence 10778, A
404	32	59.3	105	7	US-11-158-775-64	Sequence 64, Appl	477	32	59.3	222	6	US-10-467-657-4792	Sequence 4792, Ap
405	32	59.3	105	7	US-11-136-250-12	Sequence 12, Appl	478	32	59.3	234	7	US-11-128-900-17	Sequence 17, Appl
406	32	59.3	107	7	US-11-040-159-17	Sequence 17, Appl	479	32	59.3	234	7	US-11-128-900-69	Sequence 69, Appl
407	32	59.3	107	7	US-11-084-554-1	Sequence 1, Appl	480	32	59.3	236	7	US-11-086-289-4	Sequence 4, Appl
408	32	59.3	107	7	US-11-093-274-24	Sequence 24, Appl	481	32	59.3	236	7	US-11-086-289-20	Sequence 20, Appl
409	32	59.3	107	7	US-11-104-117-1	Sequence 1, Appl	482	32	59.3	241	7	US-11-054-515-1932	Sequence 1932, Ap
410	32	59.3	107	7	US-11-104-117-9	Sequence 9, Appl	483	32	59.3	241	7	US-11-054-515-2054	Sequence 2054, Ap
411	32	59.3	107	7	US-11-126-798-47	Sequence 47, Appl	484	32	59.3	241	7	US-11-266-444-2054	Sequence 2054, Ap
412	32	59.3	107	7	US-11-136-250-1	Sequence 1, Appl	485	32	59.3	244	7	US-11-054-515-82	Sequence 82, Appl
413	32	59.3	107	7	US-11-049-536-157	Sequence 157, App	486	32	59.3	244	7	US-11-054-515-164	Sequence 164, App
414	32	59.3	107	7	US-11-233-252-1	Sequence 1, Appl	487	32	59.3	244	7	US-11-054-515-261	Sequence 261, App
415	32	59.3	107	7	US-11-233-252-9	Sequence 9, Appl	488	32	59.3	244	7	US-11-054-515-280	Sequence 280, App
416	32	59.3	108	6	US-10-771-257-80	Sequence 80, Appl	489	32	59.3	244	7	US-11-266-444-82	Sequence 82, Appl
417	32	59.3	108	6	US-10-886-383-2	Sequence 2, Appl	490	32	59.3	244	7	US-11-266-444-164	Sequence 164, App
418	32	59.3	108	6	US-10-886-383-4	Sequence 4, Appl	491	32	59.3	244	7	US-11-266-444-261	Sequence 261, App
419	32	59.3	108	7	US-11-093-274-22	Sequence 22, Appl	492	32	59.3	244	7	US-11-266-444-280	Sequence 280, App
420	32	59.3	108	7	US-11-093-274-23	Sequence 23, Appl	493	32	59.3	244	7	US-11-054-515-919	Sequence 919, App
421	32	59.3	108	7	US-11-127-677-78	Sequence 78, Appl	494	32	59.3	249	7	US-11-054-515-1635	Sequence 1635, Ap
422	32	59.3	108	7	US-11-051-453-5	Sequence 5, Appl	495	32	59.3	249	7	US-11-266-444-919	Sequence 919, App
423	32	59.3	108	7	US-11-049-536-180	Sequence 180, App	496	32	59.3	249	7	US-11-266-444-1635	Sequence 1635, Ap
424	32	59.3	108	7	US-11-049-536-216	Sequence 216, App	497	32	59.3	251	7	US-11-054-515-1049	Sequence 1049, Ap
425	32	59.3	108	7	US-11-049-536-264	Sequence 264, App	498	32	59.3	251	7	US-11-266-444-1049	Sequence 1, Appl
426	32	59.3	108	7	US-11-049-536-264	Sequence 264, App	499	32	59.3	264	7	US-11-176-525-1	Sequence 52, Appl
427	32	59.3	108	7	US-11-049-536-280	Sequence 280, App	500	32	59.3	382	7	US-11-082-762-52	Sequence 7295, Ap
428	32	59.3	108	7	US-11-049-536-304	Sequence 304, App	501	32	59.3	402	7	US-11-087-099-7295	Sequence 4102, Ap
429	32	59.3	108	7	US-11-049-536-332	Sequence 332, App	502	32	59.3	421	6	US-10-467-657-4102	Sequence 2820, Ap
430	32	59.3	108	7	US-11-049-536-340	Sequence 340, App	503	32	59.3	480	6	US-10-793-626-2820	Sequence 31281, A
431	32	59.3	108	7	US-11-049-536-512	Sequence 512, App	504	32	59.3	549	7	US-11-096-568A-31281	Sequence 253, App
432	32	59.3	108	7	US-11-049-536-564	Sequence 564, App	505	32	59.3	609	6	US-10-511-538-253	Sequence 27682, A
433	32	59.3	108	7	US-11-049-536-628	Sequence 628, App	506	32	59.3	614	7	US-11-086-568A-27682	Sequence 32880, A
434	32	59.3	108	7	US-11-199-739-180	Sequence 180, App	507	32	59.3	630	7	US-11-096-568A-31280	Sequence 110, App
435	32	59.3	108	7	US-11-199-739-216	Sequence 216, App	508	32	59.3	697	7	US-11-052-554A-110	Sequence 31279, A
436	32	59.3	108	7	US-11-199-739-260	Sequence 260, App	509	32	59.3	705	7	US-11-096-568A-31279	Sequence 12, Appl
437	32	59.3	108	7	US-11-199-739-264	Sequence 264, App	510	32	59.3	94	7	US-11-097-812-12	Sequence 87, Appl
438	32	59.3	108	7	US-11-199-739-280	Sequence 280, App	511	31	57.4	95	7	US-11-054-669-87	Sequence 131, App
439	32	59.3	108	7	US-11-199-739-304	Sequence 304, App	512	31	57.4	95	7	US-11-084-554-131	Sequence 89, Appl
440	32	59.3	108	7	US-11-199-739-332	Sequence 332, App	513	31	57.4	95	7	US-11-004-590-89	Sequence 131, App
441	32	59.3	108	7	US-11-199-739-440	Sequence 440, App	514	31	57.4	95	7	US-11-136-250-131	Sequence 26, Appl
442	32	59.3	108	7	US-11-199-739-512	Sequence 512, App	515	31	57.4	102	7	US-11-049-536-26	Sequence 26, Appl
443	32	59.3	108	7	US-11-199-739-564	Sequence 564, App	516	31	57.4	102	7	US-11-199-739-26	Sequence 194, App
444	32	59.3	108	7	US-11-199-739-628	Sequence 628, App	517	31	57.4	108	6	US-10-925-366A-194	Sequence 536, App
445	32	59.3	109	6	US-10-771-257-29	Sequence 29, Appl	518	31	57.4	108	7	US-11-049-536-536	Sequence 556, App
446	32	59.3	109	6	US-10-834-397-28	Sequence 28, Appl	519	31	57.4	108	7	US-11-049-536-556	Sequence 556, App
447	32	59.3	109	6	US-10-834-397-43	Sequence 43, Appl	520	31	57.4	108	7	US-11-199-739-536	Sequence 556, App
448	32	59.3	109	7	US-11-127-677-29	Sequence 29, Appl	521	31	57.4	108	7	US-11-199-739-536	Sequence 40, Appl
449	32	59.3	109	7	US-11-049-536-176	Sequence 176, App	522	31	57.4	108	7	US-11-102-512-40	Sequence 516, App
450	32	59.3	109	7	US-11-049-536-636	Sequence 636, App	523	31	57.4	110	7	US-11-049-536-516	Sequence 516, App
451	32	59.3	109	7	US-11-049-536-660	Sequence 660, App	524	31	57.4	110	7	US-11-199-739-516	Sequence 309, App
452	32	59.3	109	7	US-11-199-739-176	Sequence 176, App	525	31	57.4	115	7	US-11-009-840A-309	Sequence 309, App
453	32	59.3	109	7	US-11-199-739-636	Sequence 636, App	526	31	57.4	115	7	US-11-009-873A-309	Sequence 309, App
454	32	59.3	109	7	US-11-199-739-660	Sequence 660, App	527	31	57.4	115	7	US-11-009-769A-309	Sequence 90, Appl
455	32	59.3	110	7	US-11-049-536-376	Sequence 376, App	528	31	57.4	119	6	US-10-993-543-90	Sequence 90, Appl
456	32	59.3	110	7	US-11-049-536-544	Sequence 544, App	529	31	57.4	121	6	US-10-993-543-154	Sequence 154, App
457	32	59.3	110	7	US-11-049-536-680	Sequence 680, App	530	31	57.4	122	6	US-10-993-543-106	Sequence 106, App
458	32	59.3	110	7	US-11-199-739-376	Sequence 376, App	531	31	57.4	139	7	US-11-128-900-22	Sequence 22, Appl
459	32	59.3	110	7	US-11-199-739-544	Sequence 544, App	532	31	57.4	139	7	US-11-128-900-96	Sequence 96, Appl
460	32	59.3	110	7	US-11-199-739-680	Sequence 680, App	533	31	57.4	154	7	US-11-096-568A-16014	Sequence 16014, A
461	32	59.3	111	7	US-11-049-536-66	Sequence 66, Appl	534	31	57.4	169	7	US-11-096-568A-16013	Sequence 16013, A
462	32	59.3	111	7	US-11-199-739-66	Sequence 66, Appl	535	31	57.4	180	7	US-11-096-568A-5388	Sequence 5388, Ap
463	32	59.3	115	7	US-11-009-840A-307	Sequence 307, App	536	31	57.4				



537	31	57.4	201	7	US-11-096-568A-5387	Sequence 5387, Ap	610	30	55.6	409	7	US-11-096-568A-3006	Sequence 3006, Ap
538	31	57.4	214	7	US-11-128-900-71	Sequence 71, Appl	611	30	55.6	421	6	US-10-793-626-1818	Sequence 1818, Ap
539	31	57.4	237	7	US-11-096-568A-5386	Sequence 5386, Ap	612	30	55.6	427	7	US-11-096-568A-28864	Sequence 28864, A
540	31	57.4	246	7	US-11-240-769-73	Sequence 73, Appl	613	30	55.6	441	6	US-10-909-769-29	Sequence 29, Appl
541	31	57.4	248	7	US-11-054-515-1104	Sequence 1104, Ap	614	30	55.6	456	7	US-11-069-642-15	Sequence 15, Appl
542	31	57.4	248	7	US-11-266-444-1104	Sequence 1104, Ap	615	30	55.6	466	7	US-11-087-099-6743	Sequence 6743, Ap
543	31	57.4	253	7	US-11-054-515-936	Sequence 936, App	616	30	55.6	514	6	US-10-506-454-1380	Sequence 1380, Ap
544	31	57.4	253	7	US-11-266-444-936	Sequence 936, App	617	30	55.6	531	7	US-11-199-544-31	Sequence 31, Appl
545	31	57.4	257	7	US-11-056-825-10	Sequence 10, Appl	618	30	55.6	672	7	US-11-294-997-36	Sequence 36, Appl
546	31	57.4	269	7	US-11-096-568A-33646	Sequence 33646, A	619	30	55.6	676	7	US-11-098-686-10486	Sequence 10486, A
547	31	57.4	353	7	US-11-096-568A-12269	Sequence 12269, A	620	30	55.6	946	7	US-11-207-626A-44	Sequence 44, Appl
548	31	57.4	362	7	US-11-012-762-62	Sequence 62, Appl	621	30	55.6	952	7	US-11-207-626A-45	Sequence 45, Appl
549	31	57.4	367	6	US-10-467-657-1440	Sequence 1440, Ap	622	30	55.6	953	7	US-11-207-626A-46	Sequence 46, Appl
550	31	57.4	376	7	US-11-096-568A-31807	Sequence 31807, A	623	30	55.6	958	7	US-11-207-626A-43	Sequence 43, Appl
551	31	57.4	385	7	US-11-096-568A-31806	Sequence 31806, A	624	30	55.6	1236	7	US-11-199-544-69	Sequence 69, Appl
552	31	57.4	471	7	US-11-096-568A-12268	Sequence 12268, A	625	30	55.6	1316	7	US-11-087-099-10229	Sequence 10229, A
553	31	57.4	506	7	US-11-096-568A-12267	Sequence 12267, A	626	30	55.6	1581	7	US-11-090-439-24	Sequence 24, Appl
554	31	57.4	619	6	US-11-098-686-10201	Sequence 10201, A	627	30	55.6	1581	7	US-11-090-439-26	Sequence 26, Appl
555	31	57.4	900	6	US-10-909-769-20	Sequence 20, Appl	628	30	55.6	1588	6	US-10-995-561-527	Sequence 527, App
556	31	57.4	1070	7	US/11/062	Sequence 4, Appl	629	29	53.7	9	7	US-11-045-024-1214	Sequence 1214, Ap
557	31	57.4	1095	7	US/11/062	Sequence 7, Appl	630	29	53.7	9	7	US-11-045-024-4107	Sequence 4107, Ap
558	31	57.4	1169	7	US-11-077-550-20	Sequence 20, Appl	631	29	53.7	9	7	US-11-045-024-6357	Sequence 6357, Ap
559	31	57.4	5024	6	US-10-793-626-2364	Sequence 2964, Ap	632	29	53.7	9	7	US-11-045-024-14142	Sequence 14142, A
560	30	55.6	11	7	US-11-203-251A-8	Sequence 8, Appl	633	29	53.7	10	7	US-11-045-024-1329	Sequence 1329, Ap
561	30	55.6	11	7	US-11-203-251A-73	Sequence 73, Appl	634	29	53.7	10	7	US-11-045-024-1331	Sequence 1331, Ap
562	30	55.6	11	7	US-11-171-567-2	Sequence 2, Appl	635	29	53.7	10	7	US-11-045-024-6360	Sequence 6360, Ap
563	30	55.6	11	7	US-11-171-567-3	Sequence 3, Appl	636	29	53.7	11	7	US-11-009-939-28	Sequence 28, Appl
564	30	55.6	11	7	US-11-171-567-10	Sequence 10, Appl	637	29	53.7	11	7	US-11-045-024-1435	Sequence 1435, Ap
565	30	55.6	79	6	US-10-746-909-10	Sequence 10, Appl	638	29	53.7	11	7	US-11-045-024-1438	Sequence 1438, Ap
566	30	55.6	95	7	US-11-054-669-93	Sequence 93, Appl	639	29	53.7	11	7	US-11-045-024-7275	Sequence 7275, Ap
567	30	55.6	95	7	US-11-084-554-106	Sequence 106, App	640	29	53.7	11	7	US-11-171-567-15	Sequence 15, Appl
568	30	55.6	95	7	US-11-061-848-49	Sequence 49, Appl	641	29	53.7	15	7	US-11-045-024-13486	Sequence 13486, A
569	30	55.6	95	7	US-11-004-590-98	Sequence 98, Appl	642	29	53.7	25	7	US-11-207-078-206	Sequence 206, Appl
570	30	55.6	107	7	US-11-112-240-8	Sequence 8, Appl	643	29	53.7	25	7	US-11-207-078-55	Sequence 55, Appl
571	30	55.6	107	7	US-11-112-304A-8	Sequence 8, Appl	644	29	53.7	95	7	US-11-054-669-90	Sequence 90, Appl
572	30	55.6	107	7	US-11-165-023-1	Sequence 1, Appl	645	29	53.7	95	7	US-11-084-554-119	Sequence 119, App
573	30	55.6	107	7	US-11-165-023-2	Sequence 2, Appl	646	29	53.7	95	7	US-11-061-848-22	Sequence 22, Appl
574	30	55.6	107	7	US-11-165-023-3	Sequence 3, Appl	647	29	53.7	95	7	US-11-061-848-69	Sequence 69, Appl
575	30	55.6	107	7	US-11-165-023-5	Sequence 5, Appl	648	29	53.7	95	7	US-11-004-590-95	Sequence 95, Appl
576	30	55.6	107	7	US-11-165-023-6	Sequence 6, Appl	649	29	53.7	95	7	US-11-136-250-119	Sequence 119, App
577	30	55.6	107	7	US-11-165-023-6	Sequence 6, Appl	650	29	53.7	102	6	US-10-771-257-104	Sequence 104, App
578	30	55.6	107	7	US-11-203-251A-65	Sequence 65, Appl	651	29	53.7	103	6	US-10-771-257-98	Sequence 98, Appl
579	30	55.6	107	7	US-11-203-251A-59	Sequence 69, Appl	652	29	53.7	103	6	US-10-771-257-100	Sequence 100, App
580	30	55.6	107	7	US-11-203-251A-65	Sequence 65, Appl	653	29	53.7	103	6	US-10-771-257-109	Sequence 109, App
581	30	55.6	107	7	US-11-203-251A-69	Sequence 69, Appl	654	29	53.7	105	7	US-11-096-074-55	Sequence 55, App
582	30	55.6	108	6	US-10-925-366A-163	Sequence 163, App	655	29	53.7	105	7	US-11-155-775-44	Sequence 44, Appl
583	30	55.6	108	6	US-10-925-366A-169	Sequence 169, App	656	29	53.7	105	7	US-11-095-822-55	Sequence 55, Appl
584	30	55.6	108	6	US-10-925-366A-288	Sequence 288, App	657	29	53.7	106	7	US-11-096-074-51	Sequence 51, Appl
585	30	55.6	108	7	US-11-165-023-4	Sequence 4, Appl	658	29	53.7	106	7	US-11-155-775-4	Sequence 4, Appl
586	30	55.6	108	7	US-11-049-536-420	Sequence 420, App	659	29	53.7	106	7	US-11-155-775-20	Sequence 20, Appl
587	30	55.6	108	7	US-11-199-739-420	Sequence 420, App	660	29	53.7	106	7	US-11-107-028-8	Sequence 8, Appl
588	30	55.6	108	7	US-11-217-919-93	Sequence 93, Appl	661	29	53.7	106	7	US-11-107-028-9	Sequence 9, Appl
589	30	55.6	114	6	US-10-925-366A-12	Sequence 12, Appl	662	29	53.7	106	7	US-11-095-822-51	Sequence 51, Appl
590	30	55.6	119	7	US-11-217-919-3	Sequence 3, Appl	663	29	53.7	106	7	US-11-016-386-1	Sequence 1, Appl
591	30	55.6	179	6	US-10-793-626-1922	Sequence 1922, Ap	664	29	53.7	107	7	US-11-064-174-160	Sequence 160, App
592	30	55.6	214	7	US-11-096-568A-3005	Sequence 3005, Ap	665	29	53.7	107	6	US-10-925-366A-141	Sequence 141, App
593	30	55.6	221	7	US-11-096-568A-28866	Sequence 28866, A	666	29	53.7	108	6	US-10-925-366A-154	Sequence 154, App
594	30	55.6	229	7	US-11-170-653-54	Sequence 54, Appl	667	29	53.7	108	6	US-10-925-366A-171	Sequence 171, App
595	30	55.6	229	7	US-11-072-512-3468	Sequence 1421, Ap	668	29	53.7	108	6	US-10-925-366A-177	Sequence 177, App
596	30	55.6	231	7	US-11-096-568A-1421	Sequence 1421, Ap	669	29	53.7	108	6	US-10-925-366A-179	Sequence 179, App
597	30	55.6	256	7	US-11-054-515-1027	Sequence 1027, Ap	670	29	53.7	108	6	US-10-925-366A-181	Sequence 181, App
598	30	55.6	256	7	US-11-266-444-1027	Sequence 1027, Ap	671	29	53.7	108	6	US-10-925-366A-184	Sequence 184, App
599	30	55.6	265	7	US-11-272-833-5	Sequence 5, Appl	672	29	53.7	108	6	US-10-771-257-78	Sequence 78, Appl
600	30	55.6	274	7	US-11-272-833-6	Sequence 6, Appl	673	29	53.7	108	7	US-11-009-939-27	Sequence 27, Appl
601	30	55.6	279	7	US-11-272-833-2	Sequence 2, Appl	674	29	53.7	108	7	US-11-127-677-76	Sequence 76, Appl
602	30	55.6	282	7	US-11-096-568A-3004	Sequence 3004, Ap	675	29	53.7	108	7	US-11-064-174-31	Sequence 31, Appl
603	30	55.6	286	7	US-11-087-099-2805	Sequence 2805, A	676	29	53.7	119	6	US-11-093-543-102	Sequence 102, App
604	30	55.6	289	7	US-11-096-568A-28865	Sequence 28865, A	677	29	53.7	128	7	US-11-116-144-147	Sequence 147, App
605	30	55.6	334	7	US-11-207-626A-22	Sequence 22, Appl	678	29	53.7	128	7	US-11-220-372-147	Sequence 147, App
606	30	55.6	341	6	US-10-793-626-2966	Sequence 2966, Ap	679	29	53.7	130	7	US-11-087-099-10148	Sequence 10148, A
607	30	55.6	343	6	US-10-453-372-1122	Sequence 1122, Ap	680	29	53.7	152	7	US-11-128-900-18	Sequence 18, Appl
608	30	55.6	373	7	US-11-087-099-6324	Sequence 6324, Ap	681	29	53.7	152	7	US-11-128-900-95	Sequence 95, Appl
609	30	55.6	409	7	US-11-096-568A-3003	Sequence 3003, Ap	682	29	53.7	180	7	US-11-096-568A-11638	Sequence 11638, A

683	29	53.7	196	7	US-11-087-099-6085	Sequence 6085, Ap	756	28	51.9	41	7	US-11-096-568A-8716	Sequence 8716, Ap
684	29	53.7	287	6	US-10-793-626-4538	Sequence 2538, Ap	757	28	51.9	47	6	US-10-973-377-41	Sequence 41, Appl
685	29	53.7	295	7	US-11-098-686-10147	Sequence 10147, A	758	28	51.9	47	6	US-10-973-377-41	Sequence 106, App
686	29	53.7	297	6	US-10-485-517-287	Sequence 287, App	759	28	51.9	92	6	US-10-968-629-31	Sequence 31, Appl
687	29	53.7	301	7	US-11-096-568A-12824	Sequence 12824, A	760	28	51.9	95	6	US-10-993-543-278	Sequence 278, App
688	29	53.7	302	7	US-11-096-568A-12823	Sequence 12823, A	761	28	51.9	95	7	US-11-054-669-70	Sequence 70, Appl
689	29	53.7	319	6	US-10-793-626-1040	Sequence 1040, Ap	762	28	51.9	95	7	US-11-054-669-72	Sequence 72, Appl
690	29	53.7	323	7	US-11-096-568A-28336	Sequence 28336, A	763	28	51.9	95	7	US-11-084-554-124	Sequence 124, App
691	29	53.7	334	7	US-11-096-568A-11637	Sequence 11637, A	764	28	51.9	95	7	US-11-084-554-134	Sequence 134, App
692	29	53.7	346	7	US-11-096-568A-17237	Sequence 17237, A	765	28	51.9	95	7	US-11-061-848-47	Sequence 47, Appl
693	29	53.7	352	7	US-11-096-568A-28335	Sequence 28335, A	766	28	51.9	95	7	US-11-061-848-56	Sequence 56, Appl
694	29	53.7	358	7	US-11-072-175-209	Sequence 209, App	767	28	51.9	95	7	US-11-061-848-71	Sequence 71, Appl
695	29	53.7	369	7	US-11-096-568A-12822	Sequence 12822, A	768	28	51.9	95	7	US-11-084-590-54	Sequence 54, Appl
696	29	53.7	370	7	US-11-087-099-7005	Sequence 7005, Ap	769	28	51.9	95	7	US-11-004-590-57	Sequence 57, Appl
697	29	53.7	376	6	US-10-501-035-289	Sequence 289, App	770	28	51.9	95	7	US-11-136-250-124	Sequence 124, App
698	29	53.7	397	7	US-11-096-568A-28928	Sequence 28928, A	771	28	51.9	95	7	US-11-136-250-134	Sequence 134, App
699	29	53.7	401	7	US-11-134-795-28	Sequence 28, Appl	772	28	51.9	101	7	US-11-049-536-34	Sequence 34, Appl
700	29	53.7	401	7	US-11-096-568A-17236	Sequence 17236, A	773	28	51.9	101	7	US-11-199-739-34	Sequence 34, Appl
701	29	53.7	405	6	US-10-506-454-650	Sequence 650, App	774	28	51.9	103	6	US-10-771-257-99	Sequence 99, Appl
702	29	53.7	407	7	US-11-087-099-9116	Sequence 9116, Ap	775	28	51.9	103	6	US-10-771-257-110	Sequence 110, App
703	29	53.7	409	7	US-11-087-099-4473	Sequence 4473, Ap	776	28	51.9	103	6	US-10-771-257-111	Sequence 111, App
704	29	53.7	411	7	US-11-096-568A-17235	Sequence 17235, A	777	28	51.9	103	6	US-10-771-257-113	Sequence 113, App
705	29	53.7	412	7	US-11-087-099-2171	Sequence 2171, Ap	778	28	51.9	105	6	US-10-771-257-103	Sequence 103, App
706	29	53.7	414	7	US-11-087-099-6301	Sequence 6301, Ap	779	28	51.9	106	7	US-11-064-174-171	Sequence 171, App
707	29	53.7	443	7	US-11-096-568A-28927	Sequence 28927, A	780	28	51.9	107	6	US-10-982-440-62	Sequence 62, Appl
708	29	53.7	447	7	US-11-096-568A-28926	Sequence 28926, A	781	28	51.9	107	6	US-10-515-241-1	Sequence 1, Appl
709	29	53.7	448	7	US-11-087-099-12070	Sequence 12070, A	782	28	51.9	107	7	US-11-064-174-34	Sequence 34, Appl
710	29	53.7	448	7	US-11-096-568A-20631	Sequence 20631, A	783	28	51.9	107	7	US-11-051-453-31	Sequence 31, Appl
711	29	53.7	451	6	US-10-467-657-366	Sequence 366, App	784	28	51.9	107	7	US-11-049-536-116	Sequence 116, App
712	29	53.7	462	7	US-11-087-099-8690	Sequence 8690, Ap	785	28	51.9	107	7	US-11-049-536-159	Sequence 159, App
713	29	53.7	467	6	US-10-467-657-2612	Sequence 2612, Ap	786	28	51.9	107	7	US-11-199-739-116	Sequence 116, App
714	29	53.7	472	7	US-11-087-099-7602	Sequence 7602, Ap	787	28	51.9	107	7	US-11-199-739-159	Sequence 159, App
715	29	53.7	487	6	US-10-980-722-2	Sequence 2, Appl	788	28	51.9	108	6	US-10-925-366A-95	Sequence 95, Appl
716	29	53.7	498	7	US-11-096-568A-17065	Sequence 17065, A	789	28	51.9	108	6	US-10-925-366A-149	Sequence 149, App
717	29	53.7	499	7	US-11-096-568A-20630	Sequence 20630, A	790	28	51.9	108	7	US-11-049-536-448	Sequence 448, App
718	29	53.7	517	7	US-11-096-568A-17054	Sequence 17054, A	791	28	51.9	108	7	US-11-199-739-448	Sequence 448, App
719	29	53.7	520	7	US-11-096-568A-17063	Sequence 17063, A	792	28	51.9	109	6	US-10-771-257-71	Sequence 71, Appl
720	29	53.7	544	6	US-10-793-626-38	Sequence 38, Appl	793	28	51.9	109	7	US-11-127-677-69	Sequence 69, Appl
721	29	53.7	581	6	US-10-506-454-1527	Sequence 1527, Ap	794	28	51.9	112	7	US-11-049-536-70	Sequence 70, Appl
722	29	53.7	608	7	US-11-024-959-481	Sequence 481, App	795	28	51.9	112	7	US-11-199-739-70	Sequence 70, Appl
723	29	53.7	657	7	US-11-227-543-15	Sequence 15, Appl	796	28	51.9	116	7	US-11-096-568A-23180	Sequence 23180, A
724	29	53.7	724	7	US-11-043-889-8	Sequence 8, Appl	797	28	51.9	116	6	US-10-993-543-170	Sequence 170, App
725	29	53.7	792	7	US-11-088-686-29	Sequence 29, Appl	798	28	51.9	119	6	US-10-968-629-32	Sequence 32, Appl
726	29	53.7	838	6	US-10-909-769-28	Sequence 28, Appl	799	28	51.9	129	6	US-10-721-763-23	Sequence 23, Appl
727	29	53.7	854	7	US-11-100-356-5	Sequence 5, Appl	800	28	51.9	129	6	US-10-721-763-23	Sequence 45, Appl
728	29	53.7	860	7	US-11-100-356-6	Sequence 6, Appl	801	28	51.9	129	7	US-11-051-453-45	Sequence 40, Appl
729	29	53.7	983	7	US-11-087-099-7483	Sequence 7483, Ap	802	28	51.9	195	7	US-11-074-176-40	Sequence 64, Appl
730	29	53.7	1046	6	US-10-392-234A-16	Sequence 16, Appl	803	28	51.9	197	6	US-10-454-437-64	Sequence 64, Appl
731	29	53.7	1250	6	US-10-531-036-37	Sequence 37, Appl	804	28	51.9	214	7	US-11-049-536-700	Sequence 700, App
732	29	53.7	1448	6	US-10-485-517-212	Sequence 212, App	805	28	51.9	214	7	US-11-199-739-700	Sequence 700, App
733	29	53.7	2053	7	US-11-013-759-9	Sequence 9, Appl	806	28	51.9	214	7	US-11-199-739-724	Sequence 724, App
734	29	53.7	2671	6	US-10-876-787-6	Sequence 6, Appl	807	28	51.9	215	6	US-10-793-626-1906	Sequence 1906, Ap
735	29	53.7	3475	7	US-11-087-099-10885	Sequence 10885, A	808	28	51.9	216	7	US-11-087-099-9611	Sequence 9611, Ap
736	28	51.9	9	7	US-11-045-024-6308	Sequence 6308, Ap	809	28	51.9	219	7	US-11-096-568A-32711	Sequence 32711, A
737	28	51.9	9	7	US-11-045-024-14146	Sequence 14146, A	810	28	51.9	223	7	US-11-050-440-17	Sequence 17, Appl
738	28	51.9	10	7	US-11-045-024-1328	Sequence 1328, Ap	811	28	51.9	223	7	US-11-050-440-18	Sequence 18, Appl
739	28	51.9	10	7	US-11-045-024-6311	Sequence 6311, Ap	812	28	51.9	224	7	US-11-050-440-4	Sequence 4, Appl
740	28	51.9	11	6	US-10-982-440-104	Sequence 104, App	813	28	51.9	227	7	US-11-096-568A-24099	Sequence 24099, A
741	28	51.9	11	7	US-11-045-024-1434	Sequence 1434, Ap	814	28	51.9	227	7	US-11-096-568A-24098	Sequence 24098, A
742	28	51.9	11	7	US-11-045-024-1437	Sequence 1437, Ap	815	28	51.9	239	7	US-11-194-246-304	Sequence 304, App
743	28	51.9	11	7	US-11-045-024-1233	Sequence 1233, Ap	816	28	51.9	244	7	US-11-087-099-4798	Sequence 4798, Ap
744	28	51.9	11	7	US-11-045-536-152	Sequence 152, App	817	28	51.9	245	7	US-11-018-868-44	Sequence 44, Appl
745	28	51.9	11	7	US-11-199-739-152	Sequence 152, App	818	28	51.9	247	6	US-10-793-626-1284	Sequence 1284, Ap
746	28	51.9	15	7	US-11-022-562-77	Sequence 77, Appl	819	28	51.9	247	6	US-10-506-454-217	Sequence 217, App
747	28	51.9	15	7	US-11-022-562-78	Sequence 78, Appl	820	28	51.9	256	7	US-11-087-099-1399	Sequence 1399, Ap
748	28	51.9	15	7	US-11-045-024-13490	Sequence 13490, A	821	28	51.9	257	7	US-11-089-551A-26	Sequence 26, Appl
749	28	51.9	18	7	US-11-033-039-1002	Sequence 1002, Ap	822	28	51.9	257	7	US-11-096-568A-32710	Sequence 32710, A
750	28	51.9	20	7	US-11-022-562-310	Sequence 310, App	823	28	51.9	265	6	US-10-502-372-8	Sequence 8, Appl
751	28	51.9	20	7	US-11-022-562-311	Sequence 311, App	824	28	51.9	266	6	US-10-793-626-2472	Sequence 2472, Ap
752	28	51.9	26	6	US-10-729-121-10	Sequence 10, Appl	825	28	51.9	269	6	US-10-485-517-348	Sequence 348, App
753	28	51.9	26	7	US-11-285-537-10	Sequence 10, Appl	826	28	51.9	275	6	US-10-485-517-348	Sequence 348, App
754	28	51.9	35	7	US-11-096-725-27	Sequence 27, Appl	827	28	51.9	276	7	US-11-098-686-10102	Sequence 10102, A
755	28	51.9	39	7	US-11-096-568A-8717	Sequence 8717, Ap	828	28	51.9	294	7	US-11-096-568A-4714	Sequence 4714, Ap

829	28	51.9	305	6	US-10-502-972-4	Sequence 4, Appli	902	28	51.9	820	6	US-10-491-468-14	Sequence 14, Appli
830	28	51.9	313	7	US-11-000-463-427	Sequence 427, App	903	28	51.9	820	7	US-11-165-819-1	Sequence 1, Appli
831	28	51.9	324	7	US-11-040-472-4	Sequence 4, Appli	904	28	51.9	829	7	US-11-194-246-296	Sequence 296, App
832	28	51.9	327	6	US-10-467-657-2408	Sequence 2408, Ap	905	28	51.9	855	6	US-10-909-769-30	Sequence 30, Appli
833	28	51.9	329	6	US-10-821-234-1381	Sequence 1381, Ap	906	28	51.9	861	7	US-11-186-641A-2	Sequence 2, Appli
834	28	51.9	329	7	US-11-096-568A-32709	Sequence 32709, A	907	28	51.9	943	7	US-11-103-957-79	Sequence 79, Appli
835	28	51.9	331	6	US-10-467-657-2646	Sequence 2646, Ap	908	28	51.9	1295	7	US-11-091-928-2	Sequence 2, Appli
836	28	51.9	333	6	US-10-467-657-8242	Sequence 8242, Ap	909	28	51.9	1320	7	US-11-098-686-10831	Sequence 10831, A
837	28	51.9	345	7	US-11-096-568A-6119	Sequence 6119, Ap	910	28	51.9	1351	7	US-11-129-741-2937	Sequence 2937, Ap
838	28	51.9	348	7	US-11-087-099-9458	Sequence 9458, Ap	911	28	51.9	1351	7	US-11-129-741-2947	Sequence 2947, Ap
839	28	51.9	349	7	US-11-087-099-2184	Sequence 2184, Ap	912	28	51.9	1385	7	US-11-129-741-3655	Sequence 3655, Ap
840	28	51.9	353	6	US-10-793-626-2730	Sequence 2730, Ap	913	28	51.9	1403	7	US-11-091-928-1	Sequence 1, Appli
841	28	51.9	363	7	US-11-000-463-335	Sequence 335, App	914	28	51.9	1857	6	US-10-055-877-252	Sequence 252, App
842	28	51.9	363	7	US-11-014-842A-41	Sequence 41, Appli	915	28	51.9	2084	6	US-10-055-877-73	Sequence 73, Appli
843	28	51.9	367	7	US-11-000-463-899	Sequence 899, App	916	28	51.9	2109	6	US-10-055-877-251	Sequence 251, App
844	28	51.9	367	7	US-11-096-568A-6118	Sequence 6118, Ap	917	27.5	50.9	218	6	US-10-714-887-158	Sequence 158, App
845	28	51.9	374	7	US-11-096-568A-6117	Sequence 6117, Ap	918	27.5	50.9	254	7	US-11-054-515-905	Sequence 905, App
846	28	51.9	388	7	US-11-072-512-3550	Sequence 3550, Ap	919	27.5	50.9	254	7	US-11-266-444-905	Sequence 905, App
847	28	51.9	391	7	US-11-087-099-1565	Sequence 1565, Ap	920	27	50.0	8	7	US-11-045-024-123	Sequence 123, App
848	28	51.9	391	7	US-11-096-568A-15545	Sequence 15545, A	921	27	50.0	8	7	US-11-045-024-4037	Sequence 4037, Ap
849	28	51.9	391	7	US-11-096-568A-34471	Sequence 34471, A	922	27	50.0	8	7	US-11-045-024-6352	Sequence 6352, Ap
850	28	51.9	402	7	US-11-096-568A-15544	Sequence 15544, A	923	27	50.0	8	7	US-11-045-024-6356	Sequence 6356, Ap
851	28	51.9	404	7	US-11-096-568A-4713	Sequence 4713, Ap	924	27	50.0	10	7	US-11-045-024-7271	Sequence 7271, Ap
852	28	51.9	410	7	US-11-096-568A-15543	Sequence 15543, A	925	27	50.0	11	6	US-10-665-658-13	Sequence 13, Appli
853	28	51.9	414	7	US-11-096-568A-34470	Sequence 34470, A	926	27	50.0	11	6	US-10-665-658-59	Sequence 59, Appli
854	28	51.9	426	7	US-11-240-769-98	Sequence 98, Appli	927	27	50.0	11	6	US-10-850-635-60	Sequence 60, Appli
855	28	51.9	435	7	US-11-240-769-97	Sequence 97, Appli	928	27	50.0	11	6	US-10-850-635-72	Sequence 72, Appli
856	28	51.9	443	7	US-11-074-176-72	Sequence 72, Appli	929	27	50.0	11	7	US-11-051-453-16	Sequence 16, Appli
857	28	51.9	450	6	US-10-763-712A-76	Sequence 76, Appli	930	27	50.0	11	7	US-11-051-453-22	Sequence 22, Appli
858	28	51.9	452	6	US-10-793-626-3092	Sequence 3092, Ap	931	27	50.0	17	6	US-10-895-064-2012	Sequence 2012, Ap
859	28	51.9	453	7	US-11-052-554A-224	Sequence 224, App	932	27	50.0	17	7	US-11-129-741-2012	Sequence 2012, Ap
860	28	51.9	476	7	US-11-062-642-19	Sequence 19, Appli	933	27	50.0	18	7	US-11-070-723A-15	Sequence 15, Appli
861	28	51.9	500	6	US-10-519-531-3	Sequence 3, Appli	934	27	50.0	49	6	US-10-467-657-3762	Sequence 3762, Ap
862	28	51.9	500	6	US-10-507-928-4	Sequence 4, Appli	935	27	50.0	76	6	US-10-467-657-780	Sequence 780, App
863	28	51.9	500	6	US-10-853-807A-11	Sequence 11, Appli	936	27	50.0	88	7	US-11-172-740-2500	Sequence 2500, Ap
864	28	51.9	500	7	US-11-042-988-11	Sequence 11, Appli	937	27	50.0	95	6	US-10-993-543-276	Sequence 276, App
865	28	51.9	500	7	US-11-022-562-339	Sequence 339, App	938	27	50.0	95	7	US-11-054-669-65	Sequence 65, Appli
866	28	51.9	500	7	US-11-023-465-4	Sequence 4, Appli	939	27	50.0	95	7	US-11-054-669-66	Sequence 66, Appli
867	28	51.9	500	7	US-11-033-039-978	Sequence 978, App	940	27	50.0	95	7	US-11-084-554-126	Sequence 126, App
868	28	51.9	500	7	US-11-129-442-44	Sequence 44, Appli	941	27	50.0	95	7	US-11-084-554-129	Sequence 129, App
869	28	51.9	501	7	US-11-129-442-23	Sequence 23, Appli	942	27	50.0	95	7	US-11-084-554-137	Sequence 137, App
870	28	51.9	504	6	US-10-507-928-6	Sequence 6, Appli	943	27	50.0	95	7	US-11-061-848-43	Sequence 43, Appli
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872	28	51.9	505	6	US-10-507-928-8	Sequence 8, Appli	945	27	50.0	95	7	US-11-061-848-58	Sequence 58, Appli
873	28	51.9	505	7	US-11-029-465-8	Sequence 8, Appli	946	27	50.0	95	7	US-11-061-848-59	Sequence 59, Appli
874	28	51.9	509	6	US-10-508-263-18	Sequence 18, Appli	947	27	50.0	95	7	US-11-004-590-59	Sequence 59, Appli
875	28	51.9	510	7	US-11-087-099-1001	Sequence 1001, Ap	948	27	50.0	95	7	US-11-004-590-60	Sequence 60, Appli
876	28	51.9	510	7	US-11-096-568A-34036	Sequence 34036, A	949	27	50.0	95	7	US-11-004-590-64	Sequence 64, Appli
877	28	51.9	512	6	US-10-519-531-4	Sequence 4, Appli	950	27	50.0	95	7	US-11-136-250-126	Sequence 126, App
878	28	51.9	512	6	US-10-519-531-5	Sequence 5, Appli	951	27	50.0	95	7	US-11-136-250-129	Sequence 129, App
879	28	51.9	512	7	US-11-009-063-25	Sequence 25, Appli	952	27	50.0	95	7	US-11-136-250-137	Sequence 137, App
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881	28	51.9	522	7	US-11-096-568A-34035	Sequence 34035, A	954	27	50.0	107	6	US-10-850-635-18	Sequence 18, Appli
882	28	51.9	524	6	US-10-508-263-60	Sequence 60, Appli	955	27	50.0	107	6	US-10-475-075-836	Sequence 836, App
883	28	51.9	570	7	US-11-096-568A-34034	Sequence 34034, A	956	27	50.0	107	6	US-10-956-008-76	Sequence 76, Appli
884	28	51.9	576	7	US-11-240-769-70	Sequence 70, Appli	957	27	50.0	107	7	US-11-107-028-49	Sequence 49, Appli
885	28	51.9	601	7	US-11-087-099-3019	Sequence 3019, Ap	958	27	50.0	107	7	US-11-107-028-51	Sequence 51, Appli
886	28	51.9	618	7	US-11-052-554A-150	Sequence 150, App	959	27	50.0	107	7	US-11-051-453-4	Sequence 4, Appli
887	28	51.9	623	6	US-10-793-626-1068	Sequence 1068, Ap	960	27	50.0	107	7	US-11-051-453-6	Sequence 6, Appli
888	28	51.9	641	7	US-11-096-568A-28382	Sequence 28382, A	961	27	50.0	107	7	US-11-051-453-30	Sequence 30, Appli
889	28	51.9	661	7	US-11-096-568A-28381	Sequence 28381, A	962	27	50.0	107	7	US-11-051-453-32	Sequence 32, Appli
890	28	51.9	668	7	US-11-096-568A-28380	Sequence 103, App	963	27	50.0	107	7	US-11-051-453-33	Sequence 33, Appli
891	28	51.9	694	6	US-10-467-657-4602	Sequence 4602, Ap	964	27	50.0	107	7	US-11-051-453-34	Sequence 34, Appli
892	28	51.9	694	6	US-10-491-468-24	Sequence 24, Appli	965	27	50.0	107	7	US-11-149-031-1	Sequence 1, Appli
893	28	51.9	694	7	US-11-078-189-16	Sequence 16, Appli	966	27	50.0	107	7	US-11-149-031-3	Sequence 3, Appli
894	28	51.9	694	7	US-11-087-099-566	Sequence 566, App	967	27	50.0	108	6	US-10-925-366A-159	Sequence 159, App
895	28	51.9	709	7	US-11-087-099-281	Sequence 281, App	968	27	50.0	108	6	US-10-925-366A-174	Sequence 174, App
896	28	51.9	745	7	US-11-096-568A-28380	Sequence 28380, A	969	27	50.0	108	6	US-10-925-366A-188	Sequence 188, App
897	28	51.9	778	6	US-10-467-962B-18	Sequence 18, Appli	970	27	50.0	108	6	US-10-925-366A-190	Sequence 190, App
898	28	51.9	782	7	US-11-145-631-9	Sequence 9, Appli	971	27	50.0	108	6	US-10-665-658-1	Sequence 1, Appli
899	28	51.9	787	6	US-10-467-657-2832	Sequence 2832, Ap	972	27	50.0	108	6	US-10-665-658-2	Sequence 2, Appli
900	28	51.9	807	7	US-11-087-099-12161	Sequence 12161, A	973	27	50.0	108	6	US-10-585-241-5	Sequence 5, Appli
901	28	51.9	807	7	US-11-165-819-2	Sequence 2, Appli	974	27	50.0	108	7	US-11-054-669-94	Sequence 94, Appli

975	27	50.0	108	7	US-11-054-669-111	Sequence 111, App
976	27	50.0	108	7	US-11-064-174-161	Sequence 161, App
977	27	50.0	108	7	US-11-064-174-177	Sequence 177, App
978	27	50.0	108	7	US-11-049-536-192	Sequence 192, App
979	27	50.0	108	7	US-11-049-536-316	Sequence 316, App
980	27	50.0	108	7	US-11-199-739-192	Sequence 192, App
981	27	50.0	108	7	US-11-199-739-316	Sequence 316, App
982	27	50.0	108	7	US-11-208-423-113	Sequence 13, Appl
983	27	50.0	113	7	US-11-074-176-334	Sequence 334, App
984	27	50.0	116	7	US-11-074-176-124	Sequence 124, App
985	27	50.0	117	7	US-11-009-840A-313	Sequence 313, App
986	27	50.0	117	7	US-11-009-873A-313	Sequence 313, App
987	27	50.0	117	7	US-11-009-769A-313	Sequence 313, App
988	27	50.0	120	7	US-11-087-099-9736	Sequence 9736, Ap
989	27	50.0	124	7	US-11-152-497-8	Sequence 8, Appl1
990	27	50.0	129	7	US-11-051-453-43	Sequence 43, Appl
991	27	50.0	129	7	US-11-051-453-44	Sequence 44, Appl
992	27	50.0	129	7	US-11-051-453-46	Sequence 46, Appl
993	27	50.0	129	7	US-11-051-433-47	Sequence 47, Appl
994	27	50.0	129	7	US-11-051-453-48	Sequence 48, Appl
995	27	50.0	129	7	US-11-051-453-52	Sequence 52, Appl
996	27	50.0	147	6	US-10-793-626-850	Sequence 850, App
997	27	50.0	162	7	US-11-096-568A-29496	Sequence 29496, A
998	27	50.0	165	6	US-10-873-528-92	Sequence 92, Appl
999	27	50.0	175	7	US-11-073-512-3190	Sequence 3190, Ap
1000	27	50.0	182	7	US-11-077-619-94	Sequence 94, Appl

## ALIGNMENTS

RESULT 1  
 US-10-473-037-6  
 ; Sequence 6, Application US/10473037  
 ; Publication No. US20050260206A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: KYOWA HAKKO KOGYO CO., LTD.  
 ; TITLE OF INVENTION: Agents for treatment of cancer using recombinant anti-GD3 antibody  
 ; TITLE OF INVENTION: the antibody fragments  
 ; FILE REFERENCE: 11374W01  
 ; CURRENT APPLICATION NUMBER: US/10/473,037  
 ; CURRENT FILING DATE: 2003-09-26  
 ; PRIOR APPLICATION NUMBER: JP2001-097483  
 ; PRIOR FILING DATE: 2001-03-29  
 ; NUMBER OF SEQ ID NOS: 50  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 6  
 ; LENGTH: 11  
 ; TYPE: PRT  
 ; ORGANISM: Mus musculus  
 ; US-10-473-037-6

RESULT 2  
US-10-473-037-10  
; Sequence 10, Application US/10473037  
; Publication No. US20050260206A1  
; GENERAL INFORMATION:  
; APPLICANT: KYOWA HAKKO KOGYO CO., LTD.  
; TITLE OF INVENTION: Agents for treatment of cancer using recombinant anti-GD3 antibody  
; FILE REFERENCE: 11374W01  
; CURRENT APPLICATION NUMBER: US/10/473,037  
; CURRENT FILING DATE: 2003-09-26  
; PRIOR APPLICATION NUMBER: JP2001-097483

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; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 10
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:synthetic protein
US-10-473-037-10

Query Match      100.0%; Score 54; DB 6; Length 108;
Best Local Similarity 100.0%; Pred. NO. 0.0021;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SASQDISNYLN 11
        |||||
Db      24 SASQDISNYLN 34

RESULT 3
US-10-473-037-50
; Sequence 50, Application US/10473037
; Publication No. US20050260206A1
; GENERAL INFORMATION:
; APPLICANT: KYOWA HAKKO KOGYO CO., LTD.
; TITLE OF INVENTION: Agents for treatment of cancer using recombinant anti-GD
; TITLE OF INVENTION: the antibody fragments
; FILE REFERENCE: 11374W01
; CURRENT APPLICATION NUMBER: US/10/473,037
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: JP2001-097483
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 50
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-473-037-50

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RESULT 4
US-11-208-422-7
; Sequence 7, Application US/11208422
; Publication No. US2006067930A1
; GENERAL INFORMATION:
; APPLICANT: Adams, Camellia W.
; APPLICANT: Lien, Samantha
; APPLICANT: Lowman, Henry B.
; APPLICANT: Marvin, Jonathan S.
; APPLICANT: Meng, Yu-Ju G.
; TITLE OF INVENTION: POLYPEPTIDE VARIANTS WITH ALTERED EFFECTOR FUNCTION
; FILE REFERENCE: P2158R1
; CURRENT APPLICATION NUMBER: US/11/208,422
; CURRENT FILING DATE: 2005-08-19
; PRIOR APPLICATION NUMBER: US 60/603,057
; PRIOR FILING DATE: 2004-08-19
; NUMBER OF SEQ ID NOS: 54
; SEQ ID NO 7
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized

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RESULT 4
US-11-208-422-7
; Sequence 7, Application US/11208422
; Publication No. US2006067930A1
; GENERAL INFORMATION:
; APPLICANT: Adams, Camellia W.
; APPLICANT: Lien, Samantha
; APPLICANT: Lowman, Henry B.
; APPLICANT: Marvin, Jonathan S.
; APPLICANT: Meng, Yu-Ju G.
; TITLE OF INVENTION: POLYPEPTIDE VARIANTS WITH ALTERED EFFECTOR FUNCTION
; FILE REFERENCE: P2158R1
; CURRENT APPLICATION NUMBER: US/11/208,422
; CURRENT FILING DATE: 2005-08-19
; PRIOR APPLICATION NUMBER: US 60/603,057
; PRIOR FILING DATE: 2004-08-19
; NUMBER OF SEQ ID NOS: 54
; SEQ ID NO 7
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized

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## US-11-208-422-7

Query Match 100.0%; Score 54; DB 7; Length 108;  
Best Local Similarity 100.0%; Pred. No. 0.0021;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SASQDISNYLN 11  
| | | | | | | | | |  
Db 24 SASQDISNYLN 34

## RESULT 5

US-11-208-422-9  
; Sequence 9, Application US/11208422  
; Publication No. US20060067930A1  
; GENERAL INFORMATION:  
; APPLICANT: Adams, Camellia W.  
; APPLICANT: Lien, Samantha  
; APPLICANT: Lowman, Henry B.  
; APPLICANT: Marvin, Jonathan S.  
; APPLICANT: Meng, Yu-Ju G.  
; TITLE OF INVENTION: POLYPEPTIDE VARIANTS WITH ALTERED EFFECTOR FUNCTION  
; FILE REFERENCE: P2158R1  
; CURRENT APPLICATION NUMBER: US/11/208,422  
; CURRENT FILING DATE: 2005-08-19  
; PRIOR APPLICATION NUMBER: US 60/603,057  
; PRIOR FILING DATE: 2004-08-19  
; NUMBER OF SEQ ID NOS: 54  
; SEQ ID NO 9  
; LENGTH: 108  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Sequence is synthesized

## US-11-208-422-9

Query Match 100.0%; Score 54; DB 7; Length 108;  
Best Local Similarity 100.0%; Pred. No. 0.0021;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SASQDISNYLN 11  
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Db 24 SASQDISNYLN 34

## RESULT 6

US-11-208-422-11  
; Sequence 11, Application US/11208422  
; Publication No. US20060067930A1  
; GENERAL INFORMATION:  
; APPLICANT: Adams, Camellia W.  
; APPLICANT: Lien, Samantha  
; APPLICANT: Lowman, Henry B.  
; APPLICANT: Marvin, Jonathan S.  
; APPLICANT: Meng, Yu-Ju G.  
; TITLE OF INVENTION: POLYPEPTIDE VARIANTS WITH ALTERED EFFECTOR FUNCTION  
; FILE REFERENCE: P2158R1  
; CURRENT APPLICATION NUMBER: US/11/208,422  
; CURRENT FILING DATE: 2005-08-19  
; PRIOR APPLICATION NUMBER: US 60/603,057  
; PRIOR FILING DATE: 2004-08-19  
; NUMBER OF SEQ ID NOS: 54  
; SEQ ID NO 11  
; LENGTH: 108  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Sequence is synthesized

## US-11-208-422-11

Query Match 100.0%; Score 54; DB 7; Length 108;  
Best Local Similarity 100.0%; Pred. No. 0.0021;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SASQDISNYLN 11  
| | | | | | | | | |  
Db 24 SASQDISNYLN 34

## RESULT 7

US-10-648-816-1  
; Sequence 1, Application US/10648816  
; Publication No. US20050244405A1  
; GENERAL INFORMATION:  
; APPLICANT: Van Bruggen, Nicholas  
; APPLICANT: Ferrara, Napoleone  
; TITLE OF INVENTION: Vascular Endothelial Cell Growth Factor Antagonists  
; FILE REFERENCE: P1717D1  
; CURRENT APPLICATION NUMBER: US/10/648,816  
; CURRENT FILING DATE: 2003-08-26  
; PRIOR APPLICATION NUMBER: US/09/718,694  
; PRIOR FILING DATE: 2000-11-21  
; PRIOR APPLICATION NUMBER: US 09/218,481  
; PRIOR FILING DATE: 1998-12-22  
; NUMBER OF SEQ ID NOS: 16  
; SEQ ID NO 1  
; LENGTH: 110  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; OTHER INFORMATION: Sequence is synthesized

## US-10-648-816-1

Query Match 100.0%; Score 54; DB 6; Length 110;  
Best Local Similarity 100.0%; Pred. No. 0.0021;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SASQDISNYLN 11  
| | | | | | | | | |  
Db 24 SASQDISNYLN 34

## RESULT 8

US-10-648-816-5  
; Sequence 5, Application US/10648816  
; Publication No. US20050244405A1  
; GENERAL INFORMATION:  
; APPLICANT: Van Bruggen, Nicholas  
; APPLICANT: Ferrara, Napoleone  
; TITLE OF INVENTION: Vascular Endothelial Cell Growth Factor Antagonists  
; FILE REFERENCE: P1717D1  
; CURRENT APPLICATION NUMBER: US/10/648,816  
; CURRENT FILING DATE: 2003-08-26  
; PRIOR APPLICATION NUMBER: US/09/718,694  
; PRIOR FILING DATE: 2000-11-21  
; PRIOR APPLICATION NUMBER: US 09/218,481  
; PRIOR FILING DATE: 1998-12-22  
; NUMBER OF SEQ ID NOS: 16  
; SEQ ID NO 5  
; LENGTH: 110  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; OTHER INFORMATION: Sequence is synthesized

## US-10-648-816-5

Query Match 100.0%; Score 54; DB 6; Length 110;  
Best Local Similarity 100.0%; Pred. No. 0.0021;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SASQDISNYLN 11  
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Db 24 SASQDISNYLN 34

## RESULT 9

US-10-473-037-2  
; Sequence 2, Application US/10473037

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; Publication No. US20050260206A1
; GENERAL INFORMATION:
; APPLICANT: KIOWA HAKKO KOGYO CO., LTD.
; TITLE OF INVENTION: Agents for treatment of cancer using recombinant anti-GD3 antibody
; FILE REFERENCE: 11374W01
; CURRENT APPLICATION NUMBER: US/10/473,037
; PRIOR APPLICATION NUMBER: 2003-09-26
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-473-037-2

Query Match          100.0%; Score 54; DB 6; Length 128;
Best Local Similarity 100.0%; Pred. No. 0.0025;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SASQDISNYLN 11
Db      44 SASQDISNYLN 54
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RESULT 10
US-11-228-293-10
; Sequence 10, Application US/11228293
; Publication No. US20060057139A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUWANA, YOSHIHISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/11/228,293
; PRIOR FILING DATE: 2005-09-19
; PRIOR APPLICATION NUMBER: US/09/225,322
; PRIOR FILING DATE: 1999-01-05
; PRIOR FILING DATE: 1995-03-21
; PRIOR FILING DATE: 1995-03-21
; PRIOR FILING DATE: 1994-08-17
; PRIOR FILING DATE: 1992-09-17
; PRIOR FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:light chain
US-11-228-293-19

Query Match          100.0%; Score 54; DB 7; Length 128;
Best Local Similarity 100.0%; Pred. No. 0.0025;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SASQDISNYLN 11
Db      44 SASQDISNYLN 54
|||||

RESULT 11
US-11-228-293-10
; Sequence 10, Application US/11228293
; Publication No. US20060057139A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUWANA, YOSHIHISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/11/228,293
; PRIOR FILING DATE: 2005-09-19
; PRIOR APPLICATION NUMBER: US/09/225,322
; PRIOR FILING DATE: 1999-01-05
; PRIOR FILING DATE: 1995-03-21
; PRIOR FILING DATE: 1995-03-21
; PRIOR FILING DATE: 1994-08-17
; PRIOR FILING DATE: 1992-09-17
; PRIOR FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: cdNA KM-641
US-11-228-293-10

Query Match          100.0%; Score 54; DB 7; Length 128;
Best Local Similarity 100.0%; Pred. No. 0.0025;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SASQDISNYLN 11
Db      44 SASQDISNYLN 54
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RESULT 11
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US-11-228-293-19
; Sequence 19, Application US/11228293
; Publication No. US20060057139A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUWANA, YOSHIHISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/11/228,293
; PRIOR FILING DATE: 2005-09-19
; PRIOR APPLICATION NUMBER: US/09/225,322
; PRIOR FILING DATE: 1999-01-05
; PRIOR FILING DATE: 1995-03-21
; PRIOR FILING DATE: 1995-03-21
; PRIOR FILING DATE: 1994-08-17
; PRIOR FILING DATE: 1992-09-17
; PRIOR FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:light chain
US-11-228-293-19

Query Match          100.0%; Score 54; DB 7; Length 128;
Best Local Similarity 100.0%; Pred. No. 0.0025;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SASQDISNYLN 11
Db      44 SASQDISNYLN 54
|||||

RESULT 12
US-11-228-319-10
; Sequence 10, Application US/11228319
; Publication No. US20060058512A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUWANA, YOSHIHISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/11/228,319
; CURRENT FILING DATE: 2005-09-19
; PRIOR APPLICATION NUMBER: US/09/225,322
; PRIOR FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: US 08/454,680
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
; PRIOR APPLICATION NUMBER: US07/947,674
; PRIOR FILING DATE: 1992-09-17
; PRIOR APPLICATION NUMBER: JP 3-238375
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
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; SEQ ID NO 10
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: cDNA KM-641
US-11-228-319-10

Query Match      100.0%; Score 54; DB 7; Length 128;
Best Local Similarity 100.0%; Pred. No. 0.0025;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SASQDISNYLN 11
      |||||
Db      44 SASQDISNYLN 54

RESULT 13
US-11-228-319-19
; Sequence 19, Application US/11228319
; Publication No. US20060058512A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KIWANA, YOSHIOHISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/11/228,319
; CURRENT FILING DATE: 2005-09-19
; PRIOR APPLICATION NUMBER: US/09/225,322
; PRIOR FILING DATE: 1998-01-05
; PRIOR APPLICATION NUMBER: US 08/454,680
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
; PRIOR APPLICATION NUMBER: US07/947,674
; PRIOR FILING DATE: 1992-09-17
; PRIOR APPLICATION NUMBER: JP 3-238375
; PRIOR FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:light chain
US-11-228-319-19

Query Match      100.0%; Score 54; DB 7; Length 128;
Best Local Similarity 100.0%; Pred. No. 0.0025;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SASQDISNYLN 11
      |||||
Db      44 SASQDISNYLN 54

RESULT 14
US-11-054-669-56
; Sequence 56, Application US/11054669
; Publication No. US20050261480A1
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: SUPER HUMANIZED ANTIBODIES
; FILE REFERENCE: 30219/US/3
; CURRENT APPLICATION NUMBER: US/11/054,669
; CURRENT FILING DATE: 2005-02-08
```

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; PRIOR APPLICATION NUMBER: US 10/194,975
; PRIOR FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 56
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-669-56

Query Match      92.6%; Score 50; DB 7; Length 95;
Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 ASQDISNYLN 11
      |||||
Db      25 ASQDISNYLN 34

RESULT 15
US-11-054-669-57
; Sequence 57, Application US/11054669
; Publication No. US20050261480A1
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: SUPER HUMANIZED ANTIBODIES
; FILE REFERENCE: 30219/US/3
; CURRENT APPLICATION NUMBER: US/11/054,669
; CURRENT FILING DATE: 2005-02-08
; PRIOR APPLICATION NUMBER: US 10/194,975
; PRIOR FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 57
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-669-57

Query Match      92.6%; Score 50; DB 7; Length 95;
Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 ASQDISNYLN 11
      |||||
Db      25 ASQDISNYLN 34

RESULT 16
US-11-084-554-145
; Sequence 145, Application US/11084554
; Publication No. US20050260679A1
; GENERAL INFORMATION:
; APPLICANT: Kellermann, Sirid-Ai
; APPLICANT: Green, Larry L.
; APPLICANT: Korver, Wouter
; TITLE OF INVENTION: REDUCING THE RISK OF HUMAN ANTI-HUMAN
; FILE REFERENCE: ABGENIX.100A
; CURRENT APPLICATION NUMBER: US/11/084,554
; CURRENT FILING DATE: 2005-03-17
; PRIOR APPLICATION NUMBER: 60/554,372
; PRIOR FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: 60/574,661
; PRIOR FILING DATE: 2004-05-24
; NUMBER OF SEQ ID NOS: 266
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 145
; LENGTH: 95
```

; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-061-848-145

Query Match 92.6%; Score 50; DB 7; Length 95;  
Best Local Similarity 100.0%; Pred. No. 0.01;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ASQDISNYLN 11  
| | | | | | | | | |  
Db 25 ASQDISNYLN 34

## RESULT 17

US-11-061-848-148

; Sequence 148, Application US/11084554

; Publication No. US2005026079A1

; GENERAL INFORMATION:

; APPLICANT: Kellermann, Sirid-Ai

; APPLICANT: Green, Larry L.

; APPLICANT: Korver, Wouter

; TITLE OF INVENTION: REDUCING THE RISK OF HUMAN ANTI-HUMAN

; FILE REFERENCE: ABGENIX.100A

; CURRENT APPLICATION NUMBER: US/11/084,554

; CURRENT FILING DATE: 2005-03-17

; PRIOR FILING DATE: 2004-03-19

; PRIOR APPLICATION NUMBER: 60/554,372

; PRIOR FILING DATE: 2004-05-24

; NUMBER OF SEQ ID NOS: 266

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 148

; LENGTH: 95

; TYPE: PRT

; ORGANISM: Homo sapiens

US-11-084-554-148

## Query Match

Best Local Similarity 92.6%; Score 50; DB 7; Length 95;

Matches 10; Conservative 0; Mismatches 0; Indels 0;

Qy 2 ASQDISNYLN 11  
| | | | | | | | | |  
Db 25 ASQDISNYLN 34

## RESULT 18

US-11-061-848-33

; Sequence 33, Application US/11061848

; Publication No. US20050288491A1

; GENERAL INFORMATION:

; APPLICANT: Nock, Steffen

; APPLICANT: Wilson, David S.

; APPLICANT: Larrick, James W.

; TITLE OF INVENTION: SUPER-HUMANIZED ANTIBODIES AGAINST RESPIRATORY SYNCYTIAL VIRUS

; FILE REFERENCE: 186280/US

; CURRENT APPLICATION NUMBER: US/11/061,848

; CURRENT FILING DATE: 2005-02-17

; PRIOR FILING DATE: 2005-02-17

; PRIOR APPLICATION NUMBER: US 60/545,011

; PRIOR FILING DATE: 2004-02-17

; NUMBER OF SEQ ID NOS: 78

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 33

; LENGTH: 95

; TYPE: PRT

; ORGANISM: Homo sapiens

US-11-061-848-33

## Query Match

Best Local Similarity 92.6%; Score 50; DB 7; Length 95;

Matches 10; Conservative 0; Mismatches 0; Indels 0;

Qy 2 ASQDISNYLN 11  
| | | | | | | | | |  
Db 25 ASQDISNYLN 34

## RESULT 19

US-11-061-848-62

; Sequence 62, Application US/11061848

; Publication No. US20050288491A1

; GENERAL INFORMATION:

; APPLICANT: Wilson, David S.

; APPLICANT: Nock, Steffen

; APPLICANT: Larrick, James W.

; TITLE OF INVENTION: SUPER-HUMANIZED ANTIBODIES AGAINST RESPIRATORY SYNCYTIAL VIRUS

; FILE REFERENCE: 186280/US

; CURRENT APPLICATION NUMBER: US/11/061,848

; CURRENT FILING DATE: 2005-02-17

; PRIOR FILING DATE: 2005-02-17

; PRIOR APPLICATION NUMBER: US 60/545,011

; NUMBER OF SEQ ID NOS: 78

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 62

; LENGTH: 95

; TYPE: PRT

; ORGANISM: Homo sapiens

US-11-061-848-62

## Query Match

Best Local Similarity 92.6%; Score 50; DB 7; Length 95;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ASQDISNYLN 11  
| | | | | | | | | |  
Db 25 ASQDISNYLN 34

## RESULT 20

US-11-061-848-68

; Sequence 68, Application US/11061848

; Publication No. US20050288491A1

; GENERAL INFORMATION:

; APPLICANT: Wilson, David S.

; APPLICANT: Nock, Steffen

; APPLICANT: Larrick, James W.

; TITLE OF INVENTION: SUPER-HUMANIZED ANTIBODIES AGAINST RESPIRATORY SYNCYTIAL VIRUS

; FILE REFERENCE: 186280/US

; CURRENT APPLICATION NUMBER: US/11/061,848

; CURRENT FILING DATE: 2005-02-17

; PRIOR FILING DATE: 2005-02-17

; PRIOR APPLICATION NUMBER: US 60/545,011

; NUMBER OF SEQ ID NOS: 78

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 68

; LENGTH: 95

; TYPE: PRT

; ORGANISM: Homo sapiens

US-11-061-848-68

## Query Match

Best Local Similarity 92.6%; Score 50; DB 7; Length 95;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ASQDISNYLN 11  
| | | | | | | | | |  
Db 25 ASQDISNYLN 34

## RESULT 21

US-11-004-590-68

; Sequence 68, Application US/11004590

; Publication No. US2006009883A1

; GENERAL INFORMATION:

; APPLICANT: Lazar, Gregory Alan



; APPLICANT: Desjarlais, John R.  
; APPLICANT: Hammond, Phillip W.  
; TITLE OF INVENTION: METHODS OF GENERATING VARIANT PROTEINS WITH INCREASED HOST STRING  
; FILE REFERENCE: 185932/US/5  
; CURRENT APPLICATION NUMBER: US/11/004,590  
; PRIOR FILING DATE: 2004-12-03  
; PRIOR APPLICATION NUMBER: US 60/527,167  
; PRIOR FILING DATE: 2003-12-04  
; PRIOR APPLICATION NUMBER: US 60/581,613  
; PRIOR FILING DATE: 2004-06-21  
; PRIOR APPLICATION NUMBER: US 60/601,665  
; PRIOR FILING DATE: 2004-08-13  
; PRIOR APPLICATION NUMBER: US 60/619,483  
; PRIOR FILING DATE: 2004-10-14  
; NUMBER OF SEQ ID NOS: 458  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 68  
; LENGTH: 95  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-004-590-68

Query Match 92.6%; Score 50; DB 7; Length 95;  
Best Local Similarity 100.0%; Pred. No. 0.01;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASQDISNYLN 11  
Db 25 ASQDISNYLN 34

RESULT 22  
US-11-004-590-69

; Sequence 69, Application US/11004590  
; Publication No. US20060008883A1  
; GENERAL INFORMATION:  
; APPLICANT: Lazar, Gregory Alan  
; APPLICANT: Desjarlais, John R.  
; APPLICANT: Hammond, Phillip W.  
; TITLE OF INVENTION: METHODS OF GENERATING VARIANT PROTEINS WITH INCREASED HOST STRING  
; FILE REFERENCE: 185932/US/5  
; CURRENT APPLICATION NUMBER: US/11/004,590  
; CURRENT FILING DATE: 2004-12-03  
; PRIOR APPLICATION NUMBER: US 60/527,167  
; PRIOR FILING DATE: 2003-12-04  
; PRIOR APPLICATION NUMBER: US 60/581,613  
; PRIOR FILING DATE: 2004-06-21  
; PRIOR APPLICATION NUMBER: US 60/601,665  
; PRIOR FILING DATE: 2004-08-13  
; PRIOR APPLICATION NUMBER: US 60/619,483  
; PRIOR FILING DATE: 2004-10-14  
; NUMBER OF SEQ ID NOS: 458  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 69  
; LENGTH: 95  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-004-590-69

Query Match 92.6%; Score 50; DB 7; Length 95;  
Best Local Similarity 100.0%; Pred. No. 0.01;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASQDISNYLN 11  
Db 25 ASQDISNYLN 34

RESULT 23  
US-11-136-250-145

; Sequence 145, Application US/11136250

; Publication No. US20060021074A1  
; GENERAL INFORMATION:  
; APPLICANT: Kellermann, Sirid-Ai  
; APPLICANT: Korver, Wouter  
; TITLE OF INVENTION: REDUCING THE RISK OF HUMAN ANTI-HUMAN  
; FILE REFERENCE: ABGENIX.100A2  
; CURRENT APPLICATION NUMBER: US/11/136,250  
; CURRENT FILING DATE: 2005-05-23  
; PRIOR APPLICATION NUMBER: 11/084,554  
; PRIOR FILING DATE: 2005-03-17  
; PRIOR APPLICATION NUMBER: PCT/US2005/009306  
; PRIOR FILING DATE: 2005-03-17  
; PRIOR APPLICATION NUMBER: 60/574,661  
; PRIOR FILING DATE: 2004-05-24  
; PRIOR APPLICATION NUMBER: 60/554,372  
; PRIOR FILING DATE: 2004-03-19  
; NUMBER OF SEQ ID NOS: 266  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 145  
; LENGTH: 95  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-136-250-145

Query Match 92.6%; Score 50; DB 7; Length 95;  
Best Local Similarity 100.0%; Pred. No. 0.01;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASQDISNYLN 11  
Db 25 ASQDISNYLN 34

RESULT 24

US-11-136-250-148  
; Sequence 148, Application US/11136250  
; Publication No. US20060021074A1  
; GENERAL INFORMATION:  
; APPLICANT: Kellermann, Sirid-Ai  
; APPLICANT: Korver, Wouter  
; TITLE OF INVENTION: REDUCING THE RISK OF HUMAN ANTI-HUMAN  
; FILE REFERENCE: ABGENIX.100A2  
; CURRENT APPLICATION NUMBER: US/11/136,250  
; CURRENT FILING DATE: 2005-05-23  
; PRIOR APPLICATION NUMBER: 11/084,554  
; PRIOR FILING DATE: 2005-03-17  
; PRIOR APPLICATION NUMBER: PCT/US2005/009306  
; PRIOR FILING DATE: 2005-03-17  
; PRIOR APPLICATION NUMBER: 60/574,661  
; PRIOR FILING DATE: 2004-05-24  
; PRIOR APPLICATION NUMBER: 60/554,372  
; PRIOR FILING DATE: 2004-03-19  
; NUMBER OF SEQ ID NOS: 266  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 148  
; LENGTH: 95  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-136-250-148

Query Match 92.6%; Score 50; DB 7; Length 95;  
Best Local Similarity 100.0%; Pred. No. 0.01;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASQDISNYLN 11  
Db 25 ASQDISNYLN 34

RESULT 25  
US-10-771-257-38  
; Sequence 38, Application US/10771257  
; Publication No. US20050288864A1  
; GENERAL INFORMATION:  
; APPLICANT: Medical Research Council  
; APPLICANT: SISSA - Scuola Superiore Internazionale di Studi Avanzati  
; APPLICANT: Cattaneo, Antonio  
; APPLICANT: Maritan, Amos  
; APPLICANT: Visintin, Michela  
; APPLICANT: Rabbitts, Terence H  
; APPLICANT: Settanni, Giovanni  
; TITLE OF INVENTION: Intracellular antibodies  
; FILE REFERENCE: 18396/2272  
; CURRENT APPLICATION NUMBER: US/10/771,257  
; CURRENT FILING DATE: 2004-02-03  
; PRIOR APPLICATION NUMBER: PCT/GB02/03512  
; PRIOR FILING DATE: 2002-08-01  
; PRIOR APPLICATION NUMBER: GB 0119004.0  
; PRIOR FILING DATE: 2001-08-03  
; PRIOR APPLICATION NUMBER: GB 0121577.1  
; PRIOR FILING DATE: 2001-09-06  
; PRIOR APPLICATION NUMBER: GB 0200928.0  
; PRIOR FILING DATE: 2002-01-16  
; PRIOR APPLICATION NUMBER: GB 0203569.9  
; PRIOR FILING DATE: 2002-02-14  
; PRIOR APPLICATION NUMBER: IT RM2001A000633  
; PRIOR FILING DATE: 2001-10-25  
; NUMBER OF SEQ ID NOS: 124  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 38  
; LENGTH: 108  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-771-257-38

Query Match 92.6%; Score 50; DB 6; Length 108;  
Best Local Similarity 100.0%; Pred. No. 0.012;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ASQDISNYLN 11  
| | | | | | | |  
Db 25 ASQDISNYLN 34

RESULT 26  
US-11-127-677-38  
; Sequence 38, Application US/11127677  
; Publication No. US20050272107A1  
; GENERAL INFORMATION:  
; APPLICANT: Medical Research Council  
; APPLICANT: Rabbitts, Terence H  
; APPLICANT: Tanaka, Tomoyuki  
; TITLE OF INVENTION: Intracellular antibodies  
; FILE REFERENCE: 18396/2462  
; CURRENT APPLICATION NUMBER: US/11/127,677  
; CURRENT FILING DATE: 2005-05-12  
; PRIOR APPLICATION NUMBER: PCT/GB03/04942  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: GB 0226729.2  
; PRIOR FILING DATE: 2002-11-15  
; NUMBER OF SEQ ID NOS: 150  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 38  
; LENGTH: 108  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Derived protein sequence of scFv  
US-11-127-677-38

Query Match 92.6%; Score 50; DB 7; Length 108;  
Best Local Similarity 100.0%; Pred. No. 0.012;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0  
Qy 2 ASQDISNYLN 11  
| | | | | | | |  
Db 25 ASQDISNYLN 34  
RESULT 27  
US-11-049-536-184  
; Sequence 184, Application US/11049536  
; Publication No. US20060024297A1  
; GENERAL INFORMATION:  
; APPLICANT: Wood, Clive R.  
; APPLICANT: Dransfield, Daniel T.  
; APPLICANT: Pieters, Henk  
; APPLICANT: Hoet, Rene  
; APPLICANT: Hufton, Simon E.  
; TITLE OF INVENTION: TIE COMPLEX BINDING PROTEINS  
; FILE REFERENCE: 10280-128001  
; CURRENT APPLICATION NUMBER: US/11/049,536  
; CURRENT FILING DATE: 2005-02-02  
; PRIOR APPLICATION NUMBER: US 10/916,840  
; PRIOR FILING DATE: 2004-08-12  
; PRIOR APPLICATION NUMBER: US 60/494,713  
; PRIOR FILING DATE: 2003-08-12  
; NUMBER OF SEQ ID NOS: 721  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 184  
; LENGTH: 108  
; TYPE: PRT  
; ORGANISM: ARTIFICIAL SEQUENCE  
; FEATURE:  
; OTHER INFORMATION: Antibody  
US-11-049-536-184

Query Match 92.6%; Score 50; DB 7; Length 108;  
Best Local Similarity 100.0%; Pred. No. 0.012;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ASQDISNYLN 11  
| | | | | | | |  
Db 26 ASQDISNYLN 35

RESULT 28  
US-11-199-739-184  
; Sequence 184, Application US/11199739  
; Publication No. US20060057138A1  
; GENERAL INFORMATION:  
; APPLICANT: Wood, Clive R.  
; APPLICANT: Dransfield, Daniel T.  
; APPLICANT: Pieters, Henk  
; APPLICANT: Hoet, Rene  
; APPLICANT: Hufton, Simon E.  
; TITLE OF INVENTION: TIE COMPLEX BINDING PROTEINS  
; FILE REFERENCE: 10280-135001  
; CURRENT APPLICATION NUMBER: US/11/199,739  
; CURRENT FILING DATE: 2005-08-09  
; PRIOR APPLICATION NUMBER: US 11/049,536  
; PRIOR FILING DATE: 2005-02-02  
; PRIOR APPLICATION NUMBER: US 10/916,840  
; PRIOR FILING DATE: 2004-08-12  
; PRIOR APPLICATION NUMBER: US 60/494,713  
; PRIOR FILING DATE: 2003-08-12  
; NUMBER OF SEQ ID NOS: 726  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 184  
; LENGTH: 108  
; TYPE: PRT  
; ORGANISM: ARTIFICIAL  
; FEATURE:  
; OTHER INFORMATION: Antibody  
US-11-199-739-184

Query Match 92.6%; Score 50; DB 7; Length 108;  
Best Local Similarity 100.0%; Pred. No. 0.012;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ASQDISNYLN 11  
Db 26 ASQDISNYLN 35

RESULT 29  
US-11-089-872-5  
; Sequence 5, Application US/11089872  
; Publication No. US2005026012A1  
; GENERAL INFORMATION:  
; APPLICANT: Zhang, Yongke  
; APPLICANT: Ramakrishnan, Vanitha  
; APPLICANT: Law, Debbie  
; TITLE OF INVENTION: ANTI-LFL2 ANTIBODIES FOR THE DIAGNOSIS, PROGNOSIS AND TREATMENT  
; TITLE OF INVENTION: OF CANCER  
; FILE REFERENCE: 05882.0223.NPUS02  
; CURRENT APPLICATION NUMBER: US/11/089,872  
; CURRENT FILING DATE: 2005-03-25  
; PRIOR APPLICATION NUMBER: 60/557,440  
; PRIOR FILING DATE: 2004-03-26  
; PRIOR APPLICATION NUMBER: 60/638,708  
; PRIOR FILING DATE: 2004-12-22  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 5  
; LENGTH: 127  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-11-089-872-5

Query Match 92.6%; Score 50; DB 7; Length 127;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ASQDISNYLN 11  
Db 44 ASQDISNYLN 53

RESULT 30  
US-10-999-866-55  
; Sequence 55, Application US/10999866  
; Publication No. US20050266004A1  
; GENERAL INFORMATION:  
; APPLICANT: GILES-KOMAR, Jill; SCALLON, Bernard J.; CAI, Ann  
; TITLE OF INVENTION: ANTI-HUMAN LYMPHOTOXIN ALPHA ANTIBODIES, COMPOSITIONS, METHODS AND  
; FILE REFERENCE: CEN5042NP  
; CURRENT APPLICATION NUMBER: US/10/999,866  
; CURRENT FILING DATE: 2004-11-30  
; PRIOR APPLICATION NUMBER: 60/527,794  
; PRIOR FILING DATE: 2003-12-08  
; NUMBER OF SEQ ID NOS: 61  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 55  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: MISC FEATURE  
; LOCATION: (1)-(11)  
; OTHER INFORMATION: LC CDR1  
US-10-999-866-55

Query Match 87.0%; Score 47; DB 6; Length 11;  
Best Local Similarity 90.0%; Pred. No. 0.0036;  
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ASQDISNYLN 11

Db 2 ASQDITNYLN 11  
|||||:||||  
RESULT 31  
US-11-009-939-38  
; Sequence 38, Application US/11009939  
; Publication No. US20050265998A1  
; GENERAL INFORMATION:  
; APPLICANT: Elson, Greg Christopher Andrew  
; TITLE OF INVENTION: Neutralizing Antibodies and Methods of Use Thereof  
; FILE REFERENCE: 23135-402  
; CURRENT APPLICATION NUMBER: US/11/009,939  
; CURRENT FILING DATE: 2005-12-10  
; PRIOR APPLICATION NUMBER: 60/528,811  
; PRIOR FILING DATE: 2003-12-10  
; PRIOR APPLICATION NUMBER: 60/528,812  
; PRIOR FILING DATE: 2003-12-10  
; PRIOR APPLICATION NUMBER: 60/528,962  
; PRIOR FILING DATE: 2003-12-10  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 38  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-11-009-939-38

Query Match 87.0%; Score 47; DB 7; Length 11;  
Best Local Similarity 90.0%; Pred. No. 0.0036;  
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ASQDISNYLN 11  
Db 2 ASQDITNYLN 11

RESULT 32  
US-10-999-866-43  
; Sequence 43, Application US/10999866  
; Publication No. US20050266004A1  
; GENERAL INFORMATION:  
; APPLICANT: GILES-KOMAR, Jill; SCALLON, Bernard J.; CAI, Ann  
; TITLE OF INVENTION: ANTI-HUMAN LYMPHOTOXIN ALPHA ANTIBODIES, COMPOSITIONS, METHODS AND  
; FILE REFERENCE: CEN5042NP  
; CURRENT APPLICATION NUMBER: US/10/999,866  
; CURRENT FILING DATE: 2004-11-30  
; PRIOR APPLICATION NUMBER: 60/527,794  
; PRIOR FILING DATE: 2003-12-08  
; NUMBER OF SEQ ID NOS: 61  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 43  
; LENGTH: 107  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: MISC FEATURE  
; LOCATION: (1)-(107)  
; OTHER INFORMATION: LC variable region  
; FEATURE:  
; NAME/KEY: MISC FEATURE  
; LOCATION: (1)-(23)  
; OTHER INFORMATION: Framework 1  
; FEATURE:  
; NAME/KEY: MISC FEATURE  
; LOCATION: (24)-(34)  
; OTHER INFORMATION: CDR1  
; FEATURE:  
; NAME/KEY: MISC FEATURE  
; LOCATION: (35)-(50)  
; OTHER INFORMATION: Framework 2  
; FEATURE:  
; NAME/KEY: MISC FEATURE

; LOCATION: (51)..(56)  
; OTHER INFORMATION: CDR2  
; FEATURE:  
; NAME/KEY: MISC FEATURE  
; LOCATION: (57)..(89)  
; OTHER INFORMATION: Framework 3  
; FEATURE:  
; NAME/KEY: MISC FEATURE  
; LOCATION: (90)..(97)  
; OTHER INFORMATION: CDR3  
; FEATURE:  
; NAME/KEY: MISC FEATURE  
; LOCATION: (98)..(107)  
; OTHER INFORMATION: Jk2  
US-10-999-866-43

Query Match 87.0%; Score 47; DB 6; Length 107;  
Best Local Similarity 90.0%; Pred. No. 0.044;  
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ASQDISNYLN 11  
Db 25 ASQDITNYLN 34

RESULT 33  
US-11-183-205-51  
; Sequence 51, Application US/11183205  
; Publication No. US20060030521A1  
; GENERAL INFORMATION:  
; APPLICANT: Neose Technologies, Inc.  
; APPLICANT: DeFrees, Shawn  
; APPLICANT: Bayer, Robert  
; APPLICANT: Bower, Caryn  
; APPLICANT: Hakes, David  
; APPLICANT: Chen, Xi  
; TITLE OF INVENTION: REMODELING AND GLYCOCONJUGATION OF PEPTIDES  
; FILE REFERENCE: 040853-01-5052-US01  
; CURRENT APPLICATION NUMBER: US/11/183,205  
; CURRENT FILING DATE: 2005-07-15  
; PRIOR FILING DATE: 2005-07-15  
; PRIOR APPLICATION NUMBER: US 60/334,233  
; PRIOR FILING DATE: 2001-11-28  
; PRIOR APPLICATION NUMBER: US 60/391,777  
; PRIOR FILING DATE: 2002-06-07  
; PRIOR APPLICATION NUMBER: US 60/387,292  
; PRIOR FILING DATE: 2002-08-16  
; PRIOR APPLICATION NUMBER: US 60/404,249  
; PRIOR FILING DATE: 2002-11-28  
; PRIOR APPLICATION NUMBER: PCT/US2002/032263  
; PRIOR FILING DATE: 2002-10-09  
; PRIOR APPLICATION NUMBER: US 10/287,994  
; PRIOR FILING DATE: 2002-11-05  
; NUMBER OF SEQ ID NOS: 62  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 51  
; LENGTH: 107  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-183-205-51

Query Match 87.0%; Score 47; DB 7; Length 107;  
Best Local Similarity 90.0%; Pred. No. 0.044;  
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ASQDISNYLN 11  
Db 25 ASQDINNYLN 34

RESULT 34  
US-11-183-205-52  
; Sequence 52, Application US/11183205  
; Publication No. US20060030521A1  
; GENERAL INFORMATION:  
; APPLICANT: Neose Technologies, Inc.  
; APPLICANT: DeFrees, Shawn  
; APPLICANT: Zopf, David  
; APPLICANT: Bayer, Robert  
; APPLICANT: Bower, Caryn  
; APPLICANT: Hakes, David  
; APPLICANT: Chen, Xi  
; TITLE OF INVENTION: REMODELING AND GLYCOCONJUGATION OF PEPTIDES  
; FILE REFERENCE: 040853-01-5052-US01  
; CURRENT APPLICATION NUMBER: US/11/183,205  
; CURRENT FILING DATE: 2005-07-15  
; PRIOR FILING DATE: 2005-07-15  
; PRIOR APPLICATION NUMBER: US 11/183,205  
; PRIOR FILING DATE: 2001-11-28  
; PRIOR APPLICATION NUMBER: US 60/334,233  
; PRIOR FILING DATE: 2002-06-25  
; PRIOR APPLICATION NUMBER: US 60/391,777  
; PRIOR FILING DATE: 2002-07-17  
; PRIOR APPLICATION NUMBER: US 60/387,292  
; PRIOR FILING DATE: 2002-08-16  
; PRIOR APPLICATION NUMBER: US 60/404,249  
; PRIOR FILING DATE: 2002-11-28  
; PRIOR APPLICATION NUMBER: PCT/US2002/032263  
; PRIOR FILING DATE: 2002-10-09  
; PRIOR APPLICATION NUMBER: US 10/287,994  
; PRIOR FILING DATE: 2002-11-05  
; NUMBER OF SEQ ID NOS: 62  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 52  
; LENGTH: 107  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-11-183-205-52

Query Match 87.0%; Score 47; DB 7; Length 107;  
Best Local Similarity 90.0%; Pred. No. 0.044;  
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ASQDISNYLN 11  
Db 25 ASQDINNYLN 34

RESULT 35  
US-11-009-939-37  
; Sequence 37, Application US/11009939  
; Publication No. US20050265998A1  
; GENERAL INFORMATION:  
; APPLICANT: Elson, Greg Christopher Andrew  
; TITLE OF INVENTION: Neutralizing Antibodies and Methods of Use Thereof  
; FILE REFERENCE: 23135-402  
; CURRENT APPLICATION NUMBER: US/11/009,939  
; CURRENT FILING DATE: 2005-12-10  
; PRIOR APPLICATION NUMBER: 60/528,811  
; PRIOR FILING DATE: 2003-12-10  
; PRIOR APPLICATION NUMBER: 60/528,812  
; PRIOR FILING DATE: 2003-12-10  
; PRIOR APPLICATION NUMBER: 60/528,962

; PRIOR FILING DATE: 2003-12-10  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 37  
; LENGTH: 108  
; TYPE: PR1  
; ORGANISM: Mus musculus  
US-11-009-939-37

Query Match 87.0%; Score 47; DB 7; Length 108;  
Best Local Similarity 90.0%; Pred. No. 0.045;  
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASQDISNYLN 11  
Db 25 ASQDITNYLN 34  
||||:||||

RESULT 36  
US-11-061-848-2  
; Sequence 2, Application US/11061848  
; Publication No. US20050288491A1  
; GENERAL INFORMATION:  
; APPLICANT: Wilson, David S.  
; APPLICANT: Nock, Steffen  
; APPLICANT: Larrick, James W.  
; TITLE OF INVENTION: SUPER-HUMANIZED ANTIBODIES AGAINST RESPIRATORY SYNCYTIAL VIRUS  
; FILE REFERENCE: 186280/US  
; CURRENT FILING DATE: 2005-02-17  
; PRIOR APPLICATION NUMBER: US 60/545,011  
; PRIOR FILING DATE: 2004-02-17  
; NUMBER OF SEQ ID NOS: 78  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 2  
; LENGTH: 108  
; TYPE: PR1  
; ORGANISM: Mus musculus  
US-11-061-848-2

Query Match 87.0%; Score 47; DB 7; Length 108;  
Best Local Similarity 90.0%; Pred. No. 0.045;  
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASQDISNYLN 11  
Db 25 ASQDINNYLN 34  
||||:||||

RESULT 37  
US-11-061-848-10  
; Sequence 10, Application US/11061848  
; Publication No. US20050288491A1  
; GENERAL INFORMATION:  
; APPLICANT: Wilson, David S.  
; APPLICANT: Nock, Steffen  
; APPLICANT: Larrick, James W.  
; TITLE OF INVENTION: SUPER-HUMANIZED ANTIBODIES AGAINST RESPIRATORY SYNCYTIAL VIRUS  
; FILE REFERENCE: 186280/US  
; CURRENT APPLICATION NUMBER: US/11/061,848  
; CURRENT FILING DATE: 2005-02-17  
; PRIOR APPLICATION NUMBER: US 60/545,011  
; PRIOR FILING DATE: 2004-02-17  
; NUMBER OF SEQ ID NOS: 78  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 10  
; LENGTH: 108  
; TYPE: PR1  
; ORGANISM: Homo sapiens  
US-11-061-848-10

Query Match 87.0%; Score 47; DB 7; Length 108;  
Best Local Similarity 90.0%; Pred. No. 0.045;

Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 2 ASQDISNYLN 11  
Db 25 ASQDINNYLN 34  
||||:||||

RESULT 38  
US-11-061-848-11  
; Sequence 11, Application US/11061848  
; Publication No. US20050288491A1  
; GENERAL INFORMATION:  
; APPLICANT: Wilson, David S.  
; APPLICANT: Nock, Steffen  
; APPLICANT: Larrick, James W.  
; TITLE OF INVENTION: SUPER-HUMANIZED ANTIBODIES AGAINST RESPIRATORY SYNCYTIAL VIRUS  
; FILE REFERENCE: 186280/US  
; CURRENT APPLICATION NUMBER: US/11/061,848  
; CURRENT FILING DATE: 2005-02-17  
; PRIOR APPLICATION NUMBER: US 60/545,011  
; PRIOR FILING DATE: 2004-02-17  
; NUMBER OF SEQ ID NOS: 78  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 11  
; LENGTH: 108  
; TYPE: PR1  
; ORGANISM: Homo sapiens  
US-11-061-848-11

Query Match 87.0%; Score 47; DB 7; Length 108;  
Best Local Similarity 90.0%; Pred. No. 0.045;  
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASQDISNYLN 11  
Db 25 ASQDINNYLN 34  
||||:||||

RESULT 39  
US-11-061-848-12  
; Sequence 12, Application US/11061848  
; Publication No. US20050288491A1  
; GENERAL INFORMATION:  
; APPLICANT: Wilson, David S.  
; APPLICANT: Nock, Steffen  
; APPLICANT: Larrick, James W.  
; TITLE OF INVENTION: SUPER-HUMANIZED ANTIBODIES AGAINST RESPIRATORY SYNCYTIAL VIRUS  
; FILE REFERENCE: 186280/US  
; CURRENT APPLICATION NUMBER: US/11/061,848  
; CURRENT FILING DATE: 2005-02-17  
; PRIOR APPLICATION NUMBER: US 60/545,011  
; PRIOR FILING DATE: 2004-02-17  
; NUMBER OF SEQ ID NOS: 78  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 12  
; LENGTH: 108  
; TYPE: PR1  
; ORGANISM: Homo sapiens  
US-11-061-848-12

Query Match 87.0%; Score 47; DB 7; Length 108;  
Best Local Similarity 90.0%; Pred. No. 0.045;  
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASQDISNYLN 11  
Db 25 ASQDINNYLN 34  
||||:||||

RESULT 40  
US-11-061-848-13  
; Sequence 13, Application US/11061848  
; Publication No. US20050288491A1

```
; GENERAL INFORMATION:
; APPLICANT: Wilson, David S.
; APPLICANT: Nock, Steffen
; APPLICANT: Larrick, James W.
; TITLE OF INVENTION: SUPER-HUMANIZED ANTIBODIES AGAINST RESPIRATORY SYNCYTIAL VIRUS
; FILE REFERENCE: 186280/US
; CURRENT APPLICATION NUMBER: US/11/061,848
; CURRENT FILING DATE: 2005-02-17
; PRIOR APPLICATION NUMBER: US 60/545,011
; PRIOR FILING DATE: 2004-02-17
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 13
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-061-848-13

Query Match      87.0%; Score 47; DB 7; Length 108;
Best Local Similarity 90.0%; Pred. No. 0.045;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      2 ASQDISNYLN 11
Db      25 ASQDINNYLN 34

RESULT 41
US-11-061-848-14
; Sequence 14, Application US/11061848
; Publication No. US20050288491A1
; GENERAL INFORMATION:
; APPLICANT: Wilson, David S.
; APPLICANT: Nock, Steffen
; APPLICANT: Larrick, James W.
; TITLE OF INVENTION: SUPER-HUMANIZED ANTIBODIES AGAINST RESPIRATORY SYNCYTIAL VIRUS
; FILE REFERENCE: 186280/US
; CURRENT APPLICATION NUMBER: US/11/061,848
; CURRENT FILING DATE: 2005-02-17
; PRIOR APPLICATION NUMBER: US 60/545,011
; PRIOR FILING DATE: 2004-02-17
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 14
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-061-848-14

Query Match      87.0%; Score 47; DB 7; Length 108;
Best Local Similarity 90.0%; Pred. No. 0.045;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      2 ASQDISNYLN 11
Db      25 ASQDINNYLN 34

RESULT 42
US-11-061-848-15
; Sequence 15, Application US/11061848
; Publication No. US20050288491A1
; GENERAL INFORMATION:
; APPLICANT: Wilson, David S.
; APPLICANT: Nock, Steffen
; APPLICANT: Larrick, James W.
; TITLE OF INVENTION: SUPER-HUMANIZED ANTIBODIES AGAINST RESPIRATORY SYNCYTIAL VIRUS
; FILE REFERENCE: 186280/US
; CURRENT APPLICATION NUMBER: US/11/061,848
; CURRENT FILING DATE: 2005-02-17
; PRIOR APPLICATION NUMBER: US 60/545,011
; PRIOR FILING DATE: 2004-02-17
; NUMBER OF SEQ ID NOS: 78
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; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 15
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-061-848-15

Query Match      87.0%; Score 47; DB 7; Length 108;
Best Local Similarity 90.0%; Pred. No. 0.045;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      2 ASQDISNYLN 11
Db      25 ASQDINNYLN 34

RESULT 43
US-11-025-712-11
; Sequence 11, Application US/11025712
; Publication No. US20050255108A1
; GENERAL INFORMATION:
; APPLICANT: Bednar, Martin M.
; APPLICANT: Thomas, G. Roger
; APPLICANT: Gross, Cordell E.
; TITLE OF INVENTION: ANTI-CD18 ANTIBODIES IN STROKE
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/025,712
; FILING DATE: 28-Dec-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/10/404,286
; FILING DATE: 31-Mar-2003
; APPLICATION NUMBER: 09/811384
; FILING DATE: 20-DEC-2000
; APPLICATION NUMBER: 09/251652
; FILING DATE: 17-FEB-2000
; APPLICATION NUMBER: 08/788800
; FILING DATE: 22-JAN-1997
; APPLICATION NUMBER: 60/093038
; FILING DATE: 23-JAN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Evans, David W.
; REGISTRATION NUMBER: NONE
; REFERENCE/DOCKET NUMBER: P1729C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1739
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 214 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-11-025-712-11

Query Match      87.0%; Score 47; DB 7; Length 214;
Best Local Similarity 90.0%; Pred. No. 0.096;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      2 ASQDISNYLN 11
```

```
Db          25 ASQDINNVLN 34
|||||:||||
; CURRENT APPLICATION NUMBER: US/11/183,205
; CURRENT FILING DATE: 2005-07-15
; PRIOR APPLICATION NUMBER: US 11/183,205
; PRIOR FILING DATE: 2005-07-15
; PRIOR APPLICATION NUMBER: US 60/334,233
; PRIOR FILING DATE: 2001-11-28
; PRIOR APPLICATION NUMBER: US 60/334,301
; PRIOR FILING DATE: 2001-11-28
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: PCT/US2002/032263
; PRIOR FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US 10/287,994
; PRIOR FILING DATE: 2002-11-05
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 55
; LENGTH: 214
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-183-205-55

Query Match      87.0%; Score 47; DB 7; Length 214;
Best Local Similarity 90.0%; Pred. No. 0.096;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      2 ASQDISNYLN 11
|||||:||||
Db      25 ASQDINNVLN 34

RESULT 46
US-10-946-836A-10
; Sequence 10, Application US/10946836A
; Publication No. US2006009382A1
; GENERAL INFORMATION:
; APPLICANT: TeGenero AG
; APPLICANT: Hanke, Thomas
; APPLICANT: Lin, Chia-Huey
; TITLE OF INVENTION: USE OF A CD28 BINDING PHARMACEUTICAL SUBSTANCE FOR MAKING A
; FILE REFERENCE: 7003/25, TEG/US/0407
; CURRENT APPLICATION NUMBER: US/10/946,836A
; CURRENT FILING DATE: 2004-09-22
; PRIOR APPLICATION NUMBER: DE 103 45 008.4
; PRIOR FILING DATE: 2003-09-22
; PRIOR APPLICATION NUMBER: DE 103 49 371.9
; PRIOR FILING DATE: 2003-10-20
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: monoclonal antibody 9D7 partial sequence
US-10-946-836A-10

Query Match      85.2%; Score 46; DB 6; Length 107;
Best Local Similarity 90.0%; Pred. No. 0.069;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      2 ASQDISNYLN 11
|||||:||||
Db      25 ASQDINNVLN 34

RESULT 45
US-11-183-205-55
; Sequence 55, Application US/11183205
; Publication No. US20060030521A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: DeFrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Bowe, Caryn
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; TITLE OF INVENTION: REMODELING AND GLYCOCONJUGATION OF PEPTIDES
; FILE REFERENCE: 040853-01-5052-US01

Db          25 ASQDINNVLN 34
|||||:||||
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/173,564
; FILING DATE: 01-JUL-2005
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/811,757
; FILING DATE: 06-MAR-1997
; CLASSIFICATION:
; APPLICATION NUMBER: 08/425,763
; FILING DATE: 20-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 00,000
; REFERENCE/DOCKET NUMBER: 941
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 214 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-11-173-564-1

Query Match      87.0%; Score 47; DB 7; Length 214;
Best Local Similarity 90.0%; Pred. No. 0.096;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      2 ASQDISNYLN 11
|||||:||||
Db      25 ASQDINNVLN 34

RESULT 45
US-11-183-205-55
; Sequence 55, Application US/11183205
; Publication No. US20060030521A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: DeFrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Bowe, Caryn
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; TITLE OF INVENTION: REMODELING AND GLYCOCONJUGATION OF PEPTIDES
; FILE REFERENCE: 040853-01-5052-US01
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RESULT 47  
US-10-988-207-10  
; Sequence 10, Application US/10988207  
; Publication No. US20060008457A1  
; GENERAL INFORMATION:  
; APPLICANT: TeGenero AG  
; APPLICANT: Hanke, Thomas  
; TITLE OF INVENTION: USE OF AN EFFECTIVE SUBSTANCE BINDING TO CD28 FOR PRODUCING A  
; FILE REFERENCE: TEG/US/0409  
; CURRENT APPLICATION NUMBER: US/10/988,207  
; CURRENT FILING DATE: 2004-11-12  
; PRIOR APPLICATION NUMBER: DE 103 52 900.4  
; PRIOR FILING DATE: 2003-11-11  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 10  
; LENGTH: 107  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: mab 5.11A partial sequence  
US-10-988-207-10

Query Match 85.2%; Score 46; DB 6; Length 107;  
Best Local Similarity 90.0%; Pred. No. 0.069;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ASQDISNYLN 11  
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Db 25 ASQDISNYLN 34

RESULT 48  
US-11-084-717-21  
; Sequence 21, Application US/11084717  
; Publication No. US20050260736A1  
; GENERAL INFORMATION:  
; APPLICANT: GEORGIOU, GEORGE  
; APPLICANT: JEONG, KI-JUN  
; APPLICANT: HARVEY, BARRETT R.  
; APPLICANT: IVERSON, BRENT L.  
; TITLE OF INVENTION: SELECTION OF BACTERIAL INNER-MEMBRANE ANCHOR POLYPEPTIDES  
; FILE REFERENCE: UTSB:723US  
; CURRENT APPLICATION NUMBER: US/11/084,717  
; CURRENT FILING DATE: 2005-03-18  
; PRIOR APPLICATION NUMBER: 60/554,324  
; PRIOR FILING DATE: 2004-03-18  
; PRIOR APPLICATION NUMBER: 10/620,278  
; PRIOR FILING DATE: 2003-07-15  
; PRIOR FILING DATE: 2002-07-15  
; NUMBER OF SEQ ID NOS: 61  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 21  
; LENGTH: 247  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: Peptide  
US-11-084-717-21

Query Match 83.3%; Score 45; DB 7; Length 247;  
Best Local Similarity 90.0%; Pred. No. 0.27;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ASQDISNYLN 11  
| | | | | | | |  
Db 25 ASQDISNYLN 34

RESULT 49  
US-11-084-717-23  
; Sequence 23, Application US/11084717  
; Publication No. US20050260736A1  
; GENERAL INFORMATION:  
; APPLICANT: GEORGIOU, GEORGE  
; APPLICANT: JEONG, KI-JUN  
; APPLICANT: HARVEY, BARRETT R.  
; APPLICANT: IVERSON, BRENT L.  
; TITLE OF INVENTION: SELECTION OF BACTERIAL INNER-MEMBRANE ANCHOR POLYPEPTIDES  
; FILE REFERENCE: UTSB:723US  
; CURRENT APPLICATION NUMBER: US/11/084,717  
; CURRENT FILING DATE: 2005-03-18  
; PRIOR APPLICATION NUMBER: 60/554,324  
; PRIOR FILING DATE: 2004-03-18  
; PRIOR APPLICATION NUMBER: 10/620,278  
; PRIOR FILING DATE: 2003-07-15  
; PRIOR APPLICATION NUMBER: 60/396,058  
; PRIOR FILING DATE: 2002-07-15  
; NUMBER OF SEQ ID NOS: 61  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 23  
; LENGTH: 247  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: Peptide  
US-11-084-717-23

Query Match 83.3%; Score 45; DB 7; Length 247;  
Best Local Similarity 90.0%; Pred. No. 0.27;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ASQDISNYLN 11  
| | | | | | | |  
Db 25 ASQDISNYLN 34

RESULT 50  
US-11-084-717-25  
; Sequence 25, Application US/11084717  
; Publication No. US20050260736A1  
; GENERAL INFORMATION:  
; APPLICANT: GEORGIOU, GEORGE  
; APPLICANT: JEONG, KI-JUN  
; APPLICANT: HARVEY, BARRETT R.  
; APPLICANT: IVERSON, BRENT L.  
; TITLE OF INVENTION: SELECTION OF BACTERIAL INNER-MEMBRANE ANCHOR POLYPEPTIDES  
; FILE REFERENCE: UTSB:723US  
; CURRENT APPLICATION NUMBER: US/11/084,717  
; CURRENT FILING DATE: 2005-03-18  
; PRIOR APPLICATION NUMBER: 60/554,324  
; PRIOR FILING DATE: 2004-03-18  
; PRIOR APPLICATION NUMBER: 10/620,278  
; PRIOR FILING DATE: 2003-07-15  
; PRIOR APPLICATION NUMBER: 60/396,058  
; PRIOR FILING DATE: 2002-07-15  
; NUMBER OF SEQ ID NOS: 61  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 25  
; LENGTH: 247  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: Peptide  
US-11-084-717-25

Query Match 83.3%; Score 45; DB 7; Length 247;  
Best Local Similarity 90.0%; Pred. No. 0.27;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;



Qy 2 ASODISNYLN 11  
| | | | |  
Db 25 ASODIRNYLN 34

Search completed: April 6, 2006, 09:23:02  
Job time : 13.1864 secs

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98	29	78.4	107	9	ADY85024	Ady85024	Monoclonal	171	28	75.7	7	9	ABE72798	Anti-LTat
99	29	78.4	108	8	ADN41877	Adn41877	Humanised	172	28	75.7	8	6	ABJ18554	Gangliosid
100	29	78.4	109	8	ADM78045	Adm78045	Human SKB	173	28	75.7	10	8	ADT39728	HSARS vir
101	29	78.4	126	2	AAR12237	Aar12237	Mouse MAB	174	28	75.7	10	8	ADS79147	SARS viru
102	29	78.4	127	2	AAR12359	Aar12359	Light (ka	175	28	75.7	10	8	ADT37258	HSARS vir
103	29	78.4	142	5	ABP28359	Abp28359	Streptoco	176	28	75.7	10	8	ABY03641	SARS coro
104	29	78.4	148	8	ADY88672	Ady88672	Streptoco	177	28	75.7	15	2	AAW59076	FMDV non-
105	29	78.4	148	8	ADY82070	Ady82070	Streptoco	178	28	75.7	31	4	AAW99873	Human exc
106	29	78.4	148	8	ADY79925	Ady79925	Streptoco	179	28	75.7	31	4	AAW43672	Human bla
107	29	78.4	166	3	AAB40975	Aab40975	Human ORF	180	28	75.7	31	8	ADF71631	Human bla
108	29	78.4	166	3	ABP11498	Abp11498	Human ORF	181	28	75.7	52	8	ADT40557	HSARS vir
109	29	78.4	214	8	ADN41870	Adn41870	Amino aci	182	28	75.7	52	8	ADT79974	SARS viru
110	29	78.4	214	9	AEC20774	Aec20774	M-CSF spe	183	28	75.7	52	8	ADT38087	HSARS vir
111	29	78.4	235	8	ADQ65818	Adq65818	Novel hum	184	28	75.7	65	5	ABP00660	Human ORF
112	29	78.4	241	6	ABU11783	Abu11783	Human MDD	185	28	75.7	66	5	ABP08962	Human ORF
113	29	78.4	264	5	ABB84602	Abb84602	Human cau	186	28	75.7	88	2	AAAR47210	Chimeric
114	29	78.4	315	9	ADW18259	Adw18259	E grandis	187	28	75.7	91	3	AAAG34427	Arabidops
115	29	78.4	329	7	ABO72445	Abot72445	Pseudomon	188	28	75.7	91	7	ADJ70926	Human hea
116	29	78.4	334	2	AAR53644	Aar53644	C-jun gen	189	28	75.7	94	5	AAU83479	Casphalia
117	29	78.4	334	5	ABE57355	Abes57355	Mouse fsc	190	28	75.7	98	7	ADH87386	Enterococ
118	29	78.4	334	7	ADSE3550	Adse3550	Rat Prote	191	28	75.7	102	3	AAAY71446	Humanised
119	29	78.4	334	7	ADSE3554	Adse3554	Rat Prote	192	28	75.7	102	3	AAAY71454	Humanised
120	29	78.4	334	7	ADD45882	Add45882	Rat Prote	193	28	75.7	105	3	AAAY71455	Humanised
121	29	78.4	334	7	ADD45882	Add45882	Rat Prote	194	28	75.7	107	2	AAAR30768	Murine an
122	29	78.4	392	3	ADC28027	Adc28027	Arabidops	195	28	75.7	107	2	AAW49812	Amino aci
123	29	78.4	405	8	ADS24320	Ads24320	Bacterial	196	28	75.7	107	2	AAW49811	Amino aci
124	29	78.4	409	3	AAAG28026	Aag28026	Arabidops	197	28	75.7	107	6	ABJ18571	Gangliosid
125	29	78.4	441	3	AAAG28025	Aag28025	Arabidops	198	28	75.7	107	6	ABJ18574	Gangliosid
126	29	78.4	464	7	ADR08646	Adr08646	Novel pro	199	28	75.7	107	6	ABR55867	Anti-glyc
127	29	78.4	465	5	AU72527	Au72527	Arabidops	200	28	75.7	107	6	ABR55866	Human imm
128	29	78.4	470	9	ADY65754	Ady65754	S. mansoni	201	28	75.7	107	6	ABP59985	Antibody
129	29	78.4	486	8	ADQ26935	Adq26935	Torafugu	202	28	75.7	107	6	ABO10814	Mouse mon
130	29	78.4	496	4	AGB22146	Agb22146	S. epider	203	28	75.7	107	6	AAO23067	Murine X8
131	29	78.4	497	5	ABP39566	Abp39566	Staphyloc	204	28	75.7	107	8	ADF69648	Humanised
132	29	78.4	497	5	ADSO5530	Adso5530	Staphyloc	205	28	75.7	107	8	ADN49402	Murine an
133	29	78.4	502	4	ABE66956	Abbe66956	Drosophi	206	28	75.7	107	8	ADN49723	Variable
134	29	78.4	504	7	ABW87730	Abw87730	Rice abio	207	28	75.7	107	8	ADN49724	Variable
135	29	78.4	504	8	ADI45243	Adi45243	Rice isop	208	28	75.7	107	8	ADU74399	Human imm
136	29	78.4	509	8	ADQ26937	Adq26937	Tetraodon	209	28	75.7	107	8	ADU74400	Mouse ant
137	29	78.4	532	8	ADR88978	Adr88978	A. thalia	210	28	75.7	107	8	ADX39145	Humanized
138	29	78.4	533	8	ADR88968	Adr88968	A. thalia	211	28	75.7	107	9	ADY85028	Monoclonal
139	29	78.4	556	8	ABO84796	Abos84796	Human can	212	28	75.7	107	9	ADZ47655	Mouse ant
140	29	78.4	564	8	ADX94234	Adx94234	Plant ful	213	28	75.7	107	9	ABE03867	B-Cell pha
141	29	78.4	603	5	AAO17253	Aao17253	A thalian	214	28	75.7	107	9	ABE72785	Anti-LTat
142	29	78.4	613	5	AAO17320	Aao17320	A thalian	215	28	75.7	108	2	AAW04177	Variant v
143	29	78.4	625	8	ADG74928	Adg74928	A thalian	216	28	75.7	108	2	AAW00834	Variable
144	29	78.4	638	8	ADR86093	Adr86093	Aspergill	217	28	75.7	108	2	AAW16620	Anti-huma
145	29	78.4	650	6	ABR62591	Abre62591	Anti-CD7	218	28	75.7	108	3	AAAY94216	Murine co
146	29	78.4	651	6	ABR62590	Abre62590	Murine ca	219	28	75.7	108	3	AAAY71450	Humanised
147	29	78.4	665	8	ABO84795	Abos84795	Murine ca	220	28	75.7	108	3	AAAY71445	Murine mo
148	29	78.4	676	2	AAR60801	Aar60801	Aspergill	221	28	75.7	108	3	AAAY56678	Anti-inte
149	29	78.4	682	8	ADI39294	Adi39294	S. hygro	222	28	75.7	108	3	AAAY56704	Murine an
150	29	78.4	685	8	ADI39262	Adi39262	S. hygro	223	28	75.7	108	6	ABO10815	Mouse mon
151	29	78.4	717	8	ADU06757	Adu06757	Novel bro	224	28	75.7	108	9	ADV86671	Anti-FLJ3
152	29	78.4	745	8	ADM48300	Adm48300	Polypepti	225	28	75.7	108	9	ADZ47742	Mouse ant
153	29	78.4	747	5	AAU97201	Aau97201	Corn Arab	226	28	75.7	108	9	ABE21885	Human DC-
154	29	78.4	747	5	ABU08326	Abu08326	Corn suga	227	28	75.7	108	9	ABE21887	Human DC-
155	29	78.4	747	8	ADG47906	Adg47906	Corn Arab	228	28	75.7	108	9	ABE21884	Human DC-
156	29	78.4	800	8	ADG47936	Adg47936	Corn Arab	229	28	75.7	108	9	ABE70912	Toll-like
157	29	78.4	867	4	ABG07270	Abg07270	Novel hum	230	28	75.7	109	2	AAAS2039	Light cha
158	29	78.4	884	4	AAW41302	Aaw41302	Human pol	231	28	75.7	109	6	ABO10818	Mouse/hum
159	29	78.4	899	4	AAW79419	Aaw79419	Human pro	232	28	75.7	109	8	ADG25821	Anti-CD30
160	29	78.4	903	4	AAW39516	Aaw39516	Human pol	233	28	75.7	109	8	ADR40433	Mouse kap
161	29	78.4	940	5	ABB91176	Abb91176	Herbicida	234	28	75.7	109	8	ADR40351	Mouse kap
162	29	78.4	961	4	AAW78435	Aaw78435	Human pro	235	28	75.7	109	9	ABE21853	Human DC-
163	29	78.4	2105	8	ADN24351	Adn24351	Bacterial	236	28	75.7	109	9	ABE21855	Human DC-
164	29	78.4	2105	8	ADN24350	Adn24350	Bacterial	237	28	75.7	109	9	ABE21858	Human DC-
165	29	78.4	2105	8	ADN24349	Adn24349	Bacterial	238	28	75.7	109	9	ABE21856	Human DC-
166	29	78.4	2215	4	AAAG64030	Aag64030	Human pol	239	28	75.7	109	9	ABE21859	Human DC-
167	28	75.7	7	3	AAU94221	Aau94221	Murine 16	240	28	75.7	110	9	ADZ47745	CDR-graft
168	28	75.7	7	7	AAU70359	Aau70359	Mouse kap	241	28	75.7	112	4	AAE00697	Human imm
169	28	75.7	7	8	ADU38481	Adu38481	Mouse ant	242	28	75.7	113	3	AAAG34763	Arabidops
170	28	75.7	7	9	ABE70914	Abet70914	Toll-like	243	28	75.7	120	4	AAAO12572	Human pol

244	28	75.7	120	8	ADS98688	Ades98688	Protein f	317	28	75.7	261	7	ADe31485	Ades31485	Plant yle
245	28	75.7	124	2	AAR47206	Aar47206	Human/mur	318	28	75.7	261	8	ADi41735	Adi41735	Plant tra
246	28	75.7	126	2	AAR29015	Aar29015	pUC-RV1-P	319	28	75.7	261	8	ADO02229	Ado02229	Thalecres
247	28	75.7	126	2	AAR29013	Aar29013	pUC-RVh-P	320	28	75.7	261	9	AEa27019	Ea27019	Stress to
248	28	75.7	126	4	ABG19080	Abg19080	Novel hum	321	28	75.7	267	4	AAG90244	Ag90244	C Glutam
249	28	75.7	126	7	ADC95167	Adc95167	B. faeciu	322	28	75.7	267	7	ADD13615	Ad13615	C. glutam
250	28	75.7	127	2	ADc28670	Adc28670	PPM-k3 pr	323	28	75.7	267	7	ADL65685	Adl65685	C. glutam
251	28	75.7	127	2	AAR32121	Aar32121	Anti-CD4	324	28	75.7	268	2	AAR44226	Ad44226	Chimeric
252	28	75.7	127	2	AAR39285	Aar39285	Mouse C4G	325	28	75.7	268	2	ABb63804	Ab63804	Drosophil
253	28	75.7	127	2	AAR99003	Aar99003	MAB VLI78	326	28	75.7	267	8	ADx92282	Adx92282	Plant ful
254	28	75.7	127	2	AAW11817	Aaw11817	Humanised	327	28	75.7	301	9	ADY65506	Ady65506	S. mangon
255	28	75.7	127	2	AAW11815	Aaw11815	Mouse ant	328	28	75.7	302	2	AAR60206	Aar60206	Bispecifi
256	28	75.7	127	2	AAW60033	Aaw60033	Mouse ant	329	28	75.7	312	5	ABb54660	Ab54660	Lactococc
257	28	75.7	127	2	AAW60035	Aaw60035	Human ant	330	28	75.7	330	5	AAE27068	Aae27068	Mouse TCR
258	28	75.7	127	2	AAW49809	Aaw49809	Variable	331	28	75.7	367	3	AAy55078	Aay55078	Single ch
259	28	75.7	127	6	AAO23066	Aao23066	Murine K8	332	28	75.7	381	3	AAy55079	Aay55079	Single ch
260	28	75.7	127	7	ABR62342	Abt62342	Anti-HLA-	333	28	75.7	391	8	ADN23479	Adn23479	Bacterial
261	28	75.7	128	2	AAR09426	Aar09426	ME4 Light	334	28	75.7	393	8	ADY12571	Ady12571	Plant ful
262	28	75.7	128	2	AAW06215	Aaw06215	MAB ME4 1	335	28	75.7	403	2	AAW88317	Aaw88317	Sugar tra
263	28	75.7	128	2	AAW85062	Aaw85062	Mouse ME4	336	28	75.7	404	7	ADCO1224	Adc01224	Enteroha
264	28	75.7	128	6	ABU58896	Abu58896	Mouse ant	337	28	75.7	421	2	AAy35514	Aay35514	Chlamydia
265	28	75.7	129	2	AAR47207	Aar47207	Human/mur	338	28	75.7	426	6	ABU24568	Abu24568	Protein e
266	28	75.7	131	2	AAR84553	Aar84553	MAB SCH94	339	28	75.7	440	3	AAb16364	Ab16364	Eucalyptu
267	28	75.7	131	8	ADJ26634	Adj26634	Human ant	340	28	75.7	440	3	ADD41540	Ad41540	Diphenol
268	28	75.7	138	3	AGG09725	Agg09725	Arabidops	341	28	75.7	444	6	ADA34105	Ada34105	Acinetoba
269	28	75.7	158	8	ADV88190	Adv88190	Streptoco	342	28	75.7	447	3	AAb42121	Ab42121	Human ORP
270	28	75.7	158	8	ADV79443	Adv79443	Streptoco	343	28	75.7	453	4	ABB68672	Abb68672	Drosophil
271	28	75.7	173	8	ADX87865	Adx87865	Plant ful	344	28	75.7	457	8	ADK74275	Adk74275	Plant ful
272	28	75.7	185	8	ADR08534	Adr08534	Human pro	345	28	75.7	467	6	ADA34091	Ada34091	Acinetoba
273	28	75.7	186	5	ABP25744	Abp25744	Streptoco	346	28	75.7	470	8	ADU38977	Adu38977	Foot-and-
274	28	75.7	186	8	ADV81618	Adv81618	Streptoco	347	28	75.7	477	4	ABB66931	Abb66931	Drosophil
275	28	75.7	198	8	ADK00579	Adk00579	HOMO prot	348	28	75.7	482	8	ADX92649	Adx92649	Plant ful
276	28	75.7	206	5	ABG79615	Abg79615	Sunflower	349	28	75.7	503	4	ABG03349	Abg03349	Novel hum
277	28	75.7	209	2	AAR64204	Aar64204	Monoclonal	350	28	75.7	504	7	ADD25787	Ad25787	Binding d
278	28	75.7	214	2	AAR30776	Aar30776	H52L6-158	351	28	75.7	504	9	ADY21738	Ady21738	Anti-CD3
279	28	75.7	214	2	AAR43338	Aar43338	Complel	352	28	75.7	512	3	AAg22915	Ag22915	Arabidops
280	28	75.7	214	2	AAW00373	Aaw00373	Anti-CD18	353	28	75.7	512	8	ADN73831	Adn73831	Thale cre
281	28	75.7	214	2	AAW34504	Aaw34504	Light cha	354	28	75.7	518	8	ADT56687	Adt56687	Plant pol
282	28	75.7	214	2	AAW34506	Aaw34506	Light cha	355	28	75.7	519	3	AAy55080	Aay55080	Single ch
283	28	75.7	214	2	AAW49815	Aaw49815	Amino aci	356	28	75.7	519	3	AAU29914	Aau29914	Arabidops
284	28	75.7	214	2	AAW95615	Aaw95615	Humanized	357	28	75.7	524	5	AAU11289	Aau11289	Ashbysa go
285	28	75.7	214	2	AAW30632	Aaw30632	Recombina	358	28	75.7	530	9	ADX27069	Adx27069	P. citrea
286	28	75.7	214	2	AAW08754	Aaw08754	Human ant	359	28	75.7	537	3	AAB03664	Ab03664	Anti-CD18
287	28	75.7	214	4	AAAB66777	Aab66777	rhuWab CD	360	28	75.7	546	3	AAy55074	Aay55074	Single ch
288	28	75.7	214	5	ABG31889	Abg31889	Humanized	361	28	75.7	555	4	AAAB19871	Ab19871	Activatin
289	28	75.7	214	8	ABR55870	Abt55870	Human imm	362	28	75.7	555	7	ADE86039	Ad86039	Anti-CD3
290	28	75.7	214	8	ADK18342	Adk18342	Amino aci	363	28	75.7	555	8	ADK00036	Adk00036	Chimaeric
291	28	75.7	214	8	ADN49727	Adn49727	Human imm	364	28	75.7	555	8	ADY22069	Ady22069	Antibody
292	28	75.7	214	8	ADU74403	Adu74403	Human imm	365	28	75.7	555	9	ADY22137	Ady22137	Antibody
293	28	75.7	214	9	ABE27968	Abt27968	Humanized	366	28	75.7	565	4	AAAB19873	Ab19873	Activatin
294	28	75.7	215	8	ADO19050	Ado19050	Murine an	367	28	75.7	577	4	AAAB19872	Ab19872	Activatin
295	28	75.7	217	7	ABM87889	Abm87889	Rice abio	368	28	75.7	601	3	AAAB07461	Ab07461	An immuno
296	28	75.7	224	5	ABB47814	Abb47814	Listeria	369	28	75.7	601	6	ABG72265	Abg72265	Recombina
297	28	75.7	227	7	ADC011394	Adc011394	Enteroha	370	28	75.7	626	3	AAy55081	Aay55081	Single ch
298	28	75.7	232	9	ADK39141	Adk39141	Humanized	371	28	75.7	627	4	AAAG63854	Aag63854	Amino aci
299	28	75.7	233	2	AAK30777	Aak30777	pH52-9.0	372	28	75.7	630	6	ADA36435	Ada36435	Acinetoba
300	28	75.7	234	9	AAAB49242	Aab49242	Chimeric	373	28	75.7	637	5	AAU753365	Aau753365	Diphtheri
301	28	75.7	234	9	ADK39101	Adk39101	Mouse mon	374	28	75.7	638	5	AAU75370	Aau75370	Diphtheri
302	28	75.7	234	9	ADK39138	Adk39138	Mouse mon	375	28	75.7	640	5	AAy55082	Aay55082	Single ch
303	28	75.7	237	2	AAW95622	Aaw95622	PS1130 ex	376	28	75.7	642	5	AAU75382	Aau75382	Diphtheri
304	28	75.7	237	2	AAW30834	Aaw30834	Recombina	377	28	75.7	642	6	AAO29675	Aao29675	Anti-T ce
305	28	75.7	237	4	AAAB66784	Aab66784	Protein e	378	28	75.7	643	5	AAU75390	Aau75390	Diphtheri
306	28	75.7	237	6	ABP72745	Abp72745	Anti-CD18	379	28	75.7	643	6	AAO29670	Aao29670	Anti-T ce
307	28	75.7	237	9	ABE27976	Abt27976	E. coli S	380	28	75.7	652	3	AAy53000	Aay53000	Human eec
308	28	75.7	244	9	ADK39104	Adk39104	Humanized	381	28	75.7	657	5	AAU75448	Aau75448	Immunotox
309	28	75.7	255	4	ABE03896	Abt03896	Human mus	382	28	75.7	656	5	AAU75383	Aau75383	Immunotox
310	28	75.7	255	6	ABU13190	Abu13190	Novel hum	383	28	75.7	657	5	AAU75389	Aau75389	Diphtheri
311	28	75.7	255	8	ADJ29216	Adj29216	Human mus	384	28	75.7	664	5	ABB94273	Abb94273	Chlamydia
312	28	75.7	256	3	AAy55072	Aay55072	Interleuk	385	28	75.7	664	6	ABU26872	Abu26872	Protein e
313	28	75.7	257	4	AAW25808	Aaw25808	Human pro	386	28	75.7	666	2	AAy34991	Aay34991	C. pneumo
314	28	75.7	260	3	AAy55075	Aay55075	Single ch	387	28	75.7	677	6	ABP97414	Abp97414	Anti-huma
315	28	75.7	261	7	ADB311793	Adb311793	Plant (A.	388	28	75.7	676	8	ADS23615	Ad23615	Bacterial
316	28	75.7	261	7	ADD30963	Add30963	Plant yle	389	28	75.7	676	6	ABU25397	Abu25397	Protein e

390	28	75.7	685	8	ADP22646	Adp22646 Sea-squir	463	27	73.0	74	6	ADB09661	Adb09661 Alloiococ
391	28	75.7	696	5	ABG93272	Abg93272 C. albica	464	27	73.0	76	3	AAB24989	Aab24989 Plant SDF
392	28	75.7	704	4	AAB19888	Aab19888 Mlv envel	465	27	73.0	76	3	AAG59155	Aag59155 Arabidops
393	28	75.7	786	5	ABU10288	Abu10288 Human lun	466	27	73.0	76	3	AAG59165	Aag59165 Arabidops
394	28	75.7	893	8	ADK40920	Adk40920 Novel hum	467	27	73.0	84	7	ADD12514	Add12514 PDZ ligan
395	28	75.7	893	8	ADR15641	Adr15641 Kinase 42	468	27	73.0	84	8	ADI33550	Adi33550 Human PDZ
396	28	75.7	895	5	AAU75369	Aau75369 Diptheri	469	27	73.0	84	8	ADM33641	Adm33641 Human PDZ
397	28	75.7	895	5	AAU75368	Aau75368 Diptheri	470	27	73.0	84	8	ADO21072	Ado21072 PDZ domai
398	28	75.7	895	5	AAU75374	Aau75374 Diptheri	471	27	73.0	84	8	ADR83013	Adr83013 PDZ domai
399	28	75.7	895	5	AAO29673	Aao29673 Anti-T ce	472	27	73.0	84	8	ADU67430	Adu67430 Human SIF
400	28	75.7	896	5	AAU75367	Aau75367 Diptheri	473	27	73.0	84	8	ADW52644	Adw52644 Human PDZ
401	28	75.7	896	5	AAU75366	Aau75366 Diptheri	474	27	73.0	87	5	ABP60748	Abp60748 Bacteriop
402	28	75.7	896	5	AAU75373	Aau75373 Diptheri	475	27	73.0	92	7	ADD12378	Add12378 PDZ ligan
403	28	75.7	896	6	AAO29672	Aao29672 Anti-T ce	476	27	73.0	92	8	ADI53395	Adi53395 Human PDZ
404	28	75.7	896	6	AAO29671	Aao29671 Anti-T ce	477	27	73.0	92	8	ADM33486	Adm33486 Human PDZ
405	28	75.7	896	6	AAO29676	Aao29676 Anti-T ce	478	27	73.0	92	8	ADO20917	Ado20917 PDZ domai
406	28	75.7	896	5	ADX01023	Adx01023 Amino aci	479	27	73.0	92	8	ADR82858	Adr82858 PDZ domai
407	28	75.7	899	5	AAU75375	Aau75375 Diptheri	480	27	73.0	92	8	ADU67275	Adu67275 Human E2R
408	28	75.7	899	6	AAO29674	Aao29674 Anti-T ce	481	27	73.0	92	9	ADM52489	Adm52489 Human PDZ
409	28	75.7	904	4	ABE862853	Abbe862853 Drosophil	482	27	73.0	97	4	AAU21288	Aau21288 Human nov
410	28	75.7	921	9	ADM17078	Adm17078 Eucalyptu	483	27	73.0	98	5	ABE07639	Abe07639 PDZ domai
411	28	75.7	1040	6	ABU03533	Abu03533 Angiogene	484	27	73.0	98	9	AEA98653	Aea98653 Human PDZ
412	28	75.7	1040	8	ADM80792	Adm80792 Human CAD	485	27	73.0	99	8	ABO56701	Abos56701 Human gen
413	28	75.7	1060	8	ADR06360	Adr06360 N meningi	486	27	73.0	99	8	ADU15847	Adu15847 EZRIN bin
414	28	75.7	1088	2	AAV00891	Aav00891 Isoleucyl	487	27	73.0	99	8	ADU16015	Adu16015 SIPI PDZ
415	28	75.7	1088	2	AAV00892	Aav00892 Isoleucyl	488	27	73.0	99	9	ABE07827	Abe07827 PDZ domai
416	28	75.7	1133	3	ABG38914	Abg38914 Arabidops	489	27	73.0	99	9	AEA98841	Aea98841 Human PDZ
417	28	75.7	1175	8	ADI45383	Adi45383 Rice isop	490	27	73.0	105	7	ADM04247	Adm04247 Human pro
418	28	75.7	1193	3	AAG38913	Aag38913 Arabidops	491	27	73.0	105	8	ADX77353	Adx77353 Plant ful
419	28	75.7	1330	6	ABU26189	Abu26189 Protein e	492	27	73.0	112	9	ABE21888	Abe21888 Human DC-
420	28	75.7	1382	8	ADU25612	L. acidop	493	27	73.0	117	5	ABB81283	Abb81283 Human FGF
421	28	75.7	1422	2	AAR82071	Aar82071 Hepatitis	494	27	73.0	119	5	ABB81284	Abb81284 Human FGF
422	28	75.7	1422	3	ABO90941	Abos90941 Hepatitis	495	27	73.0	123	3	AAB32679	Aab32679 Eucalyptu
423	28	75.7	1534	4	ABE60348	Abbe60348 Drosophil	496	27	73.0	125	5	ABB81286	Abb81286 Human FGF
424	28	75.7	2332	8	ADV94875	Adv94875 O-type fo	497	27	73.0	125	5	ABB81285	Abb81285 Human FGF
425	28	75.7	2332	3	ADM22753	Adm22753 Foot-and-	498	27	73.0	127	5	ABA47980	Aba47980 Human FGF
426	28	75.7	2496	3	ABE00347	Abes00347 SARS coro	499	27	73.0	127	8	ADF86016	Adf86016 Truncated
427	28	75.7	9893	9	AE800347	Ae800347 SARS vir	500	27	73.0	127	8	ADF86019	Adf86019 Truncated
428	28	75.7	9914	8	ADT39252	Adt39252 HSARS vir	501	27	73.0	127	8	ADF86017	Adf86017 Truncated
429	28	75.7	9914	8	ADT36782	Adt36782 HSARS vir	502	27	73.0	127	8	ADF86017	Adf86017 Truncated
430	28	75.7	9914	9	AE800350	Ae800350 SARS coro	503	27	73.0	132	5	ABY78775	Abay78775 Limnanthe
431	28	75.7	9915	8	ADU40120	Adu40120 HSARS vir	504	27	73.0	133	2	AAV41115	Aav41115 Corn eucr
432	28	75.7	9915	8	ADT37650	Adt37650 HSARS vir	505	27	73.0	135	5	ABB81299	Abb81299 Human FGF
433	28	73.0	7	9	AEA45535	Aea45535 Apolipop	506	27	73.0	136	5	ABB81300	Abb81300 Mouse FGF
434	27	73.0	7	9	ABE21462	Abes21462 Mouse ant	507	27	73.0	139	8	ADX85649	Adx85649 Plant ful
435	27	73.0	7	9	ABE31220	Abes31220 Antibody	508	27	73.0	142	5	AAR56503	Aar56503 Glia acti
436	27	73.0	15	6	ABB82628	Abb82628 Peptide a	509	27	73.0	142	5	ABB81287	Abb81287 Human FGF
437	27	73.0	16	2	AAW79048	Aaw79048 Mononucle	510	27	73.0	145	8	ADF86018	Adf86018 Truncated
438	27	73.0	23	6	ABO13302	Abos13302 Mouse zin	511	27	73.0	145	8	ADF86015	Adf86015 Truncated
439	27	73.0	29	2	AAR70342	Aar70342 RGF-9(143	512	27	73.0	145	8	ADF86014	Adf86014 Truncated
440	27	73.0	29	2	AAW82380	Aaw82380 Seq ID 15	513	27	73.0	145	8	AAU31906	Aau31906 Novel hum
441	27	73.0	29	6	ABR39387	Ab39387 Potential	514	27	73.0	147	4	ABG22962	Abg22962 Novel hum
442	27	73.0	31	9	ADX83645	Adx83645 Rat insul	515	27	73.0	149	4	ABG30352	Abg30352 Novel hum
443	27	73.0	35	9	AEA28147	Aea28147 Sericin p	516	27	73.0	151	4	ABG30352	Abg30352 Novel hum
444	27	73.0	36	4	ABB39814	Abb39814 Peptide #	517	27	73.0	152	8	ADF86020	Adf86020 Truncated
445	27	73.0	36	4	AAW33404	Aaw33404 Peptide #	518	27	73.0	152	8	ADF86021	Adf86021 Truncated
446	27	73.0	36	4	AAW73195	Aaw73195 Human bon	519	27	73.0	159	2	AAR56510	Aar56510 Glia acti
447	27	73.0	36	4	AAW60539	Aaw60539 Human bra	520	27	73.0	160	2	AAR56511	Aar56511 Glia acti
448	27	73.0	36	4	ABG54911	Abg54911 Human liv	521	27	73.0	160	6	ABP56732	Abp56732 Human SAR
449	27	73.0	36	5	ABG43042	Abg43042 Human pep	522	27	73.0	161	5	ABB81281	Abb81281 Human FGF
450	27	73.0	49	4	ABG26888	Abg26888 Novel hum	523	27	73.0	161	6	ABP56730	Abp56730 Human SAR
451	27	73.0	51	4	AAW83305	Aaw83305 Human imm	524	27	73.0	161	6	ABP56726	Abp56726 Human SAR
452	27	73.0	53	4	ABB38739	Abb38739 Peptide #	525	27	73.0	161	6	ABP56729	Abp56729 Human SAR
453	27	73.0	53	4	AAW32210	Aaw32210 Peptide #	526	27	73.0	161	6	ABP56731	Abp56731 Human SAR
454	27	73.0	53	4	AAW71929	Aaw71929 Human bon	527	27	73.0	164	5	ABB81279	Abb81279 Human FGF
455	27	73.0	53	4	AAW59374	Aaw59374 Human bra	528	27	73.0	164	5	AAB47981	Aab47981 Human FGF
456	27	73.0	53	4	ABG53612	Abg53612 Human liv	529	27	73.0	165	4	ABG05608	Abg05608 Novel hum
457	27	73.0	53	5	ABG41143	Abg41143 Human pep	530	27	73.0	167	6	ABU49863	Abu49863 Protein e
458	27	73.0	54	5	ABG61986	Abg61986 Human tum	531	27	73.0	172	4	ABG13761	Abg13761 Novel hum
459	27	73.0	54	5	ABG61987	Abg61987 Human tum	532	27	73.0	172	5	ABB81275	Abb81275 Human FGF
460	27	73.0	61	2	AAR93224	Aar93224 Partial f	533	27	73.0	172	5	ABB81277	Abb81277 Human FGF
461	27	73.0	67	3	AAB25741	Aab25741 Human sec	534	27	73.0	172	5	ABB81280	Abb81280 Human FGF
462	27	73.0	74	3	AAB34710	Aab34710 Human sec	535	27	73.0	172	7	ADE09407	Ade09407 Novel pro

536	27	73.0	172	8	ADP86013	Adf86013 Truncated	609	27	73.0	208	7	ADP55942	Human Pro
537	27	73.0	174	5	ABG62054	Abg62054 Human tum	610	27	73.0	208	7	ADP92008	Fibroblas
538	27	73.0	175	2	AAK56508	Aar56508 Glia acti	611	27	73.0	208	8	ADP86012	Human fib
539	27	73.0	176	2	AAK56509	Aar56509 Glia acti	612	27	73.0	208	8	ADM94754	Human fib
540	27	73.0	177	2	AAK27208	Aar27208 Glia acti	613	27	73.0	208	8	ADQ20388	Human eof
541	27	73.0	178	2	AAK27210	Aar27210 Glia acti	614	27	73.0	208	8	ADT97925	Human ker
542	27	73.0	178	8	ABO59224	Abos9224 Human gen	615	27	73.0	208	9	ADW47173	Human FGF
543	27	73.0	180	5	ABG93218	Abg93218 S. cerevi	616	27	73.0	208	9	ADY68646	Human FGF
544	27	73.0	182	6	ABP79009	Abp79009 N. gonorr	617	27	73.0	208	9	ADZ87304	Human fib
545	27	73.0	183	5	ABU65170	Abu65170 Human NOV	618	27	73.0	214	3	ADG16677	Arabidops
546	27	73.0	183	8	ADM61991	Adm61991 Human nov	619	27	73.0	216	3	AAK48670	Arabidops
547	27	73.0	185	7	ADP09167	Adp09167 Novel pro	620	27	73.0	214	9	ADK83648	Rat insul
548	27	73.0	186	3	AAK48671	Aag48671 Arabidops	621	27	73.0	220	2	AAW11548	Amino aci
549	27	73.0	186	3	AAK16678	Aag16678 Arabidops	622	27	73.0	220	8	ADW71820	Plant ful
550	27	73.0	190	8	ADT58116	Adt58116 Plant pol	623	27	73.0	226	7	ADD31025	Plant yie
551	27	73.0	192	4	AAK82605	Aag82605 S. epider	624	27	73.0	226	8	ADI44175	Plant tra
552	27	73.0	192	4	AAK82453	Aag82453 S. epider	625	27	73.0	233	8	ADY12452	Plant ful
553	27	73.0	192	5	ADP40134	Abp40134 Staphyloc	626	27	73.0	233	8	ADK94608	Plant ful
554	27	73.0	192	6	ADA89745	Ada89745 Staphyloc	627	27	73.0	234	9	ABP70995	Human NHE
555	27	73.0	192	8	ADP07402	Adp07402 Staphyloc	628	27	73.0	235	3	AAK25742	Human sec
556	27	73.0	194	6	AAK30473	Aae30473 Haemophil	629	27	73.0	236	7	ABM89532	Rice abio
557	27	73.0	196	4	AAK82460	Aag82460 S. epider	630	27	73.0	237	4	AAK18366	Peptide #
558	27	73.0	201	5	ABP39474	Abp39474 Staphyloc	631	27	73.0	237	4	ABK37399	Peptide #
559	27	73.0	201	8	ADP05348	Adp05348 Staphyloc	632	27	73.0	237	4	AAK30844	Peptide #
560	27	73.0	202	8	ADR10161	Adr10161 Human pro	633	27	73.0	237	4	ABK32150	Peptide #
561	27	73.0	202	9	ADZ88783	Adz88783 Breast ep	634	27	73.0	237	4	ABB22694	Protein #
562	27	73.0	203	6	ABU28516	Abu28516 Protein e	635	27	73.0	237	4	AAW70529	Human bon
563	27	73.0	205	2	AAK27209	Aar27209 Glia acti	636	27	73.0	237	4	AAK58081	Human bra
564	27	73.0	205	2	AAK56506	Aar56506 Glia acti	637	27	73.0	237	4	ABG52205	Human liv
565	27	73.0	206	2	AAK27211	Aar27211 Glia acti	638	27	73.0	237	4	AAK05966	Peptide #
566	27	73.0	206	2	AAK27212	Aar27212 Glia acti	639	27	73.0	237	5	ABG40176	Human pop
567	27	73.0	206	2	AAK56507	Aar56507 Glia acti	640	27	73.0	240	5	ABP41070	Human ova
568	27	73.0	207	2	AAK56504	Aar56504 Glia acti	641	27	73.0	243	9	ABE07641	PDZ domai
569	27	73.0	208	2	AAK27207	Aar27207 Glia acti	642	27	73.0	243	9	AEA98655	Human PDZ
570	27	73.0	208	2	AAK27213	Aar27213 Glia acti	643	27	73.0	244	2	AAK72713	Murine OR
571	27	73.0	208	2	AAK56505	Aar56505 Glia acti	644	27	73.0	245	2	AAK35673	Chlamydia
572	27	73.0	208	2	AAK70822	Aar70822 FGF-9, 3/	645	27	73.0	246	8	ADP60534	Pig TKA-1
573	27	73.0	208	2	AAK80784	Aar80784 Fibroblas	646	27	73.0	246	8	ADP60534	Bacterial
574	27	73.0	208	2	AAW11547	Aaw11547 Amino aci	647	27	73.0	246	8	ADS26704	Bacterial
575	27	73.0	208	2	AAW75719	Aaw75719 Fibroblas	648	27	73.0	246	8	ADZ26337	Bacterial
576	27	73.0	208	2	AAW53024	Aaw53024 Fibroblas	649	27	73.0	251	3	AAK58788	Breast an
577	27	73.0	208	3	AAK87856	Aay87856 Human FGF	650	27	73.0	252	6	ABP59502	Human int
578	27	73.0	208	3	AAK32341	Aay32341 Human fib	651	27	73.0	254	6	ABK39292	Protein e
579	27	73.0	208	3	AAK90418	Aay90418 FGF-9, SE	652	27	73.0	258	4	ABB63703	Drosophil
580	27	73.0	208	3	AAK10299	Aab10299 Fibroblas	653	27	73.0	258	8	ADP07938	Fly polyP
581	27	73.0	208	4	AAK50290	Aab50290 Human fib	654	27	73.0	259	9	ADZ88785	Breast ep
582	27	73.0	208	4	AAK50710	Aab50710 Human fib	655	27	73.0	261	3	AAK75036	Neisseria
583	27	73.0	208	4	AAK61663	Aab61663 FGF9 prot	656	27	73.0	263	5	ABP43601	Hypochala
584	27	73.0	208	4	AAK65655	Aag65655 Human fib	657	27	73.0	265	3	AAK16676	Arabidops
585	27	73.0	208	4	AAK504401	Aae04401 Human fib	658	27	73.0	265	3	AAK48669	Arabidops
586	27	73.0	208	4	AAK50295	Aab50295 Human fib	659	27	73.0	265	8	ADN73943	Thale cre
587	27	73.0	208	4	AAK85820	Aab85820 Human fib	660	27	73.0	269	9	ADM17209	E grandis
588	27	73.0	208	4	AAK85838	Aab85838 Murine fi	661	27	73.0	271	5	AAU10031	Human elo
589	27	73.0	208	5	AAK24994	Aae24994 Human fib	662	27	73.0	273	7	ADM03940	Human pro
590	27	73.0	208	5	ABK81276	Abk81276 Human FGF	663	27	73.0	275	9	ADZ88780	Breast ap
591	27	73.0	208	5	ABK81288	Abk81288 Human FGF	664	27	73.0	276	8	ADK77196	Plant ful
592	27	73.0	208	5	ABK81274	Abk81274 Human FGF	665	27	73.0	279	4	ABG06093	Novel hum
593	27	73.0	208	5	ABK81290	Abk81290 Chicken F	666	27	73.0	279	7	ADH87545	Enterococ
594	27	73.0	208	5	ABK81289	Abk81289 Mouse FGF	667	27	73.0	280	4	ABG23726	Novel hum
595	27	73.0	208	5	AAE18814	Aae18814 Human FGF	668	27	73.0	281	5	ABP26257	Streptoco
596	27	73.0	208	5	ABK99128	Abk99128 Human fib	669	27	73.0	281	8	ADV88127	Streptoco
597	27	73.0	208	6	ABP54432	Abp54432 Rat FGF-9	670	27	73.0	281	8	ADV79380	Streptoco
598	27	73.0	208	6	ABP54433	Abp54433 Xenopus X	671	27	73.0	281	8	ADV81558	Streptoco
599	27	73.0	208	6	ABP54431	Abp54431 Mouse FGF	672	27	73.0	285	4	ABB65204	Drosophil
600	27	73.0	208	6	ABP54430	Abp54430 Human FGF	673	27	73.0	286	6	ABU01321	S. pneumo
601	27	73.0	208	6	ABG74158	Abg74158 Human fib	674	27	73.0	286	6	ABP81579	Streptoco
602	27	73.0	208	6	ABF54279	Abf54279 Human fib	675	27	73.0	286	8	ADK48611	Novel S.
603	27	73.0	208	6	ABG72717	Abg72717 Recombina	676	27	73.0	286	8	ADR95448	Novel S.
604	27	73.0	208	6	ADK95454	Adk95454 Fibroblas	677	27	73.0	289	3	AAK58771	Streptoco
605	27	73.0	208	7	ABM74092	Abm74092 DNA clone	678	27	73.0	289	3	AAK58771	Breast an
606	27	73.0	208	7	ADC34584	Adc34584 Human fib	679	27	73.0	291	8	ADY04570	Plant ful
607	27	73.0	208	7	ADK66127	Adk66127 Fibroblas	680	27	73.0	295	4	ABG27407	Novel hum
608	27	73.0	208	7	ADP55940	Adp55940 Rat Prote	681	27	73.0	295	8	ADM87809	Human EST

682	27	73.0	296	4	ABR65333	Abb565333 Drosophil	755	27	73.0	450	2	AAV22130	Aay22130 Human tyr
683	27	73.0	296	7	ADC01826	Adc01826 C. albica	756	27	73.0	450	8	ADO60538	Ado60538 Human TKA
684	27	73.0	297	7	ADJ37953	Adj37953 D melanog	757	27	73.0	452	8	ADX72316	Adx72316 Plant ful
685	27	73.0	297	8	ADX71976	Adx71976 Plant ful	758	27	73.0	454	3	AAQ08560	Aaq08560 Arabidops
686	27	73.0	302	9	ADV16488	Adv16488 E. faecal	759	27	73.0	454	5	ABN92761	Abn92761 Herbicida
687	27	73.0	303	2	AAV74141	Aay74141 Human pro	760	27	73.0	458	8	ADN22746	Adn22746 Bacterial
688	27	73.0	306	8	ADX97067	Adx97067 Plant ful	761	27	73.0	463	8	ADT56604	Adt56604 Plant pol
689	27	73.0	306	8	ADX97272	Adx97272 Plant ful	762	27	73.0	468	9	ADZ88781	Adz88781 Breast ap
690	27	73.0	311	5	AAH71210	Aab71210 Human GPC	763	27	73.0	473	4	ABG18130	Abg18130 Novel hum
691	27	73.0	311	7	ADD12821	Add12821 Novel hum	764	27	73.0	475	8	ADK16599	Adk16599 Nanoarcha
692	27	73.0	313	8	ADX73814	Adx73814 Plant ful	765	27	73.0	480	8	ADX93344	Adx93344 Plant ful
693	27	73.0	314	5	AAU10030	Aau10030 Human ELO	766	27	73.0	494	4	ABM65461	Abm65461 Drosophil
694	27	73.0	314	5	AAE24551	Aae24551 Human ELG	767	27	73.0	506	5	ASG62055	Asg62055 Human tum
695	27	73.0	314	5	AAU81195	Aau81195 Human sec	768	27	73.0	515	8	ADT57867	Adt57867 Plant pol
696	27	73.0	314	6	ADA54388	Ada54388 Human pro	769	27	73.0	517	7	ADU08229	Adu08229 Novel pro
697	27	73.0	314	6	ABB28264	Abb28264 Human LCE	770	27	73.0	527	5	ABU05697	Abu05697 M. tuberc
698	27	73.0	314	6	ABB28263	Abb28263 Human LCE	771	27	73.0	528	4	AAAG81105	Aag81105 Mycobacte
699	27	73.0	314	8	ADM87368	Adm87368 Human pro	772	27	73.0	530	8	ADS21235	Ads21235 Bacterial
700	27	73.0	314	8	ADU06266	Adu06266 Novel bro	773	27	73.0	532	8	ADN25034	Adn25034 Bacterial
701	27	73.0	314	9	ADY17622	Ady17622 PRO polyp	774	27	73.0	538	8	ADN25034	Adn25034 Bacterial
702	27	73.0	314	9	ADZ21110	Adz21110 Human ELO	775	27	73.0	547	8	ADY07361	Ady07361 Plant ful
703	27	73.0	315	8	ADX80159	Adx80159 Plant ful	776	27	73.0	553	8	ADX96602	Adx96602 Plant ful
704	27	73.0	316	3	AAQ08562	Aaq08562 Arabidops	777	27	73.0	556	5	ABP73756	Abp73756 Candida a
705	27	73.0	318	4	ABG23725	Abg23725 Novel hum	778	27	73.0	573	6	ABU26390	Abu26390 Protein e
706	27	73.0	318	8	ADX90732	Adx90732 Plant ful	779	27	73.0	573	9	AEA22122	Aea22122 Campyloba
707	27	73.0	318	8	ADX90718	Adx90718 Plant ful	780	27	73.0	585	6	ABB80169	Abb80169 A. fumiga
708	27	73.0	318	8	ADX77989	Adx77989 Plant ful	781	27	73.0	586	4	ABG13054	Abg13054 Novel hum
709	27	73.0	321	5	ABG62063	Abg62063 Human tum	782	27	73.0	590	3	AAAG39347	Aag39347 Arabidops
710	27	73.0	323	5	ABR90591	AbR90591 Chlamydia	783	27	73.0	605	5	ABB55461	Abb55461 Lactococc
711	27	73.0	323	8	ADR99385	Adr99385 Chlamydia	784	27	73.0	612	4	ABG16046	Abg16046 Novel hum
712	27	73.0	328	2	AAV35219	Aay35219 Chlamydia	785	27	73.0	614	7	ABM88332	Abm88332 Rice abio
713	27	73.0	329	5	ABR84728	AbR84728 DNA polym	786	27	73.0	621	4	ABG28304	Abg28304 Novel hum
714	27	73.0	337	5	ABU51416	Abu51416 Helicobac	787	27	73.0	623	6	ABG74859	Abg74859 C. elegan
715	27	73.0	339	7	ADD30286	AdD30286 Plant yie	788	27	73.0	633	6	ABP78455	Abp78455 N. gonorr
716	27	73.0	339	8	ADI44171	Adi44171 Plant tra	789	27	73.0	636	6	ABP79051	Abp79051 N. gonorr
717	27	73.0	340	5	ABP52526	Abp52526 Human tra	790	27	73.0	637	6	ABU24017	Abu24017 Protein e
718	27	73.0	340	6	ADA24262	Ada24262 Human tra	791	27	73.0	638	8	ADX92515	Adx92515 Plant ful
719	27	73.0	343	4	ABG21368	Abg21368 Novel hum	792	27	73.0	644	3	AAAG39346	Aag39346 Arabidops
720	27	73.0	346	5	ABG69057	Abg69057 Amino aci	793	27	73.0	646	8	ABU00836	Abu00836 S. pneumo
721	27	73.0	355	4	ABE71043	AbE71043 Drosophil	794	27	73.0	646	8	ADK48177	Adk48177 Streptoco
722	27	73.0	358	6	ABR47594	AbR47594 Breast ca	795	27	73.0	652	6	ABU20671	Abu20671 Protein e
723	27	73.0	358	6	ADA24264	Ada24264 Human eaz	796	27	73.0	654	8	ADR95905	Adr95905 Novel S.
724	27	73.0	358	8	ADI61285	Adi61285 Human tra	797	27	73.0	654	9	AEA59775	Aea59775 Streptoco
725	27	73.0	358	8	ABM81929	Abm81929 Tumour-as	798	27	73.0	664	2	ABU26749	Abu26749 Protein e
726	27	73.0	362	4	ABG27408	Abg27408 Novel hum	799	27	73.0	667	2	AAV41118	Aay41118 Rice sucr
727	27	73.0	362	5	ABP51278	AbP51278 Human WDD	800	27	73.0	672	8	ADQ66549	Adq66549 Novel hum
728	27	73.0	367	8	ADT60338	Adt60338 Plant pol	801	27	73.0	676	8	ADN19848	Adn19848 Bacterial
729	27	73.0	368	8	ADR08612	Adr08612 Human pro	802	27	73.0	677	4	ABG09179	Abg09179 Novel hum
730	27	73.0	372	4	ABR80284	AbR80284 Human pro	803	27	73.0	677	4	ABG26012	Abg26012 Novel hum
731	27	73.0	378	5	ABU52035	Abu52035 Helicobac	804	27	73.0	677	4	ABG24683	Abg24683 Novel hum
732	27	73.0	382	5	ABE47833	AbE47833 Listeria	805	27	73.0	677	4	ABG25927	Abg25927 Novel hum
733	27	73.0	384	9	ABE39984	AbE39984 L. pneumo	806	27	73.0	681	8	ADY06544	Ady06544 Plant ful
734	27	73.0	385	5	ABU52271	AbU52271 Helicobac	807	27	73.0	683	8	ADN22276	Adn22276 Bacterial
735	27	73.0	392	9	ABE36592	AbE36592 L. pneumo	808	27	73.0	684	6	ABG74858	Abg74858 C. elegan
736	27	73.0	394	4	ABG21369	Abg21369 Novel hum	809	27	73.0	684	6	ABG74861	Abg74861 C. elegan
737	27	73.0	397	6	ABR82135	AbR82135 Bacterial	810	27	73.0	684	8	ADY05412	Ady05412 Plant ful
738	27	73.0	398	5	ABU52221	AbU52221 Helicobac	811	27	73.0	687	4	ABG04354	Abg04354 Novel hum
739	27	73.0	400	6	ABG62061	Abg62061 Human tum	812	27	73.0	689	2	AAW98483	Aaw98483 H. pylori
740	27	73.0	416	6	ABM72185	Abm72185 Staphyloc	813	27	73.0	689	4	AAU35855	Aau35855 Helicobac
741	27	73.0	424	4	ABG24823	Abg24823 Novel hum	814	27	73.0	689	6	ABU31070	Abu31070 Protein e
742	27	73.0	428	5	ABP40034	Abp40034 Staphyloc	815	27	73.0	701	3	AAV51007	Aay51007 C. vicina
743	27	73.0	428	8	ADS07976	AdS07976 Staphyloc	816	27	73.0	721	4	ABE52899	AbE52899 Escherich
744	27	73.0	434	5	ABR01749	AbR01749 Human bre	817	27	73.0	724	5	ABG62065	Abg62065 Human tum
745	27	73.0	438	8	AQO8764	AqO8764 Ciona int	818	27	73.0	775	8	ADN19941	Adn19941 Bacterial
746	27	73.0	439	4	ABG20048	AbG20048 Novel hum	819	27	73.0	850	4	AAAB74922	AaB74922 Pteris br
747	27	73.0	440	6	ABU20398	AbU20398 Protein e	820	27	73.0	852	4	AAAB94405	AaB94405 Human pro
748	27	73.0	443	3	ACG08561	Aac08561 Arabidops	821	27	73.0	852	5	ABP69464	Abp69464 Human pol
749	27	73.0	444	4	ABG68897	AbG68897 Drosophil	822	27	73.0	852	7	ADJ69529	Adj69529 Human hea
750	27	73.0	446	3	AAAG39348	Aag39348 Arabidops	823	27	73.0	895	5	ABR93775	AbR93775 Herbicida
751	27	73.0	447	2	AAE95275	Aae95275 Nisin nls	824	27	73.0	902	7	ABM64833	Abm64833 Human pro
752	27	73.0	447	2	AAW98658	Aaw98658 H. pylori	825	27	73.0	921	4	ABE50264	AbE50264 DKFp5860
753	27	73.0	450	2	AAW46606	Aaw46606 Tyrosine	826	27	73.0	921	8	ADP23117	AdP23117 PRO polyp
754	27	73.0	450	2	AAV29635	Aay29635 Human tyr	827	27	73.0	947	4	ABG20052	Abg20052 Novel hum



828	27	73.0	947	8	ADx95802	Adx95802	Plant ful	901	26	70.3	21	6	ADA03881	Ada03881	Ineulin r
829	27	73.0	965	8	ADY22208	Ady22208	Plant ful	902	26	70.3	21	7	ADH95094	Adh95094	Ineulin r
830	27	73.0	969	3	AY68833	Ay68833	A poly(AD	903	26	70.3	21	8	ADL67785	Adl67785	IGF-IR/IR
831	27	73.0	972	4	ABB71801	Abb71801	Drosophil	904	26	70.3	21	8	ADM37630	Adm37630	Anti-IR F
832	27	73.0	980	3	AY68839	Ay68839	A poly(AD	905	26	70.3	23	6	ABO12588	Abol12588	Human zin
833	27	73.0	982	2	AY28464	Ay28464	Maize pol	906	26	70.3	23	6	ABO13286	Abol13286	Mouse zin
834	27	73.0	987	4	ABG20044	Abg20044	Novel hum	907	26	70.3	23	6	ABO13297	Abol13297	Mouse zin
835	27	73.0	990	4	AAU27769	Aau27769	Human ful	908	26	70.3	23	6	ABO12729	Abol12729	Human zin
836	27	73.0	1021	7	ADF07098	Adf07098	Bacterial	909	26	70.3	23	6	ABO11774	Abol11774	Human zin
837	27	73.0	1066	2	AAW72711	Aaw72711	Alpha-1,4	910	26	70.3	23	6	AAW40986	Aaw40986	Ara h 3 a
838	27	73.0	1066	2	AAW70638	Aaw70638	M.costata	911	26	70.3	26	4	ABB23535	Abb23535	Protein #
839	27	73.0	1066	2	AAW88255	Aaw88255	Morchella	912	26	70.3	26	4	ABB16882	Abb16882	Bacteriop
840	27	73.0	1066	8	ADO50615	Ado50615	Glucan ly	913	26	70.3	41	4	AAW73436	Aaw73436	Human gen
841	27	73.0	1070	2	AAW72712	Aaw72712	Alpha-1,4	914	26	70.3	41	4	AAW73374	Aaw73374	Human gen
842	27	73.0	1070	2	AAW77083	Aaw77083	M.vulgari	915	26	70.3	41	5	ABG64276	Abg64276	Human alb
843	27	73.0	1070	2	AAW88256	Aaw88256	Morchella	916	26	70.3	41	5	ABG64277	Abg64277	Human alb
844	27	73.0	1078	8	ADO50616	Ado50616	Glucan ly	917	26	70.3	41	8	ADL77541	Adl77541	Albumin f
845	27	73.0	1078	8	ADO66807	Ado66807	Novel hum	918	26	70.3	41	8	ADL77542	Adl77542	Albumin f
846	27	73.0	1112	2	AAV13437	Aav13437	Mouse SLo	919	26	70.3	43	4	ABB10655	Abb10655	Human pan
847	27	73.0	1117	4	AAW39632	Aaw39632	Human pol	920	26	70.3	43	4	AAW92441	Aaw92441	Human dfg
848	27	73.0	1117	4	AAW39633	Aaw39633	Human pol	921	26	70.3	50	3	AAW54453	Aaw54453	Human pan
849	27	73.0	1155	2	AAW28047	Aaw28047	IRS-1 pro	922	26	70.3	50	5	ABJ10812	Abj10812	Protein o
850	27	73.0	1156	8	ADN23475	Adn23475	Bacterial	923	26	70.3	54	6	ABU43462	Abu43462	Protein e
851	27	73.0	1192	4	AAW39631	Aaw39631	Human pol	924	26	70.3	55	4	AAU60440	Aau60440	Protonib
852	27	73.0	1205	4	ABW61778	Abw61778	Drosophil	925	26	70.3	55	6	ABW56959	Abw56959	Protonib
853	27	73.0	1225	4	AAW41419	Aaw41419	Human pol	926	26	70.3	56	2	AAU02514	Aau02514	Clone eel
854	27	73.0	1225	4	AAW41418	Aaw41418	Human pol	927	26	70.3	57	6	ABU56889	Abu56889	BoNT/A Hc
855	27	73.0	1225	4	AAW41417	Aaw41417	Human pol	928	26	70.3	57	6	ABU56872	Abu56872	BoNT/A Hc
856	27	73.0	1235	6	AAW416354	Aaw416354	Rat IRSAL	929	26	70.3	57	6	ABU56874	Abu56874	BoNT/A Hc
857	27	73.0	1235	9	ADW83647	Adw83647	Rat ineul	930	26	70.3	59	4	ABB03284	Abb03284	Human muse
858	27	73.0	1235	9	ADW83656	Adw83656	Rat ineul	931	26	70.3	59	6	ABU12578	Abu12578	Novel hum
859	27	73.0	1235	9	ADW83657	Adw83657	Rat ineul	932	26	70.3	59	8	ADJ28604	Adj28604	Human mus
860	27	73.0	1361	7	ADB82702	Adb82702	Human pro	933	26	70.3	62	7	ADC74737	Adc74737	Human pro
861	27	73.0	1316	4	ABG22997	Abg22997	Novel hum	934	26	70.3	63	4	AAW96057	Aaw96057	Human reg
862	27	73.0	1332	4	ABG20051	Abg20051	Novel hum	935	26	70.3	67	8	ADH45429	Adh45429	Human mol
863	27	73.0	1442	6	ABU48905	Abu48905	Protein e	936	26	70.3	69	2	AAW20495	Aaw20495	H. pylori
864	27	73.0	1469	8	ADW89616	Adw89616	Antagonis	937	26	70.3	69	4	AAU43587	Aau43587	Protonib
865	27	73.0	1532	4	ABW68585	Abw68585	Drosophil	938	26	70.3	69	6	ABM40106	Abm40106	Protonib
866	27	73.0	1997	3	ABE18287	Abel18287	Plasmodiu	939	26	70.3	71	6	ABO14099	Abol14099	Novel hum
867	27	73.0	2042	4	ABW59689	Abw59689	Drosophil	940	26	70.3	71	6	ABO14087	Abol14087	Novel hum
868	27	73.0	2424	4	ABW68256	Abw68256	Drosophil	941	26	70.3	71	6	ABR47945	Abra47945	Human sec
869	27	73.0	3007	8	ADQ17278	Adq17278	Human eof	942	26	70.3	71	6	ABR48130	Abra48130	Human sec
870	27	73.0	4773	7	ADJ95094	Adj95094	Novel NOV	943	26	70.3	71	6	ABR00177	Abra00177	Human gen
871	27	73.0	6576	6	ABO14699	Abol14699	Novel hum	944	26	70.3	71	6	ABR00293	Abra00293	Human gen
872	27	73.0	6669	6	ABO14698	Abol14698	Novel hum	945	26	70.3	71	7	ADB91821	Adb91821	Human sec
873	27	73.0	6669	7	ADP46052	Adp46052	Human Pro	946	26	70.3	71	7	ADB91678	Adb91678	Human sec
874	27	73.0	6669	8	ADQ124530	Adq124530	Human mod	947	26	70.3	71	7	ADC74587	Adc74587	Human sec
875	27	73.0	6669	8	ADQ17209	Adq17209	Human eof	948	26	70.3	71	7	ADC74352	Adc74352	Human sec
876	27	73.0	6669	9	AEI13347	Aebi13347	Nebulin S	949	26	70.3	71	8	ADG78488	Adg78488	Human sec
877	27	73.0	6700	6	ABO14697	Abol14697	Novel hum	950	26	70.3	71	8	ADN60784	Adn60784	Human sec
878	26.5	71.6	549	8	AAW62316	Aaw62316	Yeast ER	951	26	70.3	71	8	ADN60796	Adn60796	Human sec
879	26.5	71.6	549	8	ADW43776	Adw43776	Bacterial	952	26	70.3	72	2	AAW27677	Aaw27677	Human sec
880	26	70.3	7	2	AAW75490	Aaw75490	Mouse ant	953	26	70.3	72	8	ADG78505	Adg78505	Human sec
881	26	70.3	7	5	AAE28153	Aae28153	Murine 9P	954	26	70.3	73	2	AAW20895	Aaw20895	Human pre
882	26	70.3	7	8	ADW52806	Adw52806	Anti-alpha	955	26	70.3	73	4	AAW61284	Aaw61284	Protonib
883	26	70.3	7	8	ADW38474	Adw38474	Mouse ant	956	26	70.3	73	6	ABW57803	Abw57803	Protonib
884	26	70.3	7	9	ADW95702	Adw95702	Anti-hil-	957	26	70.3	74	4	AAE01277	Aae01277	Human alb
885	26	70.3	7	9	ADW15707	Adw15707	Mouse ant	958	26	70.3	74	5	ABG63689	Abg63689	Human alb
886	26	70.3	10	2	AAW40994	Aaw40994	Ara h 3 a	959	26	70.3	74	8	ADL76954	Adl76954	Albumin f
887	26	70.3	11	9	ADW53782	Adw53782	G protein	960	26	70.3	75	4	AAU86577	Aau86577	Novel hum
888	26	70.3	12	3	AAW07957	Aaw07957	CDRI sequ	961	26	70.3	75	7	ABW59911	Abw59911	Connectiv
889	26	70.3	15	2	AAW40947	Aaw40947	Peptide 5	962	26	70.3	76	4	ABG06503	Abg06503	Novel hum
890	26	70.3	15	4	AAW63336	Aaw63336	Amino aci	963	26	70.3	80	8	ABO58149	Abol58149	Human gen
891	26	70.3	15	5	AAW60788	Abw60788	Human rib	964	26	70.3	81	8	ADL05425	Adl05425	M. catar
892	26	70.3	15	9	ADW70971	Adw70971	Rabies vi	965	26	70.3	89	2	AAW27880	Aaw27880	Amino aci
893	26	70.3	20	5	AAU70785	Aau70785	Hepatitis	966	26	70.3	89	4	ASG07217	Asg07217	Novel hum
894	26	70.3	20	5	AAU70784	Aau70784	Hepatitis	967	26	70.3	93	2	AAW20902	Aaw20902	H. pylori
895	26	70.3	20	7	ADW85038	Adw85038	HBV HBcAg	968	26	70.3	93	4	ABG24270	Abg24270	Novel hum
896	26	70.3	20	7	ADW85039	Adw85039	HBV HBcAg	969	26	70.3	99	2	AAW94292	Aaw94292	UDP-galac
897	26	70.3	20	8	ADW85039	Adw85039	HBV HBcAg	970	26	70.3	99	2	AAW92637	Aaw92637	Cyanopais
898	26	70.3	21	5	ADW14596	Adw14596	Hepatitis	971	26	70.3	100	2	AAW30455	Aaw30455	Canine co
899	26	70.3	21	8	AAU75038	Aau75038	FelV-A En	972	26	70.3	100	2	AAW30456	Aaw30456	Canine co
900	26	70.3	21	5	AAU89051	Aau89051	Insulin/I	973	26	70.3	102	5	ADK34244	Adk34244	Novel hum

974 26 70.3 103 8 ADP68200 Human GCA  
 975 26 70.3 103 8 ADG66086 Novel hum  
 976 26 70.3 104 5 ABB06787 Human rib  
 977 26 70.3 108 4 ABUS2633 Human bra  
 978 26 70.3 108 7 ADB78583 Rat F997-  
 979 26 70.3 109 1 AAP81027 V region  
 980 26 70.3 109 2 AAR21311 Light cha  
 981 26 70.3 109 8 ADR38674 Mouse lig  
 982 26 70.3 109 8 ADR38691 Mouse lig  
 983 26 70.3 109 8 ADR38672 Mouse lig  
 984 26 70.3 109 9 ADW86133 Novel cyt  
 985 26 70.3 110 9 ADW86132 Novel cyt  
 986 26 70.3 111 2 AAR25721 Humanised  
 987 26 70.3 111 2 AAY32783 HIV chemo  
 988 26 70.3 111 2 AAY32784 HIV chemo  
 989 26 70.3 111 4 AAB69662 Humanised  
 990 26 70.3 111 4 AAB69661 Murine Pd  
 991 26 70.3 111 8 ADE25831 Anti-alpha  
 992 26 70.3 111 8 ADE25830 Humanised  
 993 26 70.3 111 8 ADO47765 Humanised  
 994 26 70.3 111 8 ADO47709 Humanised  
 995 26 70.3 111 8 ADO47764 Mouse Fd7  
 996 26 70.3 111 8 ADO47708 Mouse Fd7  
 997 26 70.3 111 9 ADX16641 Humanized  
 998 26 70.3 112 2 AAR79249 Light cha  
 999 26 70.3 112 2 AAY32788 PHIV-CAT  
 1000 26 70.3 112 6 ABB98910 Variable

# ALIGNMENTS

RESULT 1  
 AAB81983  
 ID AAB81983 standard; peptide; 7 AA.

AC AAB81983;

DT 03-JUL-2001 (first entry)

DE Ganglioside GD3 specific antibody related peptide SEQ ID NO: 7.

KW Ganglioside; GD3; complementarity determining region; CDR; antibody;  
 KW cancer.

OS Mus musculus.

PN WO200123432-A1.

PD 05-APR-2001.

PF 29-SEP-2000; 2000WO-JP006774.

PR 30-SEP-1999; 99JP-00278291.

PR 06-APR-2000; 2000JP-00105088.

PA (KYOW ) KYOWA HAKKO KOGYO KK.

PI Hanai N, Shitara K, Nakamura K, Niwa R;

DR WPI; 2001-266143/27.

XX New human type complementation-determining region-transplanted antibody  
 PT and derivatives against ganglioside GD3, useful in diagnosis and therapy  
 PT of e.g. tumors, with low antigenicity, little side effects but potent  
 PT activity in cancer.

XX Claim 4; Page 142; 183pp; Japanese.

XX The present invention describes a monoclonal antibody which can react  
 CC specifically with ganglioside GD3. The antibody and its derivatives are  
 CC useful in the diagnosis and therapy of tumours, particularly cancer  
 CC diagnosis. The present sequence is a protein used in the exemplification

CC of the invention  
 XX Sequence 7 AA;

Query Match 100.0%; Score 37; DB 4; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLHS 7  
 DB 1 YSSNLHS 7

## RESULT 2

ABU11008  
 ID ABU11008 standard; peptide; 7 AA.

XX ABU11008;

XX 04-FEB-2003 (first entry)

XX Modified ganglioside GD3 antibody associated peptide #5.

XX Ganglioside GD3; anti-ganglioside GD3 antibody; tumour; melanoma.

OS Mus musculus.

PN WO200278739-A1.

PD 10-OCT-2002.

PF 29-MAR-2002; 2002WO-JP003170.

PR 29-MAR-2001; 2001JP-00097483.

PA (KYOW ) KYOWA HAKKO KOGYO KK.

PI Shitara K, Niwa R, Kanazawa J, Asada M;

DR WPI; 2003-067410/06.

XX Drugs containing genetically-modified antibody against ganglioside GD3,  
 PT its fragment, immunocompetent cell activators or/and antitumor agents in  
 PT combination, applicable in treating malignant tumor like melanoma.

XX Claim 6; Page 99; 121pp; Japanese.

XX The invention describes drugs contain a genetically-modified antibody  
 CC against ganglioside GD3 or its fragment and at least 1 of a substance  
 CC capable of activating immunocompetent cells and a substance having an  
 CC antitumor activity in combination. The drugs can be used to treat tumour  
 CC like melanoma and can provide a treatment with enhanced therapeutic  
 CC effect and little side-reactions, particularly to relieve problems of  
 CC side-effects during the conventional single administration. This sequence  
 CC represents a peptide associated with the anti- ganglioside GD3 antibody

XX Sequence 7 AA;

Query Match 100.0%; Score 37; DB 6; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLHS 7  
 DB 1 YSSNLHS 7

## RESULT 3

ADZ57814  
 ID ADZ57814 standard; peptide; 7 AA.

XX ADZ57814;

DT 30-JUN-2005 (first entry)  
 XX Ganglioside GD3 binding antibody associated CDR2 SEQ ID NO 18.  
 DE cytostatic; antibody engineering; cancer; neoplasm; ganglioside; GD3;  
 KW pharmaceutical.  
 XX Mus musculus.  
 OS WO2005035577-A1.  
 PN 21-APR-2005.  
 PD 08-OCT-2004; 2004WO-JP015314.  
 PF 08-OCT-2003; 2003JP-00350161.  
 PR (KYOW ) KYOWA HAKKO KOGYO KK.  
 XX Iida S, Satoh M, Urakubo M, Wakitani M, Uchida K, Niwa R;  
 PI Shitara K;  
 FI WPI; 2005-346195/35.  
 XX Antibody composition for treating ganglioside GD3 associated disease e.g.  
 PT cancer, comprises genetically modified antibody molecule, which  
 PT specifically binds to ganglioside GD3 and has N-glycoside-binding sugar  
 PT chain in its Fc domain.  
 XX Claim 9; SEQ ID NO 18; 124pp; Japanese.  
 PS The invention describes an antibody composition (I), comprising a  
 CC genetically modified antibody molecule which specifically binds to  
 CC ganglioside GD3 and has an N-glycoside-binding complex sugar chain in its  
 CC Fc domain, where the N-glycoside-binding complex sugar chain is a sugar  
 CC chain having no fucose attached to N-acetylglucosamine at the reducing  
 CC end of the sugar chain. Also described are: a transformant (II) capable  
 CC of producing (I), obtained by introducing DNA that encodes the antibody  
 CC molecule which specifically binds with ganglioside GD3, to a host cell;  
 CC producing (I), involving cultivating (I) in a culture medium, such that  
 CC C1 (sic) is produced and accumulated in the culture, extracting and  
 CC purifying C1 from the culture medium; a pharmaceutical (III) containing  
 CC C1 as an active ingredient; and a therapeutic agent (A1) for ganglioside  
 CC GD3 associated disease, comprising C1 as an active ingredient. (I) is  
 CC useful for treating GD3 associated disease, which involves administering  
 CC (I), where the GD3 associated diseases is cancer. (A1) is also useful for  
 CC treating GD3 associated disease. (II) is useful for producing (I). (I) is  
 CC useful for manufacturing a therapeutic agent for GD3 associated disease.  
 CC This sequence represents a ganglioside GD3 binding antibody associated  
 CC peptide.  
 XX Sequence 7 AA;  
 SQ Query Match 100.0%; Score 37; DB 9; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 2e+06; Mismatches 0; Indels 0; Gaps 0;  
 Matches 7; Conservative 0;  
 QY 1 YSSNLHS 7  
 DB 1 YSSNLHS 7  
 RESULT 4  
 AAB81988  
 ID AAB81988 standard; protein; 108 AA.  
 XX AAB81988;  
 AC 03-JUL-2001 (first entry)  
 DT Ganglioside GD3 specific antibody related protein SEQ ID NO: 54.  
 DE Ganglioside GD3; complementarity determining region; CDR; antibody;  
 KW Ganglioside; GD3; complementarity determining region; CDR; antibody;  
 XX

KW cancer.  
 XX Synthetic.  
 OS WO200123432-A1.  
 PN 05-APR-2001.  
 PD 29-SEP-2000; 2000WO-JP006774.  
 PF 30-SEP-1999; 99JP-00278291.  
 PR 06-APR-2000; 2000JP-00105088.  
 XX (KYOW ) KYOWA HAKKO KOGYO KK.  
 PA Hanai N, Shitara K, Nakamura K, Niwa R;  
 PI WPI; 2001-266143/27.  
 DR New human type complementation-determining region-transplanted antibody  
 PT and derivatives against ganglioside GD3, useful in diagnosis and therapy  
 PT of e.g. tumors, with low antigenicity, little side effects but potent  
 PT activity in cancer.  
 XX Claim 22; Page 172-173; 183pp; Japanese.  
 PS The present invention describes a monoclonal antibody which can react  
 CC specifically with ganglioside GD3. The antibody and its derivatives are  
 CC useful in the diagnosis and therapy of tumors, particularly cancer  
 CC diagnosis. The present sequence is a protein used in the exemplification  
 CC of the invention  
 XX Sequence 108 AA;  
 SQ Query Match 100.0%; Score 37; DB 4; Length 108;  
 Best Local Similarity 100.0%; Pred. No. 11; Mismatches 0; Indels 0; Gaps 0;  
 Matches 7; Conservative 0;  
 QY 1 YSSNLHS 7  
 DB 50 YSSNLHS 56  
 RESULT 5  
 AAB81986  
 ID AAB81986 standard; protein; 108 AA.  
 XX AAB81986;  
 AC 03-JUL-2001 (first entry)  
 DT Ganglioside GD3 specific antibody related protein SEQ ID NO: 10.  
 DE Ganglioside; GD3; complementarity determining region; CDR; antibody;  
 KW cancer.  
 XX Synthetic.  
 OS WO200123432-A1.  
 PN 05-APR-2001.  
 PD 29-SEP-2000; 2000WO-JP006774.  
 PF 30-SEP-1999; 99JP-00278291.  
 PR 06-APR-2000; 2000JP-00105088.  
 XX (KYOW ) KYOWA HAKKO KOGYO KK.  
 PA Hanai N, Shitara K, Nakamura K, Niwa R;  
 PI WPI; 2001-266143/27.  
 DR

PT New human type complementation-determining region-transplanted antibody  
 PT and derivatives against ganglioside GD3; useful in diagnosis and therapy  
 PT of e.g. tumors, with low antigenicity, little side effects but potent  
 PT activity in cancer.

XX Example 1; Page 143-144; 183pp; Japanese.

XX The present invention describes a monoclonal antibody which can react  
 CC specifically with ganglioside GD3. The antibody and its derivatives are  
 CC useful in the diagnosis and therapy of tumors, particularly cancer  
 CC diagnosis. The present sequence is a protein used in the exemplification  
 CC of the invention

XX Sequence 108 AA;

Query Match 100.0%; Score 37; DB 4; Length 108;  
 Best Local Similarity 100.0%; Pred. No. 11;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSSNLHS 7  
 |||||  
 Db 50 YSSNLHS 56

#### RESULT 6

AA81990  
 ID AAB81990 standard; protein; 108 AA.

AC AAB81990;

DT 03-JUL-2001 (first entry)

DE Ganglioside GD3 specific antibody related protein SEQ ID NO: 56.

KW Ganglioside; GD3; complementarity determining region; CDR; antibody;  
 KW cancer.

OS Mus musculus.

PN WO200123432-A1.

PD 05-APR-2001.

PF 29-SEP-2000; 2000WO-JP006774.

PR 30-SEP-1999; 99JP-00278291.

PR 06-APR-2000; 2000JP-00105088.

PA (KYOW ) KYOWA HAKKO KOGYO KK.

PI Hanai N, Shitara K, Nakamura K, Niwa R;

DR WPI; 2001-266143/27.

PT New human type complementation-determining region-transplanted antibody  
 PT and derivatives against ganglioside GD3; useful in diagnosis and therapy  
 PT of e.g. tumors, with low antigenicity, little side effects but potent  
 PT activity in cancer.

PS Claim 11; Page 174-175; 183pp; Japanese.

XX The present invention describes a monoclonal antibody which can react  
 CC specifically with ganglioside GD3. The antibody and its derivatives are  
 CC useful in the diagnosis and therapy of tumors, particularly cancer  
 CC diagnosis. The present sequence is a protein used in the exemplification  
 CC of the invention

XX Sequence 108 AA;

Query Match 100.0%; Score 37; DB 4; Length 108;  
 Best Local Similarity 100.0%; Pred. No. 11;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSSNLHS 7  
 |||||  
 Db 50 YSSNLHS 56

#### RESULT 7

ABU11011

ID ABU11011 standard; protein; 108 AA.

AC ABU11011;

DT 04-FEB-2003 (first entry)

DE Modified ganglioside GD3 antibody associated protein #4.

KW Ganglioside GD3; anti-ganglioside GD3 antibody; tumour; melanoma.

OS Synthetic.

PN WO200278739-A1.

PD 10-OCT-2002.

PF 29-MAR-2002; 2002WO-JP003170.

PR 29-MAR-2001; 2001JP-00097483.

PA (KYOW ) KYOWA HAKKO KOGYO KK.

PI Shitara K, Niwa R, Kanazawa J, Asada M;

DR WPI; 2003-067410/06.

PT Drugs containing genetically-modified antibody against ganglioside GD3,  
 PT its fragment, immunocompetent cell activators or/and antitumor agents in  
 PT combination, applicable in treating malignant tumor like melanoma.

PS Claim 8; Page 100; 121pp; Japanese.

XX The invention describes drugs contain a genetically-modified antibody  
 CC against ganglioside GD3 or its fragment and at least 1 of a substance  
 CC capable of activating immunocompetent cells and a substance having an  
 CC antitumor activity in combination. The drugs can be used to treat tumour  
 CC like melanoma and can provide a treatment with enhanced therapeutic  
 CC effect and little side-reactions, particularly to relieve problems of  
 CC side-effects during the conventional single administration. This sequence  
 CC represents a protein associated with the anti- ganglioside GD3 antibody

SQ Sequence 108 AA;

Query Match 100.0%; Score 37; DB 6; Length 108;  
 Best Local Similarity 100.0%; Pred. No. 11;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSSNLHS 7  
 |||||  
 Db 50 YSSNLHS 56

#### RESULT 8

ABU11013

ID ABU11013 standard; protein; 108 AA.

AC ABU11013;

DT 04-FEB-2003 (first entry)

DE Modified ganglioside GD3 antibody associated protein #6.

KW Ganglioside GD3; anti-ganglioside GD3 antibody; tumour; melanoma.

OS Mus musculus.

PN WO200278739-A1.  
 XX 10-OCT-2002.  
 XX  
 XX 29-MAR-2002; 2002WO-JP0031170.  
 XX  
 XX 29-MAR-2001; 2001JP-00097483.  
 XX  
 XX (KYOW ) KYOWA HAKKO KOGYO KK.  
 XX  
 XX Shitara K, Niwa R, Kanazawa J, Asada M;  
 XX WPI; 2003-067410/06.  
 XX  
 XX Drugs containing genetically-modified antibody against ganglioside GD3,  
 PT its fragment, immunocompetent cell activators or/and antitumor agents in  
 PT combination, applicable in treating malignant tumor like melanoma.  
 XX  
 XX Claim 7; Page 113; 121pp; Japanese.  
 XX  
 XX The invention describes drugs contain a genetically-modified antibody  
 CC against ganglioside GD3 or its fragment and at least 1 of a substance  
 CC capable of activating immunocompetent cells and a substance having an  
 CC antitumor activity in combination. The drugs can be used to treat tumour  
 CC like melanoma and can provide a treatment with enhanced therapeutic  
 CC effect and little side-reactions, particularly to relieve problems of  
 CC side-effects during the conventional single administration. This sequence  
 CC represents a protein associated with the anti- ganglioside GD3 antibody  
 XX  
 XX Sequence 108 AA;  
 SQ  
 Query Match 100.0%; Score 37; DB 6; Length 108;  
 Best Local Similarity 100.0%; Pred. No. 11;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YSSNLHS 7  
 DB 50 YSSNLHS 56  
 |||||  
 RESULT 9  
 ADZ57819  
 ID ADZ57819 standard; protein; 108 AA.  
 XX  
 XX AC ADZ57819;  
 XX  
 XX DT 30-JUN-2005 (first entry)  
 XX  
 XX DE Ganglioside GD3 binding antibody associated protein SEQ ID NO 23.  
 XX  
 XX KW cytostatic; antibody engineering; cancer; neoplasm; ganglioside; GD3;  
 XX pharmaceutical.  
 XX  
 XX OS Synthetic.  
 XX  
 XX PN WO2005035577-A1.  
 XX  
 XX PD 21-APR-2005.  
 XX  
 XX PF 08-OCT-2004; 2004WO-JP015314.  
 XX  
 XX PR 08-OCT-2003; 2003JP-00350161.  
 XX  
 XX PA (KYOW ) KYOWA HAKKO KOGYO KK.  
 XX  
 XX PI Iida S, Satoh M, Urakubo M, Wakitani M, Uchida K, Niwa R;  
 XX Shitara K;  
 XX  
 XX DR WPI; 2005-346195/35.  
 XX  
 XX Antibody composition for treating ganglioside GD3 associated disease e.g.  
 PT cancer, comprises genetically modified antibody molecule, which  
 PT specifically binds to ganglioside GD3 and has N-glycoside-binding sugar  
 PT chain in its Fc domain.  
 XX  
 XX Claim 25; SEQ ID NO 26; 124pp; Japanese.  
 XX  
 XX The invention describes an antibody composition (I), comprising a

PT chain in its Fc domain.  
 XX  
 XX Claim 20; SEQ ID NO 23; 124pp; Japanese.  
 XX  
 XX The invention describes an antibody composition (I), comprising a  
 CC genetically modified antibody molecule which specifically binds to  
 CC ganglioside GD3 and has an N-glycoside-binding complex sugar chain in its  
 CC Fc domain, where the N-glycoside-binding complex sugar chain is a sugar  
 CC chain having no fucose attached to N-acetylglucosamine at the reducing  
 CC end of the sugar chain. Also described are: a transformant (II) capable  
 CC of producing (I), obtained by introducing DNA that encodes the antibody  
 CC molecule which specifically binds with ganglioside GD3, to a host cell;  
 CC producing (I), involving cultivating (I) in a culture medium, such that  
 CC Cl (sic) is produced and accumulated in the culture, extracting and  
 CC purifying Cl from the culture medium; a pharmaceutical (III) containing  
 CC Cl as an active ingredient; and a therapeutic agent (A1) for ganglioside  
 CC GD3 associated disease, comprising Cl as an active ingredient. (I) is  
 CC useful for treating GD3 associated disease, which involves administering  
 CC (I), where the GD3 associated diseases is cancer. (A1) is also useful for  
 CC treating GD3 associated disease. (II) is useful for producing (I). (I) is  
 CC useful for manufacturing a therapeutic agent for GD3 associated disease.  
 CC This sequence represents a ganglioside GD3 binding antibody associated  
 CC protein.  
 XX  
 XX Sequence 108 AA;  
 SQ  
 Query Match 100.0%; Score 37; DB 9; Length 108;  
 Best Local Similarity 100.0%; Pred. No. 11;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YSSNLHS 7  
 DB 50 YSSNLHS 56  
 |||||  
 RESULT 10  
 ADZ57822  
 ID ADZ57822 standard; protein; 108 AA.  
 XX  
 XX AC ADZ57822;  
 XX  
 XX DT 30-JUN-2005 (first entry)  
 XX  
 XX DE Ganglioside GD3 binding antibody associated protein SEQ ID NO 26.  
 XX  
 XX KW cytostatic; antibody engineering; cancer; neoplasm; ganglioside; GD3;  
 XX pharmaceutical.  
 XX  
 XX OS Synthetic.  
 XX  
 XX PN WO2005035577-A1.  
 XX  
 XX PD 21-APR-2005.  
 XX  
 XX PF 08-OCT-2004; 2004WO-JP015314.  
 XX  
 XX PR 08-OCT-2003; 2003JP-00350161.  
 XX  
 XX PA (KYOW ) KYOWA HAKKO KOGYO KK.  
 XX  
 XX PI Iida S, Satoh M, Urakubo M, Wakitani M, Uchida K, Niwa R;  
 XX Shitara K;  
 XX  
 XX DR WPI; 2005-346195/35.  
 XX  
 XX Antibody composition for treating ganglioside GD3 associated disease e.g.  
 PT cancer, comprises genetically modified antibody molecule, which  
 PT specifically binds to ganglioside GD3 and has N-glycoside-binding sugar  
 PT chain in its Fc domain.  
 XX  
 XX Claim 25; SEQ ID NO 26; 124pp; Japanese.  
 XX  
 XX The invention describes an antibody composition (I), comprising a

CC genetically modified antibody molecule which specifically binds to  
 CC ganglioside GD3 and has an N-glycoside-binding complex sugar chain in its  
 CC Fc domain, where the N-glycoside-binding complex sugar chain is a sugar  
 CC chain having no fucose attached to N-acetylglucosamine at the reducing  
 CC end of the sugar chain. Also described are: a transformant (II) capable  
 CC of producing (I), obtained by introducing DNA that encodes the antibody  
 CC molecule which specifically binds with ganglioside GD3, to a host cell;  
 CC producing (I), involving cultivating (I) in a culture medium, such that  
 CC C1 (sic) is produced and accumulated in the culture, extracting and  
 CC purifying C1 from the culture medium; a pharmaceutical (III) containing  
 CC C1 as an active ingredient; and a therapeutic agent (A1) for ganglioside  
 CC GD3 associated disease, comprising C1 as an active ingredient. (I) is  
 CC useful for treating GD3 associated disease, which involves administering  
 CC (I), where the GD3 associated disease is cancer. (A1) is also useful for  
 CC treating GD3 associated disease. (II) is useful for producing (I). (I) is  
 CC useful for manufacturing a therapeutic agent for GD3 associated disease.  
 CC This sequence represents a ganglioside GD3 binding antibody associated  
 CC protein.

XX Sequence 108 AA;

Query Match 100.0%; Score 37; DB 9; Length 108;  
 Best Local Similarity 100.0%; Pred. No. 11;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLS 7  
 |||||  
 Db 50 YSSNLS 56

#### RESULT 11

ADZ57823  
 ID ADZ57823 standard; protein; 108 AA.

XX AC ADZ57823;

XX DT 30-JUN-2005 (first entry)

XX DE Ganglioside GD3 binding antibody associated protein SEQ ID NO 27.

XX KW cytotatic; antibody engineering; cancer; neoplasm; ganglioside; GD3;  
 XX pharmaceutical.

XX OS Synthetic.

XX WO2005035577-A1.

XX PD 21-APR-2005.

XX PF 08-OCT-2004; 2004WO-JP015314.

XX PR 08-OCT-2003; 2003JP-00350161.

XX PA (KYOW ) KYOWA HAKKO KOGYO KK.

XX PI Iida S, Satoh M, Urakubo M, Wakitani M, Uchida K, Niwa R;  
 XX PI Shitara K;

XX DR WPI; 2005-346195/35.

XX Antibody composition for treating ganglioside GD3 associated disease e.g.  
 PT cancer, comprises genetically modified antibody molecule, which  
 PT specifically binds to ganglioside GD3 and has N-glycoside-binding sugar  
 PT chain in its Fc domain.

XX Claim 25; SEQ ID NO 27; 124pp; Japanese.

XX The invention describes an antibody composition (I), comprising a  
 CC genetically modified antibody molecule which specifically binds to  
 CC ganglioside GD3 and has an N-glycoside-binding complex sugar chain in its  
 CC Fc domain, where the N-glycoside-binding complex sugar chain is a sugar  
 CC chain having no fucose attached to N-acetylglucosamine at the reducing  
 CC end of the sugar chain. Also described are: a transformant (II) capable

CC of producing (I), obtained by introducing DNA that encodes the antibody  
 CC molecule which specifically binds with ganglioside GD3, to a host cell;  
 CC producing (I), involving cultivating (I) in a culture medium, such that  
 CC C1 (sic) is produced and accumulated in the culture, extracting and  
 CC purifying C1 from the culture medium; a pharmaceutical (III) containing  
 CC C1 as an active ingredient; and a therapeutic agent (A1) for ganglioside  
 CC GD3 associated disease, comprising C1 as an active ingredient. (I) is  
 CC useful for treating GD3 associated disease, which involves administering  
 CC (I), where the GD3 associated disease is cancer. (A1) is also useful for  
 CC treating GD3 associated disease. (II) is useful for producing (I). (I) is  
 CC useful for manufacturing a therapeutic agent for GD3 associated disease.  
 CC This sequence represents a ganglioside GD3 binding antibody associated  
 CC protein.

XX Sequence 108 AA;

Query Match 100.0%; Score 37; DB 9; Length 108;  
 Best Local Similarity 100.0%; Pred. No. 11;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLS 7  
 |||||  
 Db 50 YSSNLS 56

#### RESULT 12

ADZ57817  
 ID ADZ57817 standard; protein; 108 AA.

XX AC ADZ57817;

XX DT 30-JUN-2005 (first entry)

XX DE Ganglioside GD3 binding antibody associated protein SEQ ID NO 21.

XX KW cytotatic; antibody engineering; cancer; neoplasm; ganglioside; GD3;  
 XX pharmaceutical.

XX OS Mus musculus.

XX WO2005035577-A1.

XX PD 21-APR-2005.

XX PF 08-OCT-2004; 2004WO-JP015314.

XX PR 08-OCT-2003; 2003JP-00350161.

XX PA (KYOW ) KYOWA HAKKO KOGYO KK.

XX PI Iida S, Satoh M, Urakubo M, Wakitani M, Uchida K, Niwa R;  
 XX PI Shitara K;

XX DR WPI; 2005-346195/35.

XX Antibody composition for treating ganglioside GD3 associated disease e.g.  
 PT cancer, comprises genetically modified antibody molecule, which  
 PT specifically binds to ganglioside GD3 and has N-glycoside-binding sugar  
 PT chain in its Fc domain.

XX Claim 14; SEQ ID NO 21; 124pp; Japanese.

XX The invention describes an antibody composition (I), comprising a  
 CC genetically modified antibody molecule which specifically binds to  
 CC ganglioside GD3 and has an N-glycoside-binding complex sugar chain in its  
 CC Fc domain, where the N-glycoside-binding complex sugar chain is a sugar  
 CC chain having no fucose attached to N-acetylglucosamine at the reducing  
 CC end of the sugar chain. Also described are: a transformant (II) capable  
 CC of producing (I), obtained by introducing DNA that encodes the antibody  
 CC molecule which specifically binds with ganglioside GD3, to a host cell;  
 CC producing (I), involving cultivating (I) in a culture medium, such that  
 CC C1 (sic) is produced and accumulated in the culture, extracting and  
 CC purifying C1 from the culture medium; a pharmaceutical (III) containing

CC C1 as an active ingredient; and a therapeutic agent (A1) for ganglioside  
 CC GD3 associated disease, comprising C1 as an active ingredient. (I) is  
 CC useful for treating GD3 associated disease, which involves administering  
 CC (I), where the GD3 associated disease is cancer. (A1) is also useful for  
 CC treating GD3 associated disease. (II) is useful for producing (I). (I) is  
 CC useful for manufacturing a therapeutic agent for GD3 associated disease.  
 CC This sequence represents a ganglioside GD3 binding antibody associated  
 CC protein.  
 XX Sequence 108 AA;  
 SQ

Query Match 100.0%; Score 37; DB 9; Length 108;  
 Best Local Similarity 100.0%; Pred. No. 11;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLHS 7  
 |||||  
 DB 50 YSSNLHS 56

RESULT 13  
 ADZ57820  
 ID ADZ57820 standard; protein; 108 AA.  
 XX  
 AC ADZ57820;  
 XX  
 DT 30-JUN-2005 (first entry)  
 XX  
 DE Ganglioside GD3 binding antibody associated protein SEQ ID NO 24.  
 XX  
 KW cytotatic; antibody engineering; cancer; neoplasm; ganglioside; GD3;  
 KW pharmaceutical.  
 XX  
 OS Synthetic.  
 XX  
 PN WO2005035577-A1.  
 XX  
 PD 21-APR-2005.  
 XX  
 PF 08-OCT-2004; 2004WO-JP015314.  
 XX  
 PR 08-OCT-2003; 2003JP-00350161.  
 XX  
 PA (KYOW ) KYOWA HAKKO KOGYO KK.  
 XX  
 PI Iida S, Satoh M, Urakubo M, Wakitani M, Uchida K, Niwa R;  
 PI Shitara K;  
 XX  
 DR WPI; 2005-346195/35.  
 XX  
 PT Antibody composition for treating ganglioside GD3 associated disease e.g.  
 PT cancer, comprises genetically modified antibody molecule, which  
 PT specifically binds to ganglioside GD3 and has N-glycoside-binding sugar  
 PT chain in its Fc domain.  
 XX  
 PS Claim 21; SEQ ID NO 24; 124pp; Japanese.  
 XX  
 CC The invention describes an antibody composition (I), comprising a  
 CC genetically modified antibody molecule which specifically binds to  
 CC ganglioside GD3 and has an N-glycoside-binding complex sugar chain in its  
 CC Fc domain, where the N-glycoside-binding complex sugar chain is a sugar  
 CC chain having no fucose attached to N-acetylglucosamine at the reducing  
 CC end of the sugar chain. Also described are: a transformant (II) capable  
 CC of producing (I), obtained by introducing DNA that encodes the antibody  
 CC molecule which specifically binds with ganglioside GD3, to a host cell;  
 CC producing (I), involving cultivating (I) in a culture medium, such that  
 CC C1 (Ic) is produced and accumulated in the culture, extracting and  
 CC purifying C1 from the culture medium; a pharmaceutical (III) containing  
 CC C1 as an active ingredient; and a therapeutic agent (A1) for ganglioside  
 CC GD3 associated disease, comprising C1 as an active ingredient. (I) is  
 CC useful for treating GD3 associated disease, which involves administering  
 CC (I), where the GD3 associated disease is cancer. (A1) is also useful for  
 CC treating GD3 associated disease. (II) is useful for producing (I). (I) is

CC useful for manufacturing a therapeutic agent for GD3 associated disease.  
 CC This sequence represents a ganglioside GD3 binding antibody associated  
 CC protein.  
 XX Sequence 108 AA;  
 SQ

Query Match 100.0%; Score 37; DB 9; Length 108;  
 Best Local Similarity 100.0%; Pred. No. 11;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLHS 7  
 |||||  
 DB 50 YSSNLHS 56

RESULT 14  
 AAR33257  
 ID AAR33257 standard; protein; 128 AA.  
 XX  
 AC AAR33257;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 12-JUL-1993 (first entry)  
 XX  
 DE Rat immunoglobulin L chain variable region of pKM641LA2.  
 XX  
 KW Promoter; variable; region; rat; immunoglobulin; heavy; H; chain;  
 KW humanised; chimeric; antibody; expression vector.  
 XX  
 OS Rattus rattus.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..20 /note= "Signal peptide"  
 FT Protein 21..128  
 FT /note= "Mature protein"  
 XX  
 PN EP533199-A2.  
 XX  
 PD 24-MAR-1993.  
 XX  
 PF 18-SEP-1992; 92EP-00116026.  
 XX  
 PR 18-SEP-1991; 91JP-00238375.  
 XX  
 PA (KYOW ) KYOWA HAKKO KOGYO CO LTD.  
 XX  
 PI Shitara K, Hanai N, Hasegawa M, Miyaji H, Kuwana Y;  
 XX  
 DR WPI; 1993-095510/12.  
 DR N-PSDB; AAR33258.  
 XX  
 PT Humanised chimeric antibody prodn. against ganglioside GD3 - for treating  
 PT cancers, such as melanoma, neuroblastoma, etc.  
 XX  
 PS Claim 6; Page 30-31; 63pp; English.  
 XX  
 CC The sequences given in AAR33256-57 represent rat heavy and light chain  
 CC variable regions respectively. The DNA sequences encoding these proteins  
 CC were used in the construction of humanised chimeric antibody expression  
 CC vectors. In these humanised antibodies none of the amino acids of the non  
 CC -human animal Ab variable region have been changed. (Updated on 25-MAR-  
 CC 2003 to correct PN field.)  
 XX  
 SQ Sequence 128 AA;  
 CC

Query Match 100.0%; Score 37; DB 2; Length 128;  
 Best Local Similarity 100.0%; Pred. No. 13;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLHS 7  
 |||||  
 DB 70 YSSNLHS 76

```

RESULT 15
AAR53340
ID AAR53340 standard; protein; 128 AA.
XX
AC AAR53340;
XX
DT 18-NOV-1994 (first entry)
XX
DE KM641 H chain variable region.
XX
KW Monoclonal antibody; Ab; ganglioside GM2; chimera; chimeric antibody;
KW expression vector; heavy; light; chain; hypervariable region; CDR;
KW constant region; hybridoma; Ig; immunoglobulin; promoter; enhancer.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT Peptide
FT 1..20
FT /label= sig_peptide
XX
PN AU9346181-A.
XX
PD 17-MAR-1994.
XX
PF 07-SEP-1993; 93AU-00046181.
XX
PR 07-SEP-1992; 92JP-00238452.
XX
PA (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI Nakamura K, Koike M, Shitara K, Hanai N, Kuwana Y, Hasegawa M;
XX WPI; 1994-126857/16.
XX DR N-PSDB; AAQ45438.
XX
PT Humanised antibody specific for ganglioside GM2 - used for producing a
PT cytotoxic effect on cancers such as melanoma, neuroblastoma and glioma.
XX
PS Example 2; Page 115-116; 191pp; English.
XX
CC Example 2 describes the construction of the vector pChi641HA1 for
CC chimeric human antibody H chain expression. mRNA from mouse anti-GD3
CC monoclonal Ab KM641-producing cells was isolated and KM641 H and L chain
CC cDNAs isolated. The base sequences of the Ig variable regions in KM641 H
CC chain cDNA (pKM641HA3) and KM641 L chain cDNA (pKM641LA2) are given in
CC AA045438-39. A KM641-derived chimeric human Ab H chain expression vector
CC was constructed by joining the H chain variable region gene from
CC pKM641HA3 to a vector for chimeric human Ab H chain expression using the
CC synthetic DNAs given in AAQ63439 and AAQ63440
XX
SQ Sequence 128 AA;
Query Match 100.0%; Score 37; DB 2; Length 128;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 YSSNLHS 7
Db 70 YSSNLHS 76

RESULT 16
AAV28368
ID AAV28368 standard; protein; 128 AA.
XX
AC AAV28368;
XX
DT 04-NOV-1999 (first entry)
XX
DE pKM641 LA2 immunoglobulin light chain.
XX

```

```

KW antibody; nucleotide; genomic; hypervariable region; chimeric;
KW light chain; amino acid.
XX
OS Mus sp.
XX
PN US939532-A.
XX
PD 17-AUG-1999.
XX
PF 07-JUN-1995; 95US-00483528.
XX
PR 07-SEP-1993; 93US-00116778.
XX
PA (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI Nakamura K, Hanai N, Kuwana Y, Hasegawa M, Koike M, Shitara K;
XX WPI; 1999-469416/39.
XX DR N-PSDB; AAX99481.
XX
PT Chimeric human antibody expression vectors.
XX
PS Example 1; Col 99; 188pp; English.
XX
CC This immunoglobulin region was isolated from pKM641LA2.A methionine
CC codon, presumably the initiation codon ATG, was found in the vicinity of
CC the 5' terminus and the sequence has a full length leader sequence. The
CC chimeric human antibodies are useful in the treatment of cancer,
CC especially that which is of neural ectodermal origin. In contrast to
CC prior art constructs based on mouse monoclonal antibodies, the chimeric
CC human antibodies do not cause anti-mouse immunoglobulin production. The
CC chimeric human antibodies have a prolonged half-life and a reduced
CC frequency of adverse effects when compared to mouse monoclonal antibodies
XX
SQ Sequence 128 AA;
Query Match 100.0%; Score 37; DB 2; Length 128;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 YSSNLHS 7
Db 70 YSSNLHS 76

RESULT 17
AAB01628
ID AAB01628 standard; protein; 128 AA.
XX
AC AAB01628;
XX
DT 07-DEC-2000 (first entry)
XX
DE Murine immunoglobulin light chain variable region.
XX
KW Mouse; immunoglobulin; L chain; light chain; variable region; cancer;
KW humanised antibody.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FT Peptide
FT 1..20
FT /label= signal_peptide
FT Protein
FT 21..128
FT /label= mature_immunoglobulin_light_chain_v_region
XX
PN EP1013761-A2.
XX
PD 28-JUN-2000.
XX
PF 18-SEP-1992; 99EP-00124345.
XX
PR 18-SEP-1991; 91JP-00238375.
XX

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```

PR 18-SEP-1992; 92EP-00116026.
XX
XX (KYOW ) KYOWA HAKKO KOGYO KK.
XX
XX Shitara K, Hanai N, Hasegawa M, Miyaji H, Kuwana Y;
XX
XX WPI; 2000-402204/35.
XX N-PSDB; AAS1004.
XX
XX New humanized chimera antibody KM-871 useful for treating cancer,
XX comprises variable region of mouse monoclonal antibody, reactive with
XX ganglioside and human antibody constant region.
XX
XX Claim 14; Page 28-29; 65pp; English.
XX
XX The present sequence is a murine immunoglobulin light chain variable
XX region from plasmid KM-641. The coding sequence was used in the creation
XX of an expression vector, along with the sequence for a human antibody, to
XX produce humanised chimaeric antibodies, which can be used to treat
XX cancer. Humanised chimaeric antibodies are more effective than mouse
XX antibodies as they do not provoke a reaction in the human and side
XX effects, such as the formation of anti-mouse immunoglobulin antibody and
XX the rapid half-life of the immunoglobulins, do not occur
XX
XX Sequence 128 AA;
SQ
Query Match 100.0%; Score 37; DB 3; Length 128;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YSSNLHS 7
DB 70 YSSNLHS 76
|||||
RESULTS
AAB81994
ID AAB81994 standard; protein; 128 AA.
XX
XX AAB81994;
XX
XX 03-JUL-2001 (first entry)
XX
XX Ganglioside GD3 specific antibody related protein #3.
XX
XX Ganglioside; GD3; complementarity determining region; CDR; antibody;
XX cancer.
XX Synthetic.
XX
XX WO200123432-A1.
XX
XX 05-APR-2001.
XX
XX 29-SEP-2000; 2000WO-JP006774.
XX
XX 30-SEP-1999; 99JP-00278291.
XX 06-APR-2000; 2000JP-00105088.
XX
XX (KYOW ) KYOWA HAKKO KOGYO KK.
XX
XX Hanai N, Shitara K, Nakamura K, Niwa R;
XX
XX WPI; 2001-266143/27.
XX N-PSDB; AAF86901.
XX
XX New human type complementation-determining region-transplanted antibody
XX and derivatives against ganglioside GD3, useful in diagnosis and therapy
XX of e.g. tumors, with low antigenicity, little side effects but potent
XX activity in cancer.
XX Synthetic.
XX
XX WO200123432-A1.
XX
XX 05-APR-2001.
XX
XX 29-SEP-2000; 2000WO-JP006774.
XX
XX 30-SEP-1999; 99JP-00278291.
XX 06-APR-2000; 2000JP-00105088.
XX
XX (KYOW ) KYOWA HAKKO KOGYO KK.
XX
XX Hanai N, Shitara K, Nakamura K, Niwa R;
XX
XX WPI; 2001-266143/27.
XX N-PSDB; AAF86898.
XX
XX New human type complementation-determining region-transplanted antibody
XX and derivatives against ganglioside GD3, useful in diagnosis and therapy
XX of e.g. tumors, with low antigenicity, little side effects but potent
XX activity in cancer.
XX Synthetic.
XX
XX 155-156; 183pp; Japanese.
XX

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```

CC The present invention describes a monoclonal antibody which can react
CC specifically with ganglioside GD3. The antibody and its derivatives are
CC useful in the diagnosis and therapy of tumours, particularly cancer
CC diagnosis. The present sequence is a protein used in the exemplification
CC of the invention
XX
XX Sequence 128 AA;
SQ
Query Match 100.0%; Score 37; DB 4; Length 128;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YSSNLHS 7
DB 70 YSSNLHS 76
|||||
RESULTS
AAB81995
ID AAB81995 standard; protein; 128 AA.
XX
XX AAB81995;
XX
XX 03-JUL-2001 (first entry)
XX
XX Ganglioside GD3 specific antibody related protein #4.
XX
XX Ganglioside; GD3; complementarity determining region; CDR; antibody;
XX cancer.
XX Synthetic.
XX
XX WO200123432-A1.
XX
XX 05-APR-2001.
XX
XX 29-SEP-2000; 2000WO-JP006774.
XX
XX 30-SEP-1999; 99JP-00278291.
XX 06-APR-2000; 2000JP-00105088.
XX
XX (KYOW ) KYOWA HAKKO KOGYO KK.
XX
XX Hanai N, Shitara K, Nakamura K, Niwa R;
XX
XX WPI; 2001-266143/27.
XX N-PSDB; AAF86901.
XX
XX New human type complementation-determining region-transplanted antibody
XX and derivatives against ganglioside GD3, useful in diagnosis and therapy
XX of e.g. tumors, with low antigenicity, little side effects but potent
XX activity in cancer.
XX Synthetic.
XX
XX 157-158; 183pp; Japanese.
XX
XX The present invention describes a monoclonal antibody which can react
XX specifically with ganglioside GD3. The antibody and its derivatives are
XX useful in the diagnosis and therapy of tumours, particularly cancer
XX diagnosis. The present sequence is a protein used in the exemplification
XX of the invention
XX
XX Sequence 128 AA;
SQ
Query Match 100.0%; Score 37; DB 4; Length 128;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YSSNLHS 7
DB 70 YSSNLHS 76
|||||
RESULTS
AAB81994
ID AAB81994 standard; protein; 128 AA.
XX
XX AAB81994;
XX
XX 03-JUL-2001 (first entry)
XX
XX Ganglioside GD3 specific antibody related protein #3.
XX
XX Ganglioside; GD3; complementarity determining region; CDR; antibody;
XX cancer.
XX Synthetic.
XX
XX WO200123432-A1.
XX
XX 05-APR-2001.
XX
XX 29-SEP-2000; 2000WO-JP006774.
XX
XX 30-SEP-1999; 99JP-00278291.
XX 06-APR-2000; 2000JP-00105088.
XX
XX (KYOW ) KYOWA HAKKO KOGYO KK.
XX
XX Hanai N, Shitara K, Nakamura K, Niwa R;
XX
XX WPI; 2001-266143/27.
XX N-PSDB; AAF86898.
XX
XX New human type complementation-determining region-transplanted antibody
XX and derivatives against ganglioside GD3, useful in diagnosis and therapy
XX of e.g. tumors, with low antigenicity, little side effects but potent
XX activity in cancer.
XX Synthetic.
XX
XX 155-156; 183pp; Japanese.
XX

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```
AAB81997
ID AAB81997 standard; protein; 128 AA.
XX
AC AAB81997;
XX
DT 03-JUL-2001 (first entry)
XX
DE Ganglioside GD3 specific antibody related protein #6.
XX
KW Ganglioside; GD3; complementarity determining region; CDR; antibody;
XX
OS Synthetic.
XX
PN WO200123432-A1.
XX
PD 05-APR-2001.
XX
PF 29-SEP-2000; 2000WO-JP006774.
XX
PR 30-SEP-1999; 99JP-00278291.
XX
PR 06-APR-2000; 2000JP-00105088.
XX
PA (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI Hanai N, Shitara K, Nakamura K, Niwa R;
XX
DR WPI; 2001-266143/27.
XX
PT New human type complementation-determining region-transplanted antibody
PT and derivatives against ganglioside GD3; useful in diagnosis and therapy
PT of e.g. tumors, with low antigenicity, little side effects but potent
PT activity in cancer.
XX
SQ Sequence 128 AA;
XX
Query Match 100.0%; Score 37; DB 4; Length 128;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YSSNLHS 7
DB 70 YSSNLHS 76
XX
RESULT 21
AAB81978
ID AAB81978 standard; protein; 128 AA.
XX
AC AAB81978;
XX
DT 03-JUL-2001 (first entry)
XX
DE Ganglioside GD3 specific antibody related protein SEQ ID NO: 2.
XX
KW Ganglioside; GD3; complementarity determining region; CDR; antibody;
XX
OS Mus musculus.
XX
PN WO200123432-A1.
XX
PD 05-APR-2001.
XX
Query Match 100.0%; Score 37; DB 4; Length 128;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YSSNLHS 7
DB 70 YSSNLHS 76
XX
RESULT 22
AAB81996
ID AAB81996 standard; protein; 128 AA.
XX
AC AAB81996;
XX
DT 03-JUL-2001 (first entry)
XX
DE Ganglioside GD3 specific antibody related protein #5.
XX
KW Ganglioside; GD3; complementarity determining region; CDR; antibody;
XX
OS Synthetic.
XX
PN WO200123432-A1.
XX
PD 05-APR-2001.
XX
PF 29-SEP-2000; 2000WO-JP006774.
XX
PR 30-SEP-1999; 99JP-00278291.
XX
PR 06-APR-2000; 2000JP-00105088.
XX
PA (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI Hanai N, Shitara K, Nakamura K, Niwa R;
XX
DR WPI; 2001-266143/27.
XX
PT New human type complementation-determining region-transplanted antibody
PT and derivatives against ganglioside GD3; useful in diagnosis and therapy
PT of e.g. tumors, with low antigenicity, little side effects but potent
PT activity in cancer.
XX
PS Example 1; Page 159-160; 183pp; Japanese.
XX
CC The present invention describes a monoclonal antibody which can react
CC specifically with ganglioside GD3. The antibody and its derivatives are
CC useful in the diagnosis and therapy of tumors, particularly cancer
CC diagnosis. The present sequence is a protein used in the exemplification
CC of the invention
XX
SQ Sequence 128 AA;
XX
Query Match 100.0%; Score 37; DB 4; Length 128;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YSSNLHS 7
DB 70 YSSNLHS 76
XX
RESULT 23
AAB81997
ID AAB81997 standard; protein; 128 AA.
XX
AC AAB81997;
XX
DT 03-JUL-2001 (first entry)
XX
DE Ganglioside GD3 specific antibody related protein #6.
XX
KW Ganglioside; GD3; complementarity determining region; CDR; antibody;
XX
OS Synthetic.
XX
PN WO200123432-A1.
XX
PD 05-APR-2001.
XX
PF 29-SEP-2000; 2000WO-JP006774.
XX
PR 30-SEP-1999; 99JP-00278291.
XX
PR 06-APR-2000; 2000JP-00105088.
XX
PA (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI Hanai N, Shitara K, Nakamura K, Niwa R;
XX
DR WPI; 2001-266143/27.
XX
PT New human type complementation-determining region-transplanted antibody
PT and derivatives against ganglioside GD3; useful in diagnosis and therapy
PT of e.g. tumors, with low antigenicity, little side effects but potent
PT activity in cancer.
XX
PS Example 1; Page 159-160; 183pp; Japanese.
XX
CC The present invention describes a monoclonal antibody which can react
CC specifically with ganglioside GD3. The antibody and its derivatives are
CC useful in the diagnosis and therapy of tumors, particularly cancer
CC diagnosis. The present sequence is a protein used in the exemplification
CC of the invention
XX
SQ Sequence 128 AA;
XX
Query Match 100.0%; Score 37; DB 4; Length 128;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YSSNLHS 7
DB 70 YSSNLHS 76
XX
```

CC The present invention describes a monoclonal antibody which can react specifically with ganglioside GD3. The antibody and its derivatives are useful in the diagnosis and therapy of tumours, particularly cancer diagnosis. The present sequence is a protein used in the exemplification of the invention

XX Sequence 128 AA;

Query Match 100.0%; Score 37; DB 4; Length 128;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSSNLHS 7  
|||||  
Db 70 YSSNLHS 76

## RESULT 23

AAB81999  
ID AAB81999 standard; protein; 128 AA.

XX AAB81999;  
AC AAB81999;

XX 03-JUL-2001 (first entry)

XX Ganglioside GD3 specific antibody related protein #8.

DE Ganglioside; GD3; complementarity determining region; CDR; antibody;  
KW cancer.  
XX Synthetic.

XX WO200123432-A1.  
PN  
XX 05-APR-2001.

XX 29-SEP-2000; 2000WO-JP006774.  
PF  
XX 30-SEP-1999; 99JP-00278291.  
PR  
XX 06-APR-2000; 2000JP-00105088.

XX (KYOW ) KYOWA HAKKO KOGYO KK.  
PA  
XX Hanai N, Shitara K, Nakamura K, Niwa R;  
PI

XX WPI; 2001-266143/27.  
DR  
XX N-PSDB; AAF86913.

XX New human type complementation-determining region-transplanted antibody and derivatives against ganglioside GD3, useful in diagnosis and therapy of e.g. tumors, with low antigenicity, little side effects but potent activity in cancer.  
PT  
XX Example 1; Page 166; 183pp; Japanese.

PS The present invention describes a monoclonal antibody which can react specifically with ganglioside GD3. The antibody and its derivatives are useful in the diagnosis and therapy of tumours, particularly cancer diagnosis. The present sequence is a protein used in the exemplification of the invention

XX Sequence 128 AA;  
Query Match 100.0%; Score 37; DB 4; Length 128;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSSNLHS 7  
|||||  
Db 70 YSSNLHS 76

## RESULT 24

AAB81999  
ID AAB81999 standard; protein; 128 AA.

XX AAB81999;  
AC AAB81992;

XX 03-JUL-2001 (first entry)

XX Ganglioside GD3 specific antibody related protein #1.

DE Ganglioside; GD3; complementarity determining region; CDR; antibody;  
KW cancer.  
XX Synthetic.

XX WO200123432-A1.  
PN  
XX 05-APR-2001.

XX

## AAB81999

ID AAB81993 standard; protein; 128 AA.

XX AAB81993;  
AC

XX 03-JUL-2001 (first entry)

XX Ganglioside GD3 specific antibody related protein #2.

DE Ganglioside; GD3; complementarity determining region; CDR; antibody;  
KW cancer.  
XX Synthetic.

XX WO200123432-A1.  
PN  
XX 05-APR-2001.

XX 29-SEP-2000; 2000WO-JP006774.  
PF  
XX 30-SEP-1999; 99JP-00278291.  
PR  
XX 06-APR-2000; 2000JP-00105088.

XX (KYOW ) KYOWA HAKKO KOGYO KK.  
PA  
XX Hanai N, Shitara K, Nakamura K, Niwa R;  
PI

XX WPI; 2001-266143/27.  
DR  
XX N-PSDB; AAF86895.

XX New human type complementation-determining region-transplanted antibody and derivatives against ganglioside GD3, useful in diagnosis and therapy of e.g. tumors, with low antigenicity, little side effects but potent activity in cancer.  
PT  
XX Example 1; Page 153; 183pp; Japanese.

PS The present invention describes a monoclonal antibody which can react specifically with ganglioside GD3. The antibody and its derivatives are useful in the diagnosis and therapy of tumours, particularly cancer diagnosis. The present sequence is a protein used in the exemplification of the invention

XX Sequence 128 AA;  
Query Match 100.0%; Score 37; DB 4; Length 128;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSSNLHS 7  
|||||  
Db 70 YSSNLHS 76

## RESULT 25

AAB81992  
ID AAB81992 standard; protein; 128 AA.

XX AAB81992;  
AC

XX 03-JUL-2001 (first entry)

XX Ganglioside GD3 specific antibody related protein #1.

DE Ganglioside; GD3; complementarity determining region; CDR; antibody;  
KW cancer.  
XX Synthetic.

XX WO200123432-A1.  
PN  
XX 05-APR-2001.

XX

```

PF 29-SEP-2000; 2000WO-JP006774.
XX
XX The present invention describes a monoclonal antibody which can react
CC specifically with ganglioside GD3. The antibody and its derivatives are
CC useful in the diagnosis and therapy of tumours, particularly cancer
PR 30-SEP-1999; 99JP-00278291.
XX
XX 06-APR-2000; 2000JP-00105088.
XX
XX (KYOW ) KYOWA HAKKO KOGYO KK.
XX
XX Hanai N, Shitara K, Nakamura K, Niwa R;
PI WPI; 2001-266143/27.
XX
XX N-PSDB; AAF86892.
DR
XX
XX New human type complementation-determining region-transplanted antibody
PT and derivatives against ganglioside GD3; useful in diagnosis and therapy
PT of e.g. tumors, with low antigenicity, little side effects but potent
PT activity in cancer.
XX
XX Example 1; Page 150-151; 183pp; Japanese.
PS
XX
XX The present invention describes a monoclonal antibody which can react
CC specifically with ganglioside GD3. The antibody and its derivatives are
CC useful in the diagnosis and therapy of tumours, particularly cancer
CC diagnosis. The present sequence is a protein used in the exemplification
CC of the invention
XX
XX Sequence 128 AA;
SQ
Query Match 100.0%; Score 37; DB 4; Length 128;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YSSNLHS 7
DB 70 YSSNLHS 76
|||||
|

RESULT 26
AAB81998
ID AAB81998 standard; protein; 128 AA.
XX
XX AAB81998;
AC
XX 03-JUL-2001 (first entry)
DT
XX
XX Ganglioside GD3 specific antibody related protein #7.
DE
XX
XX Ganglioside; GD3; complementarity determining region; CDR; antibody;
KW cancer.
XX
XX Synthetic.
OS
XX WO200123432-A1.
FN
XX
XX 05-APR-2001.
XX
XX 29-SEP-2000; 2000WO-JP006774.
PF
XX
XX 30-SEP-1999; 99JP-00278291.
PR
XX 06-APR-2000; 2000JP-00105088.
XX
XX (KYOW ) KYOWA HAKKO KOGYO KK.
PA
XX
XX Hanai N, Shitara K, Nakamura K, Niwa R;
PI WPI; 2001-266143/27.
XX
XX N-PSDB; AAF86912.
DR
XX
XX New human type complementation-determining region-transplanted antibody
PT and derivatives against ganglioside GD3; useful in diagnosis and therapy
PT of e.g. tumors, with low antigenicity, little side effects but potent
PT activity in cancer.
XX
XX Example 3; Page 164-165; 183pp; Japanese.
PS

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XX The present invention describes a monoclonal antibody which can react
CC specifically with ganglioside GD3. The antibody and its derivatives are
CC useful in the diagnosis and therapy of tumours, particularly cancer
CC diagnosis. The present sequence is a protein used in the exemplification
CC of the invention
XX
XX Sequence 128 AA;
SQ
Query Match 100.0%; Score 37; DB 4; Length 128;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YSSNLHS 7
DB 70 YSSNLHS 76
|||||
|

RESULT 27
ABU11003
ID ABU11003 standard; protein; 128 AA.
XX
XX ABU11003;
AC
XX 04-FEB-2003 (first entry)
DT
XX
XX Modified ganglioside GD3 antibody associated protein #2.
DE
XX
XX Ganglioside GD3; anti-ganglioside GD3 antibody; tumour; melanoma.
KW
XX
XX Mus musculus.
OS
XX WO200278739-A1.
FN
XX 10-OCT-2002.
PD
XX
XX 29-MAR-2002; 2002WO-JP003170.
PF
XX
XX 29-MAR-2001; 2001JP-00097483.
PR
XX
XX (KYOW ) KYOWA HAKKO KOGYO KK.
PA
XX Shitara K, Niwa R, Kanazawa J, Asada M;
PI WPI; 2003-067410/06.
XX
XX Drugs containing genetically-modified antibody against ganglioside GD3,
PT its fragment, immunocompetent cell activators or/and antitumor agents in
PT combination, applicable in treating malignant tumor like melanoma.
XX
XX Example 3; Page 98; 121pp; Japanese.
PS
XX
XX The invention describes drugs contain a genetically-modified antibody
CC against ganglioside GD3 or its fragment and at least 1 of a substance
CC capable of activating immunocompetent cells and a substance having an
CC antitumor activity in combination. The drugs can be used to treat tumour
CC like melanoma and can provide a treatment with enhanced therapeutic
CC effect and little side-reactions, particularly to relieve problems of
CC side-effects during the conventional single administration. This sequence
CC represents a protein associated with the anti- ganglioside GD3 antibody
XX
XX Sequence 128 AA;
SQ
Query Match 100.0%; Score 37; DB 6; Length 128;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YSSNLHS 7
DB 70 YSSNLHS 76
|||||
|

RESULT 28

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ADQ09630
ID ADQ09630 standard; protein; 107 AA.
XX
AC ADQ09630;
XX
DT 07-OCT-2004 (first entry)
XX
DE Variable light chain protein of murine anti-human GPR64-16 antibody ID16.
XX
KW murine; mouse; antibody; GPR64; cytotoxic; ovarian cancer;
KW uterine cancer; Ewing's sarcoma; cell death; cytostatic; gene therapy;
KW immunotherapy; cellular proliferation.
XX
OS Mus sp.
XX
PN WO2004058171-A2.
XX
PD 15-JUL-2004.
XX
PF 19-DEC-2003; 2003WO-US040820.
XX
PR 20-DEC-2002; 2002US-0435618P.
XX
PA (PROT-) PROTEIN DESIGN LABS INC.
XX
PI Law D, Wang Q, Dubridge R, Bhaskar V;
XX
DR WPI; 2004-525780/50.
DR N-PSDB; ADQ09620.
XX
XX
PT New antibody that inhibits binding of a GPR64 polypeptide to an antibody
PT comprising GPR64-18, GPR64-81, GPR64-93 or GPR64-101, useful in preparing
PT a composition for diagnosing or treating ovarian cancer.
XX
PS Example 2; SEQ ID NO 16; 75pp; English.
XX
CC This invention relates to novel antibodies that bind to the G protein
CC coupled receptor protein identified as GPR64, namely GPR64-1, GPR64-16,
CC GPR64-18, GPR64-20 and GPR64-48. Specifically, it refers to the use of
CC these anti-GPR64 antibodies as selective cytotoxic agents against GPR64
CC expressing tumour cells such as those associated with ovarian cancer,
CC uterine cancer and Ewing's sarcoma. The present invention describes
CC epitope mapping of those antibodies that show high affinity binding to
CC GPR64 through competitive binding analyses, such that the antibodies can
CC be assessed for GPR64 dependent cell death in vitro. Accordingly, they
CC can be used to develop cytostatic compositions for gene therapy or
CC immunotherapy that inhibit cellular proliferation of an ovarian cancerous
CC cell and furthermore can diagnose and inhibit growth of tumour cells.
CC This polypeptide is encoded by a light chain variable region DNA sequence
CC of a murine anti-human GPR64 antibody of the invention.
XX
SQ Sequence 107 AA;
Query Match 91.9%; Score 34; DB 8; Length 107;
Best Local Similarity 85.7%; Pred. No. 45;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLHS 7
DB 50 YTSNLHS 56
|:|||||
|:|||||

RESULT 29
AAR52865
ID AAR52865 standard; protein; 273 AA.
XX
AC AAR52865;
XX
DT 27-AUG-2003 (revised)
DT 25-MAR-2003 (revised)
DT 09-SEP-1994 (first entry)
XX
DE Anti-influenza N10 scFv.

XX Monoclonal antibody N10; target binding polypeptide; scFv; scFv;
KW single chain antibody; protein secretion; FLAG; Escherichia coli;
XX antibody engineering; humanized antibody; influenza virus; neuraminidase.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT Peptide 1..22
FT Peptide /label= Sig_peptide
FT Peptide 266..273
FT /note= "C-terminal FLAG tail"
XX
PN WO9407921-A1.
XX
PD 14-APR-1994.
XX
PF 24-SEP-1993; 93WO-AU000491.
XX
PR 25-SEP-1992; 92AU-00004973.
XX
PA (CSIR ) COMMONWEALTH SCI & IND RES ORG.
XX
PI Hudson PJ, Lah M, Kortt A, Irving RA, Atwell JL, Malby RL;
PI Power BE, Colman PM;
XX
DR WPI; 1994-135515/16.
DR N-PSDB; AAQ62957.
XX
XX
PT New target-binding polypeptide(s) used for diagnosis, etc. - having a
PT stable core polypeptide region with at least one target-binding region
PT covalently attached, opt. mutated to alter specificity, etc.
XX
PS Disclosure; Page 41; 67pp; English.
XX
CC An scFv fragment of NC10 (a monoclonal antibody that recognises influenza
CC virus N9 neuraminidase) was expressed in Escherichia coli. The N-terminal
CC PeB signal peptide directed the scFv fragment into the periplasm where
CC it became associated with the insoluble membrane fraction. An octapeptide
CC FLAG tail was fused to the C-terminus of scFv and used to monitor scFv
CC during purification. (Updated on 25-MAR-2003 to correct PN field.)
CC (Updated on 25-MAR-2003 to correct PI field.) (Updated on 27-AUG-2003 to
CC correct OS field.)
XX
SQ Sequence 273 AA;
Query Match 91.9%; Score 34; DB 2; Length 273;
Best Local Similarity 85.7%; Pred. No. 1.3e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLHS 7
DB 208 YTSNLHS 214
|:|||||
|:|||||

RESULT 30
ADE62374
ID ADE62374 standard; protein; 744 AA.
XX
AC ADE62374;
XX
DT 29-JAN-2004 (first entry)
XX
DE Rat Protein AAB60512, SEQ ID NO 8303.
XX
KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
XX
OS Rattus norvegicus.
XX
PN WO2003016475-A2.
XX
PD 27-FEB-2003.

```

XX 14-AUG-2002; 2002WO-US025765.  
 PF 14-AUG-2001; 2001US-0312147P.  
 PR 01-NOV-2001; 2001US-0346382P.  
 PR 26-NOV-2001; 2001US-0333347P.  
 XX (GEHO ) GEN HOSPITAL CORP.  
 PA (FARB ) BAYER AG.  
 XX  
 PI Woolf C, D'urso D, Befort K, Costigan M;  
 XX  
 XX WPI: 2003-268312/26.  
 DR GENBANK; AAB60512.  
 DR  
 XX New composition comprising two or more isolated polypeptides, useful for  
 PT preparing a medicament for treating pain in an animal.  
 PT  
 XX Claim 1; Page; 1017pp; English.  
 PS  
 XX The invention discloses a composition comprising two or more isolated rat  
 CC or human polynucleotides or a polynucleotide which represents a fragment,  
 CC derivative or allelic variation of the nucleic acid sequence. Also  
 CC claimed are a vector comprising the novel polynucleotide, a host cell  
 CC comprising the vector, a method for identifying a nucleotide sequence  
 CC which is differentially regulated in an animal subjected to pain and a  
 CC kit to perform the method, an array, a method for identifying an agent  
 CC that increases or decreases the expression of the polynucleotide sequence  
 CC that is differentially expressed in neuronal tissue of a first animal  
 CC subjected to pain, a method for identifying a compound which regulates  
 CC the expression of a polynucleotide sequence which is differentially  
 CC expressed in an animal subjected to pain, a method for identifying a  
 CC compound that regulates the activity of one or more of the  
 CC polynucleotides, a method for producing a pharmaceutical composition, a  
 CC method for identifying a compound or small molecule that regulates the  
 CC activity in an animal of one or more of the polypeptides given in the  
 CC specification, a method for identifying a compound useful in treating  
 CC pain and a pharmaceutical composition comprising the one or more  
 CC polypeptides or their antibodies. The polynucleotide or the compound that  
 CC modulates its activity is useful for preparing a medicament for treating  
 CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction  
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene  
 CC therapy). The sequence presented is a rat protein (shown in Table 2 of  
 CC the specification) which is differentially expressed during pain. Note:  
 CC The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic form directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences.  
 XX  
 SQ Sequence 744 AA;  
 Query Match 91.9%; Score 34; DB 7; Length 744;  
 Best Local Similarity 85.7%; Pred. No. 3.9e+02;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YSSNLHS 7  
 Db 501 YSSNLHT 507  
 RESULT 31  
 ADX80263  
 ID ADX80263 standard; protein; 306 AA.  
 XX  
 AC ADX80263;  
 XX  
 XX 21-APR-2005 (first entry)  
 DE Plant full length insert polypeptide seqid 49629.  
 XX  
 XX plant protectant; plant growth regulant; gene therapy; plant;  
 KW recombinant DNA construct; physical array; plant breeding marker;  
 KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;  
 KW extreme osmotic condition; pathogen tolerance; pest tolerance;  
 KW growth rate; cell cycle pathway; disease resistance;  
 KW galactomannan production; lignin production; plant growth regulator;  
 KW yield; plant growth; plant development; seed oil; protein yield;  
 XX Unidentified.  
 OS  
 XX US2004034888-A1.  
 FN  
 XX 19-FEB-2004.  
 PD  
 XX 28-APR-2003; 2003US-00425114.  
 PF  
 XX 06-MAY-1999; 99US-00304517.  
 PR  
 PR 05-NOV-2001; 2001US-00985678.  
 XX  
 XX (LIUJ/) LIU J.  
 PA (ZHOU/) ZHOU Y.  
 PA (KOVA/) KOVALIC D K.  
 PA (SCRE/) SCREEN S E.  
 PA (TABAS/) TABASKA J E.  
 PA (CAOY/) CAO Y.  
 XX  
 PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;  
 XX WPI: 2004-180133/17.  
 DR  
 XX New recombinant DNA construct, useful for improving plant tolerance to  
 PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or  
 PT pests, for conferring increased resistance to plant disease, or for  
 PT improving yield.  
 PT  
 XX Claim 1; SEQ ID NO 49629; 15pp; English.  
 PS  
 XX The invention describes a recombinant DNA construct comprising a  
 CC polynucleotide consisting of a sequence encoding an amino acid sequence  
 CC available in electronic form from the US patent office at  
 CC ftp.segdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide  
 CC of the invention are also useful in physical arrays of molecules and as  
 CC plant breeding markers. The recombinant DNA construct is useful for  
 CC improving plant tolerance to cold, heat, drought, herbicides, extreme  
 CC osmotic conditions, pathogens or pests, for manipulating growth rate in  
 CC plant cells by modification of the cell cycle pathway, for conferring  
 CC increased resistance to plant disease, for producing galactomannan,  
 CC lignin or plant growth regulators, for increasing the rate of homologous  
 CC recombination in plants, for improving yield by modification of  
 CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake  
 CC or by providing improved plant growth and development under at least one  
 CC stress condition or for modifying seed oil or protein yield and/or  
 CC content. This is the amino acid sequence of a plant full length insert  
 CC polypeptide that can be used in the recombinant DNA construct of the  
 CC invention.  
 CC  
 XX Sequence 306 AA;  
 Query Match 89.2%; Score 33; DB 8; Length 306;  
 Best Local Similarity 85.7%; Pred. No. 2.3e+02;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YSSNLHS 7  
 Db 12 FSSNLHS 18  
 RESULT 32  
 ABB55521  
 ID ABB55521 standard; protein; 368 AA.  
 XX  
 AC ABB55521;  
 XX  
 XX 29-AUG-2003 (revised)  
 DT 16-MAY-2002 (first entry)  
 XX

DE Lactococcus lactis protein yweB.  
 XX Biosynthesis; biodegradation; lactic bacterium; yogurt; cheese.  
 KW Lactococcus lactis; IL1403.  
 OS FR2807446-A1.  
 XX 12-OCT-2001.  
 XX 11-APR-2000; 2000FR-00004630.  
 XX 11-APR-2000; 2000FR-00004630.  
 XX (INRG ) INRA INST NAT RECH AGRONOMIQUE.  
 XX Bolotine A, Sorokine A, Renault P, Ehrlich SD;  
 PI WPI; 2002-043418/06.  
 DR New nucleotide sequence useful in the identification of Lactococcus  
 XX lactis and related species.  
 PT Claim 6; SEQ ID NO 2223; 2504pp; French.  
 PS The present invention is related to a Lactococcus lactis nucleotide  
 CC sequence (ABA90521) and related proteins (ABB53300-ABB55621). The nucleic  
 CC acid sequence is useful in the detection and/or amplification of nucleic  
 CC acid sequence, particularly to identify Lactococcus lactis or related  
 CC species. The proteins of the invention are useful for the biosynthesis or  
 CC biodegradation of a composition of interest. The invention helps research  
 CC in lactic bacteria, particularly useful in the production of yogurt and  
 CC cheese. Note: The sequence data for this patent is based on equivalent  
 CC patent WO20017734 (published 18-OCT-2001) which is available in  
 CC electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences. (Updated on 29-AUG-2003 to  
 CC standardise OS field)  
 XX Sequence 368 AA;  
 SQ

Query Match 89.2%; Score 33; DB 5; Length 368;  
 Best Local Similarity 85.7%; Pred. No. 2.9e+02;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLHS 7  
 :|||||  
 Db 121 FSSNLHS 127

RESULT 33  
 AAY23802  
 ID AAY23802 standard; protein; 474 AA.  
 AC AAY23802;  
 XX 14-SEP-1999 (first entry)  
 DT A gyrase protein sequence.  
 DE Identification; detection; microbe; gyrase gene; gyrase protein.  
 KW Unidentified.  
 XX JP11169175-A.  
 XX 29-JUN-1999.  
 PD 12-DEC-1997; 97JP-00343316.  
 PF 12-DEC-1997; 97JP-00343316.  
 PR (KAIY-) KAIYO BIOTECHNOLOGY KENKYUSHO KK.  
 PA

DR WPI; 1999-422615/36.  
 DR N-PSDB; AAX86009.  
 XX Identification and detection of a microbe - by detection of a gyrase  
 PT gene.  
 PT Example 12; Page 31-32; 42pp; Japanese.  
 PS The specification describes a method for the identification or detection  
 XX of a microbe, using the gyrase gene as the index. The method involves the  
 CC use of PCR primers to amplify DNA from the microbe, which is then  
 CC identified or detected depending on its base sequence. The method can be  
 CC used to classify and identify an unidentified microbe strain rapidly and  
 CC with high precision. The present sequence represents a gyrase protein  
 XX Sequence 474 AA;  
 SQ

Query Match 89.2%; Score 33; DB 2; Length 474;  
 Best Local Similarity 85.7%; Pred. No. 3.8e+02;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSNLHS 7  
 :|||||  
 Db 164 YSENLS 170

RESULT 34  
 AAY69824  
 ID AAY69824 standard; peptide; 36 AA.  
 XX AAY69824;  
 AC AAY69824;  
 XX 20-APR-2000 (first entry)  
 DT HIV-1 gp41 envelope protein amino acids 628-663 mutant 2.  
 DE Cytostatic; human immunodeficiency virus gp41 envelope protein; antibody;  
 KW antiviral; vaccine; human; pathogenic retrovirus; immunodominant zone;  
 KW immune response; mutein.  
 XX Human immunodeficiency virus 1.  
 OS Synthetic.  
 OS FR2771011-A1.  
 PN 21-MAY-1999.  
 PD 17-NOV-1997; 97FR-00014387.  
 PF 17-NOV-1997; 97FR-00014387.  
 PR 17-NOV-1997; 97FR-00014387.  
 XX (HIPP-) HIPPOCAMPE SA.  
 PA Serres PF, Geourjon C, Deleage G, Combet C;  
 PI WPI; 2000-099991/09.  
 DR Vaccine against retroviral infection containing modified envelope  
 XX protein.  
 PT Claim 4; Page 31; 37pp; French.  
 PS This sequence corresponds to a mutant of amino acids 628-663 of the gp41  
 CC envelope protein of the human immunodeficiency virus type 1 (HIV-1). The  
 CC invention relates to the generation of vaccine against the effects of  
 CC infection, in humans or animals, and comprises a modified polypeptide  
 CC containing at least part of an envelope protein of a pathogenic  
 CC retrovirus. The polypeptide can enter a target cell via a membrane  
 CC receptor for a host protein. The part of the envelope protein in includes  
 CC at least a fragment of an immunodominant zone and contains at least one  
 CC amino acid that is conserved in the immunodominant zone and present in  
 CC the pathogenic retroviral strain. When unmodified, the polypeptide  
 CC induces an immune response against both the immunodominant zone and the

CC host protein, and the modified polypeptide induces such a response  
 CC against the immunodominant zone only. The vaccines are particularly used  
 CC to protect against human or feline immune deficiency viruses. The  
 CC modified polypeptide may also be used to raise specific antibodies for  
 CC treatment of retroviral infections, particularly in the early stages  
 XX  
 SQ Sequence 36 AA;

Query Match 86.5%; Score 32; DB 3; Length 36;  
 Best Local Similarity 71.4%; Pred. No. 34;  
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLHS 7  
 |:|:|:|  
 Db 16 YTSNIHS 22

RESULT 35  
 ADO10396  
 ID ADO10396 standard; peptide; 36 AA.  
 AC ADO10396;  
 XX  
 DT 01-JUL-2004 (first entry)  
 XX  
 DE HIV1 glycoprotein 41 (gp41) mutant peptide #28.  
 XX  
 KW HIV1; glycoprotein 41; gp41; retrovirus; membrane receptor;  
 KW immune response; envelope protein; retroviral infection; HIV infection;  
 KW FIV infection; anti-HIV; virucide; cytokine; mutant; mutein.  
 XX  
 OS Human immunodeficiency virus 1.  
 OS Synthetic.  
 XX

US2004014046-A1.  
 XX  
 PD 22-JAN-2004.  
 XX  
 PF 22-JUL-2002; 2002US-00198938.  
 XX  
 PR 22-JUL-2002; 2002US-00198938.  
 XX  
 PA (MYME-) MYMETICS SA.  
 XX  
 PI Serres PF;  
 XX  
 DR WPI; 2004-121552/12.  
 XX  
 PT Obtaining vaccines for preventing pathogenic effects of a retroviral  
 PT (e.g. HIV) infection in a host comprises selecting a modified polypeptide  
 PT that induces an immune response against the immunodominant region of an  
 PT envelope protein.  
 XX

Example 3; Page 14; 17pp; English.  
 XX  
 PS The invention relates to a method of searching for and obtaining a  
 CC vaccine against pathogenic effects related to infection of an animal or  
 CC human host by a retrovirus capable of penetrating into a target cell of  
 CC the host, the target cell possessing a membrane receptor for a protein of  
 CC the host, comprising selecting as the vaccine a modified polypeptide that  
 CC induces an immune response directed against the immunodominant region of  
 CC an envelope protein and not against a protein of the host. The invention  
 CC also relates to a vaccine obtained by the method, an antibody obtained by  
 CC immunising a host with the aid of the vaccine, where the antibody  
 CC recognises the envelope protein and not the protein of the host and a  
 CC pharmaceutical composition containing the antibody. The method is useful  
 CC in obtaining vaccines for preventing the pathogenic effects related to a  
 CC retroviral (e.g. HIV or FIV) infection. This sequence represents an HIV1  
 CC glycoprotein 41 (gp41) mutant peptide used in the scope of the invention.  
 XX  
 SQ Sequence 36 AA;

Query Match 86.5%; Score 32; DB 8; Length 36;

Best Local Similarity 71.4%; Pred. No. 34;  
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YSSNLHS 7  
 |:|:|:|  
 Db 16 YTSNIHS 22

RESULT 36  
 ABB93504  
 ID ABB93504 standard; protein; 481 AA.  
 XX  
 AC ABB93504;  
 XX  
 DT 31-MAY-2002 (first entry)  
 XX  
 DE Herbicidally active polypeptide SEQ ID NO 2715.  
 XX  
 KW Herbicidal; plant; agriculture; herbicide.  
 XX  
 OS Arabidopsis thaliana.  
 XX  
 PN WO200210210-A2.  
 XX  
 PD 07-FEB-2002.  
 XX  
 PF 28-AUG-2001; 2001WO-EP009892.  
 XX  
 PR 28-AUG-2001; 2001WO-EP009892.  
 XX  
 PA (FARB ) BAYER AG.  
 XX  
 PI Tietjen K, Weidler M;  
 XX  
 DR WPI; 2002-269010/31.  
 XX  
 PT Identifying plant target proteins for herbicidally active compounds,  
 PT comprising aligning and comparing nucleic acid or amino acid sequences  
 PT from plant with nucleic acid or amino acid sequences from non-plant  
 PT organisms.  
 XX  
 PS Claim 5; SEQ ID NO 2715; 261pp + Sequence Listing; English.  
 XX  
 CC The invention relates to identifying target proteins (ABB90790-ABB94016)  
 CC for herbicidally active compounds, comprising aligning and comparing  
 CC nucleic acid or amino acid sequences from plant with nucleic acid or  
 CC amino acid sequences from non-plant organisms using suitable search  
 CC parameters, where plant sequences having an E-value greater by a factor  
 CC of 3 than the E-value of most similar non-plant sequences are selected.  
 CC The polypeptides or nucleic acids encoding them are useful for  
 CC identifying modulators. The identified modulators are useful as  
 CC herbicides  
 XX  
 SQ Sequence 481 AA;

Query Match 86.5%; Score 32; DB 5; Length 481;  
 Best Local Similarity 85.7%; Pred. No. 6.2e+02;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YSSNLHS 7  
 |:|:|:|  
 Db 6 YSSSLHS 12  
 RESULT 37  
 ADD14911  
 ID ADD14911 standard; protein; 500 AA.  
 XX  
 AC ADD14911;  
 XX  
 DT 15-JAN-2004 (first entry)  
 XX  
 DE N. tabacum Ntcel2 protein.



```

XX Tobacco; cyst and root knot nematode responsive promoter; promoter;
KW endo-1,4-beta-glucanase; EGase; Ntcel2; nematode; plant; Ti plasmid;
KW microparticle; ballistic transformation; protoplast; transgenic plant;
KW insecticidal protein; crystal protein; toxic; insect; dicot; monocot;
KW Ntcel2; enzyme.
XX
XX Nicotiana tabacum.
XX
XX US2003106092-A1.
XX
XX 05-JUN-2003.
XX
XX 02-OCT-2001; 2001US-00970367.
XX
XX 02-OCT-2001; 2001US-00970367.
XX
XX (DAVI/) DAVIS E L.
XX (GOEL/) GOELLNER M.
XX
XX Davis EL, Goellner M;
XX
XX WPI; 2003-810836/76.
XX N-PSDB; ADD14910.
XX
XX Nucleic acid construct for controlling cyst and root knot nematodes,
PT comprises a cyst and root knot nematode responsive promoter and
PT optionally a heterologous nucleic acid.
XX
XX Disclosure; SEQ ID NO 2; 32pp; English.
XX
XX The invention discloses a nucleic acid construct comprising, in the 5' to
CC 3' direction, a cyst and root knot nematode responsive promoter and,
CC optionally, a heterologous nucleic acid positioned downstream from the
CC promoter. The cyst and root knot nematode responsive promoter preferably
CC comprises the Nicotiana endo-1,4-beta-glucanase (EGase), Ntcel2, promoter
CC and, optionally, a heterologous nucleic acid positioned downstream from
CC the promoter and operably associated with it, where the heterologous
CC nucleic acid encodes a product disruptive of nematode attack. Also
CC claimed is a plant cell transformed with the construct making a
CC transformed plant, comprising regenerating a plant from the construct, an
CC Agrobacterium tumefaciens cell containing the construct comprising a Ti
CC plasmid, a microparticle carrying the construct, suitable for the
CC ballistic transformation of a plant cell, a plant cell protoplast
CC comprising the construct and a seed obtained from the transgenic plant.
CC The heterologous nucleic acid segment may be a gene encoding for an
CC insecticidal protein, preferably a Bacillus thuringiensis crystal protein
CC toxic to insects, but may be a product toxic to the plant cell. The
CC transgenic plant is a dicot or monocot, preferably a tobacco (Nicotiana
CC tabacum) plant. The construct is used for making a transgenic plant, such
CC as a tobacco plant, that is resistant to cyst and root knot nematodes. An
CC advantage of the invention is that two or more promoters can be daisy-
CC chained to a single structural gene. The sequence presented is the N.
CC tabacum Ntcel2 protein.
XX
XX Sequence 500 AA;
SQ
Query Match 86.5%; Score 32; DB 7; Length 500;
Best Local Similarity 85.7%; Pred. No. 6.4e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLHS 7
Db 228 YSSSLHS 234
|||||

RESULT 38
AEB57114
ID AEB57114 standard; protein; 500 AA.
XX
XX AEB57114;
XX
XX 06-OCT-2005. (first entry)
XX

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```

XX Endo-1,4-beta-glucanase, Ntcel2, SEQ ID 2.
XX
XX Plant; nematode resistance; crop improvement; cyst nematode;
KW root-knot nematode; nematode infection; endo-1; 4-beta-glucanase; enzyme.
XX
XX Nicotiana tabacum.
XX
XX US2005166285-A1.
XX
XX 28-JUL-2005.
XX
XX 04-MAR-2005; 2005US-00072129.
XX
XX 02-OCT-2001; 2001US-00970367.
XX
XX (DAVI/) DAVIS E L.
XX (GOEL/) GOELLNER M.
XX
XX Davis EL, Goellner M;
XX
XX WPI; 2005-521451/53.
XX N-PSDB; AEB57113.
XX
XX New nucleic acid construct comprising, in the 5' to 3' direction, a cyst
PT and root knot nematode responsive promoter, and a heterologous nucleic
PT acid, useful for making a transformed plant resistant to nematode
PT infections.
XX
XX Example 3; SEQ ID NO 2; 32pp; English.
XX
XX The present invention relates to a nucleic acid construct comprising, in
CC the 5' to 3' direction, a cyst and root-knot nematode responsive promoter
CC (Nicotiana Ntcel2 promoter, AEB57113), and a heterologous nucleic acid
CC positioned downstream from the promoter. The heterologous nucleic acid
CC can be a gene coding for an insecticidal protein. The nucleic acid
CC construct is useful for making a transformed plant that is resistant to
CC nematode infections. Also disclosed are endo-1,4-beta-glucanases, which
CC are found to be upregulated in cyst and root-knot nematode feeding cells.
CC The present sequence is one such endo-1,4-beta-glucanase.
XX
XX Sequence 500 AA;
SQ
Query Match 86.5%; Score 32; DB 9; Length 500;
Best Local Similarity 85.7%; Pred. No. 6.4e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLHS 7
Db 228 YSSSLHS 234
|||||

RESULT 39
ABU25460
ID ABU25460 standard; protein; 277 AA.
XX
XX ABU25460;
XX
XX 19-JUN-2003 (first entry)
XX
XX Protein encoded by Prokaryotic essential gene #10987.
DE
XX
XX Antisense; prokaryotic essential gene; cell proliferation; drug design.
KW
XX Clostridium difficile.
XX
XX WO200277183-A2.
XX
XX 03-OCT-2002.
XX
XX 21-MAR-2002; 2002WO-US009107.
XX
XX 21-MAR-2001; 2001US-00815242.
XX

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PR 06-SEP-2001; 2001US-00948993.  
PR 25-OCT-2001; 2001US-0342923P.  
PR 08-FEB-2002; 2002US-00072851.  
PR 06-MAR-2002; 2002US-0362699P.  
XX  
PA (ELIT-) ELITRA PHARM INC.  
XX  
PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;  
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;  
XX  
DR WPI; 2003-029926/02.  
DR N-PSDB; ACA29330.  
XX  
XX New antisense nucleic acids, useful for identifying proteins or screening  
PT for homologous nucleic acids required for cellular proliferation to  
PT isolate candidate molecules for rational drug discovery programs.  
XX  
XX Claim 25; SEQ ID NO 53384; 1766pp; English.  
XX  
XX The invention relates to an isolated nucleic acid comprising any one of  
CC the 6213 antisense sequences given in the specification where expression  
CC of the nucleic acid inhibits proliferation of a cell. Also included are:  
CC (1) a vector comprising a promoter operably linked to the nucleic acid  
CC encoding a polypeptide whose expression is inhibited by the antisense  
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated  
CC polypeptide or its fragment whose expression is inhibited by the  
CC antisense nucleic acid; (4) an antibody capable of specifically binding  
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
CC proliferation; or the activity of a gene in an operon required for  
CC proliferation; (7) identifying a compound that influences the activity of  
CC the gene product or that has an activity against a biological pathway  
CC required for proliferation, or that inhibits cellular proliferation; (8)  
CC identifying a gene required for cellular proliferation or the biological  
CC pathway in which a proliferation-required gene or its gene product lies  
CC or a gene on which the test compound that inhibits proliferation of an  
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a  
CC compound's activity; (11) a culture comprising strains in which the gene  
CC product is overexpressed or underexpressed; (12) determining the extent  
CC to which each of the strains is present in a culture or collection of  
CC strains; or (13) identifying the target of a compound that inhibits the  
CC proliferation of an organism. The antisense nucleic acids are useful for  
CC identifying proteins or screening for homologous nucleic acids required  
CC for cellular proliferation to isolate candidate molecules for rational  
CC drug discovery programs, or for screening homologous nucleic acids  
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,  
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of  
CC the target prokaryotic essential genes. Note: The sequence data for this  
CC patent did not form part of the printed specification, but was obtained  
CC in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 277 AA;  
Query Match 83.8%; Score 31; DB 6; Length 277;  
Best Local Similarity 83.3%; Pred. No. 5.3e+02; Indels 0; Gaps 0;  
Matches 5; Conservative 1; Mismatches 0;  
QY 1 YSSNLH 6  
|||||  
DB 94 YSSNIH 99  
RESULT 40  
AAAY97205  
ID AAAY97205 standard; protein; 347 AA.  
XX  
AC AAAY97205;  
XX  
XX 12-SEP-2003 (revised)  
DT 22-DEC-2000 (first entry)  
XX  
XX Campylobacter jejuni OH4384 Beta-1,4-GalNAC transferase.  
XX

KW Biosynthetic locus; biosynthesis; lipid A biosynthesis;  
KW acetyltransferase; glycosyltransferase; Beta-1,4-GalNAC transferase;  
KW Beta-1,3-galactosyltransferase; alpha-2,3-sialyltransferase;  
KW sialic acid synthase; CMP-sialic acid synthetase; mimic; antibody;  
KW immunity; immunogen; ganglioside.  
XX  
OS Campylobacter jejuni; OH4384.  
XX  
XX WO200046379-A1.  
XX  
XX 10-AUG-2000.  
XX  
XX 01-FEB-2000; 2000WO-CA000086.  
XX  
XX 01-FEB-1999; 99US-0118213P.  
XX 31-JAN-2000; 2000US-00495406.  
XX  
XX (CANA ) NAT RES COUNCIL CANADA.  
XX  
XX Gilbert M, Wakarchuk WW;  
XX  
XX WPI; 2000-524418/47.  
DR N-PSDB; AAA53722, AAA53720.  
XX  
XX Novel glycosyltransferase polypeptides and polynucleotides useful for  
PT biosynthesis of ganglioside and ganglioside mimics, as diagnostic  
PT reagents and as immunogen for producing antibodies.  
XX  
XX Claim 13; Page 100-101; 120pp; English.  
XX  
XX A reaction mixture for the synthesis of a sialylated oligosaccharide is  
CC useful for synthesising sialylated oligosaccharides such as ganglioside,  
CC lysoganglioside or their mimics. Glycosyltransferases are useful for  
CC chemo-enzymatic synthesis of oligosaccharides, including gangliosides and  
CC other oligosaccharides that have biological activity. The enzymes and  
CC nucleic acids that encode them are useful for studies of the pathogenesis  
CC mechanisms of organisms that synthesize ganglioside mimics, such as *C.*  
CC *jejuni* and the nucleic acids are used as probes to study expression of  
CC genes involved in ganglioside mimetic synthesis. Antibodies raised  
CC against the glycosyltransferases are also useful for analyzing the  
CC expression patterns of these genes involved in pathogenesis. The nucleic  
CC acids are also useful for designing antisense oligonucleotides for  
CC inhibiting expression of the Campylobacter enzymes that are involved in  
CC the biosynthesis of ganglioside mimics that can mask the pathogens from  
CC the host's immune system. The oligosaccharides are useful as diagnosing  
CC reagents or as therapeutics and as immunogens for producing antibodies.  
CC Bacterial glycosyltransferase can be used to catalyse the formation of  
CC oligosaccharides that are identical to the corresponding mammalian  
CC structures and are easier and less expensive to produce in large  
CC quantity, compared to the mammalian glycosyltransferase. The bacterial  
CC origin of the enzymes facilitates expression of large quantities of the  
CC enzymes using relatively inexpensive prokaryotic expression systems.  
XX  
XX (Updated on 12-SEP-2003 to standardise OS field)  
XX  
SQ Sequence 347 AA;  
Query Match 83.8%; Score 31; DB 3; Length 347;  
Best Local Similarity 71.4%; Pred. No. 6.9e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 YSSNLHS 7  
:|||:  
DB 268 FSSNIHS 274  
RESULT 41  
ABJ18486  
ID ABJ18486 standard; protein; 347 AA.  
XX  
AC ABJ18486;  
XX  
XX 07-FEB-2003 (first entry)  
XX

DE Campylobacter jejuni bifunctional sialtransferase cstII #7.  
 XX  
 KW Enzyme; gene therapy; acyltransferase; glycosyltransferase;  
 KW GalNAc transferase; N-Acetylgalactosamine transferase;  
 KW galactosyltransferase; sialyltransferase; sialic acid synthase;  
 KW cytidine 5'-monophosphate sialic acid synthetase;  
 KW CMP sialic acid synthetase; acetyltransferase; ganglioside synthesis;  
 KW ganglioside mimetics; inflammation; tumour metastasis.  
 XX  
 OS Campylobacter jejuni.  
 XX  
 PN WO200274942-A2.  
 XX  
 XX 26-SEP-2002.  
 PD  
 XX 22-FEB-2002; 2002WO-CA000229.  
 PF  
 XX 21-MAR-2001; 2001US-00816028.  
 PR  
 XX (CANADA) NAT RES COUNCIL CANADA.  
 PA  
 XX Gilbert M, Wakarchuk WW;  
 PI  
 XX WPI; 2003-040554/03.  
 DR  
 XX N-PSDB; ABT13673.  
 DR  
 XX New glycosyltransferases from Campylobacter, useful for synthesizing  
 PT gangliosides and ganglioside mimetics, and in studying the pathogenesis  
 PT mechanisms of organisms that synthesize ganglioside mimetics.  
 PT  
 XX  
 PS Claim 5; Page 101; 107pp; English.  
 XX  
 CC The invention comprises the amino acid and coding sequences of  
 CC Campylobacter jejuni proteins. The C. jejuni proteins of the invention  
 CC may be either an: acyltransferase; glycosyltransferase; GalNAc (N-  
 CC Acetylgalactosamine) transferase; galactosyltransferase;  
 CC sialyltransferase; sialic acid synthase; cytidine 5'-monophosphate (CMP)  
 CC sialic acid synthetase; acetyltransferase. The C. jejuni DNA and protein  
 CC sequences of the invention are useful for ganglioside synthesis, studying  
 CC ganglioside mimetics, and for designing oligonucleotides to inhibit  
 CC expression of Campylobacter enzymes involved in the biosynthesis of  
 CC ganglioside mimetics that can mask the pathogen's from the host's immune  
 CC system. The C. jejuni oligosaccharides of the invention may be used as  
 CC diagnostic reagents (e.g. to locate areas of inflammation or tumour  
 CC metastasis). The present amino acid sequence represents a Campylobacter  
 CC jejuni protein of the invention  
 CC  
 XX  
 SQ Sequence 347 AA;  
 Query Match 83.8%; Score 31; DB 6; Length 347;  
 Best Local Similarity 71.4%; Pred. No. 6.9e+02;  
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YSSNLHS 7  
 :|||:|  
 Db 268 FSSNIHS 274  
 RESULT 42  
 ABP80364  
 ID ABP80364 standard; protein; 380 AA.  
 XX  
 AC ABP80364;  
 XX  
 XX 07-MAR-2003 (first entry)  
 DT  
 XX N. gonorrhoeae amino acid sequence SEQ ID 7258.  
 DE  
 XX Antibacterial; infection; vaccine; gene therapy.  
 KW  
 XX Neisseria gonorrhoeae.  
 OS  
 XX WO200279243-A2.  
 PN

XX 10-OCT-2002.  
 PD  
 XX 12-FEB-2002; 2002WO-IB002069.  
 PF  
 XX 12-FEB-2001; 2001GB-00003424.  
 PR  
 XX (CHIR-) CHIRON SPA.  
 PA  
 XX Fontana MR, Pizza M, Massignani V, Monaci E;  
 PI  
 XX WPI; 2003-058415/05.  
 DR  
 XX N-PSDB; ABZ41334.  
 DR  
 XX New protein from Neisseria gonorrhoeae, useful for the manufacture of a  
 PT medicament for treating or preventing N. gonorrhoeae infection.  
 PT  
 XX  
 PS Disclosure; Page 716; 815pp; English.  
 XX  
 CC The present invention relates to proteins from Neisseria gonorrhoeae.  
 CC Also disclosed are the nucleic acid molecules encoding the proteins and  
 CC antibodies that specifically bind to the proteins. The composition  
 CC comprising the protein, nucleic acid or antibody is useful for the  
 CC manufacture of a medicament for treating or preventing N. gonorrhoeae  
 CC infection, this may be in the form of a vaccine or gene therapy.  
 CC  
 CC Sequences given in records ABP76736-ABP81046 represent nucleic acid  
 CC molecules of the invention  
 CC  
 XX  
 SQ Sequence 380 AA;  
 Query Match 83.8%; Score 31; DB 6; Length 380;  
 Best Local Similarity 71.4%; Pred. No. 7.6e+02;  
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YSSNLHS 7  
 :|||:|  
 Db 48 YANLHS 54  
 RESULT 43  
 ADT57543  
 ID ADT57543 standard; protein; 385 AA.  
 XX  
 AC ADT57543;  
 XX  
 XX 13-JAN-2005 (first entry)  
 DT  
 XX Plant polypeptide, SEQ ID 7620.  
 DE  
 XX  
 XX Plant; transgenic; cold tolerance; growth rate; drought tolerance;  
 KW disease resistance; galactomannan production; plant growth regulator;  
 KW heat tolerance; herbicide tolerance; lignin production;  
 KW extreme osmotic condition tolerance; pathogens resistance;  
 KW pest resistance; yield improvement; seed oil yield; seed protein yield.  
 KW  
 XX Viridiplantae.  
 OS  
 XX US2004216190-A1.  
 PN  
 XX 28-OCT-2004.  
 PD  
 XX 18-DEC-2003; 2003US-00739930.  
 PF  
 XX 28-APR-2003; 2003US-00424599.  
 PR  
 XX 28-APR-2003; 2003US-00425115.  
 PR  
 XX (KOVA/) KOVALIC D K.  
 PA  
 XX Kovalic DK;  
 PI  
 XX WPI; 2004-757369/74.  
 DR  
 XX New recombinant DNA constructs useful in the field of biochemistry and  
 PT

PT genetics, and in particular for producing transgenic plants with improved  
 PT biological characteristics.

XX Claim 2; SEQ ID NO 7620; 14pp; English.

XX The invention relates a recombinant DNA construct comprising a  
 CC polynucleotide having any of 5544 nucleotide sequences (cDNAs SEQ ID NO:  
 CC 1-5544) and encoding a polypeptide with any of 5544 amino acid sequences  
 CC (SEQ ID NO: 5545-11088). The cDNAs and proteins are from corn, soybean,  
 CC Arabidopsis, wheat and rape but the specification does not indicate which  
 CC sequences is derived from which organism. Also included is a method of  
 CC producing a plant having an improved property, comprising transforming a  
 CC plant with a recombinant DNA construct comprising a promoter region  
 CC functional in a plant cell operably joined to a polynucleotide encoding a  
 CC polypeptide associated with the property, and growing the transformed  
 CC plant. The property is selected from improving plant cold tolerance, for  
 CC manipulating growth rate in plant cells by modification of the cell cycle  
 CC pathway, for improving plant drought tolerance, for providing increased  
 CC resistance to plant disease, for galactomannan production, for production  
 CC of plant growth regulators, for improving plant heat tolerance, for  
 CC improving plant tolerance to herbicides, for increasing the rate of  
 CC homologous recombination in plants, for lignin production, for improving  
 CC plant tolerance to extreme osmotic conditions, for improving plant  
 CC tolerance to pathogens or pests, for yield improvement by modification of  
 CC photosynthesis, for modifying seed oil yield and/or content, for  
 CC modifying seed protein yield and/or content, for yield improvement by  
 CC modification of carbohydrate, nitrogen or phosphorus use and/or uptake  
 CC and for yield improvement by providing improved plant growth and  
 CC development under at least one stress condition. The polynucleotide may  
 CC also encode a plant transcription factor. The methods and compositions of  
 CC the present invention are useful in the field of biochemistry and  
 CC genetics, in particular for producing transgenic plants with improved  
 CC biological characteristics such as increased yield, improved nitrogen  
 CC flow, increasing plant tolerance to cold or heat, improving plant  
 CC tolerance to extreme osmotic and drought conditions, and improving plant  
 CC tolerance to plant pests or pathogens. They can also be used in physical  
 CC arrays of molecules, plant breeding markers, computer-based storage and  
 CC analysis systems. The present sequence is one of the 5544 plant protein  
 CC sequences of the invention. Note: The sequence data for this patent did  
 CC not form part of the printed specification, but was obtained in  
 CC electronic format directly from USPTO at  
 CC seqdata.uspto.gov/sequence.html?DocID=20040216190.

XX Sequence 385 AA;

Query Match 83.8%; Score 31; DB 8; Length 385;  
 Best Local Similarity 85.7%; Pred. No. 7.7e+02;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSNLHS 7

Db 165 YSSNQHS 171

RESULT 44

ADX79662  
 ID ADX79662 standard; protein; 392 AA.

XX AC ADX79662;

XX 21-APR-2005 (first entry)

XX Plant full length insert polypeptide seqid 49028.

XX plant protectant; plant growth regulant; gene therapy; plant;  
 KW recombinant DNA construct; physical array; plant breeding marker;  
 KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;  
 KW extreme osmotic condition; pathogen tolerance; pest tolerance;  
 KW growth rate; cell cycle pathway; disease resistance;  
 KW galactomannan production; lignin production; plant growth regulator;  
 KW yield; plant growth; plant development; seed oil; protein yield;  
 KW protein content.

OS Unidentified.

XX US2004034888-A1.

XX 19-FEB-2004.

XX 28-APR-2003; 2003US-00425114.

XX 06-MAY-1999; 99US-00304517.

XX 05-NOV-2001; 2001US-00985678.

XX (LIUJ/) LIU J.

XX (ZHOU/) ZHOU Y.

XX (KOVA/) KOVALIC D K.

XX (SCRE/) SCREEN S E.

XX (TAB/) TABASKA J E.

XX (CAO/) CAO Y.

PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;

XX WPI; 2004-180133/17.

XX New recombinant DNA construct, useful for improving plant tolerance to  
 PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or  
 PT pests, for conferring increased resistance to plant disease, or for  
 PT improving yield.

XX Claim 1; SEQ ID NO 49028; 15pp; English.

XX The invention describes a recombinant DNA construct comprising a  
 CC polynucleotide consisting of a sequence encoding an amino acid sequence  
 CC available in electronic form from the US patent office at  
 CC ftp.seqdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide  
 CC of the invention are also useful in physical arrays of molecules and as  
 CC plant breeding markers. The recombinant DNA construct is useful for  
 CC improving plant tolerance to cold, heat, drought, herbicides, extreme  
 CC osmotic conditions, pathogens or pests, for manipulating growth rate in  
 CC plant cells by modification of the cell cycle pathway, for conferring  
 CC increased resistance to plant disease, for producing galactomannan,  
 CC lignin or plant growth regulators, for increasing the rate of homologous  
 CC recombination in plants, for improving yield by modification of  
 CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake  
 CC or by providing improved plant growth and development under at least one  
 CC stress condition or for modifying seed oil or protein yield and/or  
 CC content. This is the amino acid sequence of a plant full length insert  
 CC polypeptide that can be used in the recombinant DNA construct of the  
 CC invention.

XX Sequence 392 AA;

Query Match 83.8%; Score 31; DB 8; Length 392;

Best Local Similarity 85.7%; Pred. No. 7.9e+02;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSNLHS 7

Db 195 YSSGLHS 201

RESULT 45

ADY08554

ID ADY08554 standard; protein; 407 AA.

XX AC ADY08554;

XX 21-APR-2005 (first entry)

XX Plant full length insert polypeptide seqid 64369.

XX plant protectant; plant growth regulant; gene therapy; plant;  
 KW recombinant DNA construct; physical array; plant breeding marker;  
 KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;  
 KW extreme osmotic condition; pathogen tolerance; pest tolerance;

KW growth rate; cell cycle pathway; disease resistance;  
 KW galactomannan production; lignin production; plant growth regulator;  
 KW yield; plant growth; plant development; seed oil; protein yield;  
 KW protein content.  
 XX Unidentified.  
 XX US2004034888-A1.  
 PN 19-FEB-2004.  
 PD 28-APR-2003; 2003US-00425114.  
 XX 06-MAY-1999; 99US-00304517.  
 PR 05-NOV-2001; 2001US-00985678.  
 XX (LIUJ/) LIU J.  
 PA (ZHOU/) ZHOU Y.  
 PA (KOVA/) KOVALIC D K.  
 PA (SCRE/) SCREEN S E.  
 PA (TABA/) TABASKA J E.  
 PA (CAOY/) CAO Y.  
 XX Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;  
 PI WPI; 2004-180133/17.  
 DR New recombinant DNA construct, useful for improving plant tolerance to  
 PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or  
 PT pests, for conferring increased resistance to plant disease, or for  
 PT improving yield.  
 XX Claim 1; SEQ ID NO 64369; 15pp; English.  
 PS The invention describes a recombinant DNA construct comprising a  
 CC polynucleotide consisting of a sequence encoding an amino acid sequence  
 CC available in electronic form from the US patent office at  
 CC ftp.seqdata.uspto.gov/sequence.html?docid:2004034888. The polynucleotide  
 CC of the invention are also useful in physical arrays of molecules and as  
 CC plant breeding markers. The recombinant DNA construct is useful for  
 CC improving plant tolerance to cold, heat, drought, herbicides, extreme  
 CC osmotic conditions, pathogens or pests, for manipulating growth rate in  
 CC plant cells by modification of the cell cycle pathway, for conferring  
 CC increased resistance to plant disease, for producing galactomannan,  
 CC lignin or plant growth regulators, for increasing the rate of homologous  
 CC recombination in plants, for improving yield by modification of  
 CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake  
 CC or by providing improved plant growth and development under at least one  
 CC stress condition or for modifying seed oil or protein yield and/or  
 CC content. This is the amino acid sequence of a plant full length insert  
 CC polypeptide that can be used in the recombinant DNA construct of the  
 CC invention.  
 XX SQ Sequence 407 AA;  
 Query Match 83.8%; Score 31; DB 8; Length 407;  
 Best Local Similarity 85.7%; Pred. No. 8.2e-02;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 YSSNLHS 7  
 DB 187 YSSNQHS 193  
 RESULT 46  
 AAM97437  
 ID AAM97437 standard; peptide; 14 AA.  
 XX AAM97437;  
 XX 24-JAN-2002 (first entry)  
 DT Human peptide #712 encoded by a SNP oligonucleotide.  
 DE

XX Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;  
 KW neuroprotective; antimicrobial; gene therapy; vaccine; amyloid;  
 KW amyloid protein; angiotensin; apoptosis related protein; cadherin;  
 KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;  
 KW complement related protein; cytochrome; kinesis; cytokine; interferon;  
 KW interleukin; G-protein coupled receptor; thioesterase; inflammation;  
 KW multifactorial disease; autoimmune disease; infection;  
 KW nervous system disease.  
 XX Homo sapiens.  
 OS WO200147944-A2.  
 PN 05-JUL-2001.  
 PD 28-DEC-2000; 2000WO-US035498.  
 PF 28-DEC-1999; 99US-0173419P.  
 PR 27-DEC-2000; 2000US-00173419.  
 XX (CURA-) CURAGEN CORP.  
 XX Shimkets RA, Leach M;  
 PI WPI; 2001-465210/50.  
 DR Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,  
 PT oncogenes and histones, useful for diagnosing and treating, e.g. cancer,  
 PT autoimmune diseases and infections.  
 XX Disclosure; Page 3823; 4143pp; English.  
 PS The present invention relates to oligonucleotides (see AAL26793-AAL34659)  
 CC encoding polymorphic variants of proteins related to amylases, amyloid  
 CC proteins, angiotensin, apoptosis related proteins, cadherin, cyclin,  
 CC polymerase, oncogenes, histones, kinases, colony stimulating factors,  
 CC complement related proteins, cytochromes, kinesins, cytokines,  
 CC interferons, interleukins, G-protein coupled receptors and thioesterases.  
 CC The present sequence is a peptide encoded by one such oligonucleotide.  
 CC The oligonucleotides and the peptides encoded by them may be used in the  
 CC prevention, diagnosis and treatment of diseases associated with  
 CC inappropriate expression of the proteins listed above. Disorders that may  
 CC be prevented, diagnosed and/or treated include multifactorial diseases  
 CC with a genetic component, such as autoimmune diseases (e.g. rheumatoid  
 CC arthritis, multiple sclerosis, diabetes, systemic lupus erythematosus  
 CC and Grave's disease), inflammation, cancer (e.g. cancers of the bladder,  
 CC brain, breast, colon and kidney, leukaemia), diseases of the nervous  
 CC system and an infection of pathogenic organisms  
 XX SQ Sequence 14 AA;  
 Query Match 81.1%; Score 30; DB 4; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 30;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 SSNLHS 7  
 DB 2 SSNLHS 7  
 RESULT 47  
 ABO12747  
 ID ABO12747 standard; peptide; 23 AA.  
 XX ABO12747;  
 XX 25-AUG-2003 (first entry)  
 DT Human zinc finger DNA binding domain #1046.  
 DE Composite binding polypeptide; zinc finger nucleic acid binding domain;  
 KW autoimmune disorder; immunosuppressive; zinc finger DNA binding domain;

```

KW human.
XX
XX OS Homo sapiens.
XX PN WO200299084-A2.
XX PD 12-DEC-2002.
XX
XX PF 04-APR-2002; 2002WO-US022272.
XX PR 04-APR-2001; 2001GB-00008491.
XX PA (SANG-) SANGMO BIOSCIENCES INC.
XX PI Moore M, Sepp A, Isalan M, Choo Y;
XX WI; 2003-278214/27.
XX
XX PT New composite binding zinc finger polypeptide, useful for designing
XX PT sequence-specific binding proteins regulating gene expression in the
XX PT fields of molecular biology, and for the diagnosis and treatment of
XX PT autoimmune disorders.
XX
XX PS Example 2; Page 93; 157pp; English.
XX
XX CC The invention relates to a composite binding polypeptide comprising a
XX CC first natural binding domain derived from a first natural binding
XX CC polypeptide and a second natural binding domain derived from a second
XX CC natural binding polypeptide, where the first and second natural binding
XX CC polypeptides may be the same or different and where the polypeptide binds
XX CC to a target differing from the natural target of both the first and
XX CC second binding polypeptides. The invention also relates to a chimeric
XX CC polypeptide comprising a binding polypeptide cited above and a biological
XX CC effector domain, a library of natural binding domains, a library of
XX CC natural zinc finger nucleic acid binding domains comprising a linker
XX CC attached to it, a method for selecting a binding polypeptide capable of
XX CC binding to a target site and a method for designing a composite binding
XX CC polypeptide. The methods and compositions of the present invention are
XX CC useful for designing sequence-specific binding proteins for regulation of
XX CC gene expression in the fields of molecular biology. They can also be used
XX CC for the diagnosis and treatment of autoimmune disorders, and as research
XX CC tools and in transgenic animals. This sequence represents a human zinc
XX CC finger DNA binding domain used in the scope of the invention
XX
XX SQ Sequence 23 AA;
    Query Match      81.1%; Score 30; DB 6; Length 23;
    Best Local Similarity 100.0%; Pred. No. 52;
    Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 SSNLHS 7
Db 13 SSNLHS 18
    |||||
    |||||

RESULT 48
ABP03340
ID ABP03340 standard; protein; 56 AA.
XX
XX AC ABP03340;
XX
XX DT 24-JUN-2002 (first entry)
XX
XX DE Human ORFX protein sequence SEQ ID NO:6662.
XX
XX KW Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis;
XX KW hyperproliferative disorder; psoriasis; benign tumour; haemorrhage;
XX KW degenerative disorder; osteoarthritis; neurodegenerative disorder;
XX KW cardiovascular disease; diabetes mellitus; systemic lupus erythematosus;
XX KW hypertension; hypothyroidism; cholesterol ester storage disease;
XX KW immune deficiency; immune disorder; infectious disease;
XX KW autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;
XX KW myasthenia gravis.

KW Homo sapiens.
XX WO200192523-A2.
XX 06-DEC-2001.
XX
XX PF 29-MAY-2001; 2001WO-US010836.
XX PR 30-MAY-2000; 2000US-0206132P.
XX PR 29-AUG-2000; 2000US-0228716P.
XX PA (CURA-) CURAGEN CORP.
XX
XX PI Shimkets RA, Leach MD;
XX WI; 2002-106308/14.
XX DR N-PSDB; ABN19092.
XX
XX PT Novel human polypeptides and polynucleotides useful for diagnosing,
XX PT preventing and treating cardiovascular disease, neurodegenerative,
XX PT hyperproliferative disorders and autoimmune disorders.
XX
XX PS Disclosure; SEQ ID NO 6662; 1037pp; English.
XX
XX CC The present invention describes substantially purified human proteins
XX CC (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1
XX CC in the specification). ABN15762 to ABN27252 encode the human ORFX
XX CC proteins given in ABP00010 to ABP11500. ORFX proteins are useful for
XX CC treating or preventing a pathology associated with an ORFX-associated
XX CC disorder in humans, and in the manufacture of a medicament for treating a
XX CC syndrome associated with ORFX-associated disorder. ORFX polynucleotide
XX CC sequences can be used in gene therapy. ORFX sequences can be used in the
XX CC treatment of cancer, hyperproliferative disorders, cirrhosis of liver,
XX CC psoriasis, benign tumours, keloid, degenerative disorders, haemorrhage,
XX CC osteoarthritis, neurodegenerative disorders, diabetes mellitus, systemic
XX CC lupus erythematosus, hypertension, hypothyroidism, cholesterol ester
XX CC storage disease, various immune deficiencies and disorders, infectious
XX CC diseases, autoimmune disorders such as multiple sclerosis, rheumatoid
XX CC arthritis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host
XX CC disease and autoimmune inflammatory eye disease. ORFX proteins are also
XX CC useful for treating burns, incisions, ulcers, for treating osteoporosis,
XX CC bone degenerative disorders, or periodontal disease, and for gut
XX CC protection or regeneration and treatment of lung or liver fibrosis,
XX CC reperfusion injury in various tissues and conditions resulting from
XX CC systemic cytokine damage. N.B. The sequence data for this patent did not
XX CC form part of the printed specification, but was obtained in electronic
XX CC format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 56 AA;
    Query Match      81.1%; Score 30; DB 5; Length 56;
    Best Local Similarity 71.4%; Pred. No. 1,46+02;
    Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 YSSNLHS 7
Db 17 YSSHLHS 23
    |||||
    |||||

RESULT 49
AAU59057
ID AAU59057 standard; protein; 83 AA.
XX
XX AC AAU59057;
XX
XX DT 13-FEB-2002 (first entry)
XX
XX DE Propionibacterium acnes immunogenic protein #19953.
XX
XX KW SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
XX KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;

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GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: April 6, 2006, 08:56:41 ; Search time 7 Seconds  
(without alignments)  
96.217 Million cell updates/sec

Title: US-10-089-500-7

Perfect score: 37

Sequence: 1 YSNNLHS 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

1: PIR 80:\*

2: PIR1:\*

3: PIR3:\*

4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33	89.2	219	2 T30122	hypothetical prote
2	33	89.2	368	2 G86895	hypothetical prote
3	32	86.5	324	2 S61447	cellulase (EC 3.2.
4	32	86.5	489	2 T06350	cellulase (EC 3.2.
5	31	83.8	107	2 A48677	Ig kappa chain V-J
6	31	83.8	380	2 A81198	conserved hypotet
7	31	83.8	380	2 A81833	probable transcrip
8	30	81.1	243	2 AF0777	hypothetical prote
9	30	81.1	290	2 AI2054	hypothetical prote
10	30	81.1	313	2 T48439	probable RNA-bind
11	30	81.1	412	2 S72617	alcohol dehydrogen
12	30	81.1	424	2 G86247	hypothetical prote
13	30	81.1	427	2 T23954	hypothetical prote
14	30	81.1	458	2 F97296	UDP-N-acetylmuram
15	30	81.1	459	2 AF2847	two component sens
16	30	81.1	459	2 E97624	osmolarity sensor
17	30	81.1	472	2 AD5332	hypothetical prote
18	30	81.1	816	2 T17257	hypothetical prote
19	30	81.1	844	2 B83136	probable fibrillar
20	30	81.1	1042	1 GBECE	beta-galactosidase
21	30	81.1	1042	2 E85968	evolved beta-D-gal
22	30	81.1	1042	2 F91123	evolved beta-D-gal
23	30	81.1	1723	2 H86357	polymorphic membra
24	30	81.1	1723	2 E72067	polymorphic membra
25	30	81.1	1732	2 C81601	polymorphic membra
26	29	78.4	108	1 KVM573	Ig kappa chain V r
27	29	78.4	111	2 G38740	Ig kappa chain V r
28	29	78.4	111	2 A38740	Ig kappa chain V r
29	29	78.4	111	2 E38740	Ig kappa chain V r

30	29	78.4	111	2 C38740	Ig kappa chain V r
31	29	78.4	227	2 T11242	ribosomal protein
32	29	78.4	243	2 G8567	protein T08A9.2 [i
33	29	78.4	334	1 TVNSJA	transcription fact
34	29	78.4	334	2 S12742	hypothetical prote
35	29	78.4	347	2 T25192	hypothetical prote
36	29	78.4	391	2 T38822	glucose-6-phosphat
37	29	78.4	451	2 B69675	unknown protein, 2
38	29	78.4	465	2 G96655	hypothetical prote
39	29	78.4	516	2 T33061	hypothetical prote
40	29	78.4	550	2 F90407	molybdopterin bios
41	29	78.4	572	2 T51525	hypothetical prote
42	29	78.4	732	2 AI2158	hypothetical prote
43	29	78.4	746	2 S74219	alpha-galactosidas
44	29	78.4	787	2 T00798	hypothetical prote
45	29	78.4	867	2 T14777	hypothetical prote
46	29	78.4	947	2 G86420	probable receptor-
47	29	78.4	2105	2 T18968	probable serine-ty
48	28	75.7	48	2 T43063	RAD51 protein, lon
49	28	75.7	79	2 S38466	hypothetical prote
50	28	75.7	93	2 S38564	Ig kappa chain V r
51	28	75.7	107	2 S69901	Ig kappa chain (cl
52	28	75.7	107	2 B48677	Ig kappa chain V-J
53	28	75.7	107	2 C48677	Ig light chain V-J
54	28	75.7	107	2 A28044	Ig kappa chain V r
55	28	75.7	107	2 D48677	Ig kappa chain V-J
56	28	75.7	107	2 B28044	Ig kappa chain V r
57	28	75.7	107	2 B49026	Ig kappa chain V r
58	28	75.7	107	2 S69906	Ig kappa chain (cl
59	28	75.7	108	1 KVM5AR	Ig kappa chain V r
60	28	75.7	108	2 S11124	Ig kappa chain V r
61	28	75.7	108	2 S38862	Ig kappa chain V r
62	28	75.7	108	2 S69902	Ig kappa chain (cl
63	28	75.7	108	2 S69900	Ig kappa chain (cl
64	28	75.7	108	2 S19970	Ig kappa chain V r
65	28	75.7	108	2 S69903	Ig kappa chain (cl
66	28	75.7	109	2 P80888	Ig kappa chain V r
67	28	75.7	115	2 A53276	Ig kappa chain V r
68	28	75.7	122	2 JL0080	Ig kappa chain pre
69	28	75.7	122	2 A29380	Ig kappa chain pre
70	28	75.7	126	2 A34904	Ig kappa chain pre
71	28	75.7	127	2 PH1224	Ig kappa chain pre
72	28	75.7	128	2 A26406	Ig kappa chain V r
73	28	75.7	129	2 A86162	protein F1003.7 [i
74	28	75.7	145	2 AH1768	wall teichoic acid
75	28	75.7	224	2 AC1188	phosphoglycerate m
76	28	75.7	224	2 AC1546	phosphoglycerate m
77	28	75.7	227	2 G90631	probable fibrillar
78	28	75.7	227	2 F85482	probable chaparon
79	28	75.7	250	2 C90606	hypothetical prote
80	28	75.7	261	2 E86354	hypothetical prote
81	28	75.7	270	2 S17828	nuclease S1 - Peni
82	28	75.7	270	2 JE0408	3'-nucleotidase [E
83	28	75.7	271	1 S34678	short-chain alcoh
84	28	75.7	277	2 S59781	hypothetical prote
85	28	75.7	312	2 C86790	2-dehydropanoate
86	28	75.7	342	2 T46909	hypothetical prote
87	28	75.7	348	2 T12281	NADH2 dehydrogen
88	28	75.7	370	2 E97316	response regulator
89	28	75.7	379	2 D81515	cell shape-determi
90	28	75.7	391	2 T28822	hypothetical prote
91	28	75.7	404	2 C85829	glycosyl transfera
92	28	75.7	404	2 H90983	probable glycosyl
93	28	75.7	409	2 T40633	hypothetical prote
94	28	75.7	415	2 A86599	rod shape protein
95	28	75.7	415	2 C72026	rod shape protein
96	28	75.7	451	2 T19491	hypothetical prote
97	28	75.7	451	2 S02068	RNA-directed RNA p
98	28	75.7	471	2 A31103	membrane glycoprot
99	28	75.7	475	2 T48986	hypothetical prote
100	28	75.7	512	2 H84698	hypothetical prote
101	28	75.7	526	2 E86149	T1N6.20 protein -
102	28	75.7	529	2 A24031	genome polypeptin

103	28	75.7	664	2	B86539	glycogen hydrolase	176	27	73.0	422	2	H85872	dihydrofolate foly
104	28	75.7	664	2	B72084	Glycosyl hydrolase	177	27	73.0	422	2	G91028	dihydrofolate foly
105	28	75.7	743	2	T42557	tegument protein 1	178	27	73.0	445	2	AT0483	metalloproteinase
106	28	75.7	1583	2	AB2137	hypothetical prote	179	27	73.0	447	2	C64640	hypothetical prote
107	28	75.7	1628	1	T43682	nucleoporin - fibs	180	27	73.0	447	2	S44133	histidine kinase -
108	28	75.7	2332	1	GNNY4F	genome polyprotein	181	27	73.0	448	2	AF1942	hypothetical prote
109	28	75.7	2332	1	GNNYP	genome polyprotein	182	27	73.0	450	2	G01158	tyrosine kinase ac
110	28	75.7	2333	1	GNNY2F	genome polyprotein	183	27	73.0	452	2	T70223	hypothetical prote
111	28	75.7	2358	1	T39569	probable alpha-glu	184	27	73.0	454	2	T48005	hypothetical prote
112	28	75.7	2371	2	T43432	alpha-glucan synth	185	27	73.0	458	2	T16041	hypothetical prote
113	28	75.7	2496	2	A71616	secreted protein P	186	27	73.0	486	2	T26483	hypothetical prote
114	28	75.7	3071	2	T50345	vacuolar protein s	187	27	73.0	496	2	T38197	probable myb-like
115	28	75.7	3655	2	T38084	TRAP-like protein	188	27	73.0	497	2	F83651	hypothetical prote
116	27	73.0	50	2	G97836	hypothetical prote	189	27	73.0	515	2	T39031	hypothetical prote
117	27	73.0	71	2	T17985	hypothetical prote	190	27	73.0	527	2	B70700	hypothetical prote
118	27	73.0	87	1	TXBPT4	thioredoxin [valid	191	27	73.0	530	2	B86326	probable oxidoredu
119	27	73.0	138	2	S15556	K222 protein - hum	192	27	73.0	573	2	E81385	hypothetical prote
120	27	73.0	159	2	S72326	glucan 1,3-beta-gl	193	27	73.0	577	2	T22460	hypothetical prote
121	27	73.0	159	2	G70841	hypothetical prote	194	27	73.0	605	2	C96888	hypothetical prote
122	27	73.0	165	2	B64121	nonheme ferritin h	195	27	73.0	611	2	T38908	probable gamma-glu
123	27	73.0	167	2	AG0306	probable DNA-bind	196	27	73.0	637	2	C97191	threonyl-tRNA synt
124	27	73.0	175	2	T43424	hypothetical prote	197	27	73.0	645	2	T39614	kinase-binding pro
125	27	73.0	175	2	A97194	hypothetical prote	198	27	73.0	645	2	T21829	hypothetical prote
126	27	73.0	180	2	S54502	ypt-interacting pr	199	27	73.0	646	2	T48644	negative regulator
127	27	73.0	194	2	G64124	transcription init	200	27	73.0	646	2	A95055	hypothetical prote
128	27	73.0	201	2	T16878	hypothetical prote	201	27	73.0	646	2	F97924	hypothetical prote
129	27	73.0	203	1	XX8CTG	galactoside O-acet	202	27	73.0	661	1	S95633	endo-1,4-beta-xyla
130	27	73.0	203	2	C90678	thiogalactoside ac	203	27	73.0	664	2	B81269	hypothetical prote
131	27	73.0	203	2	G85528	thiogalactoside ac	204	27	73.0	689	2	F64698	conserved hypother
132	27	73.0	208	2	S66486	fibroblast growth	205	27	73.0	691	2	B81937	competence protein
133	27	73.0	208	2	A48137	fibroblast growth	206	27	73.0	692	2	F71821	hypothetical prote
134	27	73.0	208	2	JC7082	fibroblast sonatol	207	27	73.0	748	2	S54505	hypothetical prote
135	27	73.0	208	2	A70253	antigen, P35 homol	208	27	73.0	749	2	T34090	hypothetical prote
136	27	73.0	219	2	B81534	hypothetical prote	209	27	73.0	765	2	G64502	hypothetical prote
137	27	73.0	228	2	F97323	protein-disulfide	210	27	73.0	775	2	T45136	WD repeat protein
138	27	73.0	244	2	G86617	hypothetical prote	211	27	73.0	808	2	A82877	hypothetical prote
139	27	73.0	244	2	H72006	hypothetical prote	212	27	73.0	829	2	D90324	penicillin acylase
140	27	73.0	252	2	E84083	nitrogen fixation	213	27	73.0	873	2	T50171	hypothetical prote
141	27	73.0	260	1	CRQ01R	carbonate dehydrat	214	27	73.0	880	2	S56828	finger protein YUL
142	27	73.0	280	2	F84765	hypothetical prote	215	27	73.0	931	2	T25148	hypothetical prote
143	27	73.0	286	2	C97974	spermidine synthas	216	27	73.0	969	2	T03657	NAD ADP-ribosyltra
144	27	73.0	286	2	A95106	spermidine synthas	217	27	73.0	1112	2	T42383	probable calcium-a
145	27	73.0	286	2	C97220	spermidine synthas	218	27	73.0	1156	2	T23308	hypothetical prote
146	27	73.0	291	2	H69521	4-hydroxybenzoate	219	27	73.0	1170	2	A57650	repair protein XPG
147	27	73.0	296	2	T25585	hypothetical prote	220	27	73.0	1235	1	S16948	insulin receptor s
148	27	73.0	312	2	T45739	transcription fact	221	27	73.0	1236	2	B36329	hypothetical prote
149	27	73.0	319	2	A70340	conserved hypother	222	27	73.0	1316	2	T00381	KRAA0633 protein -
150	27	73.0	323	2	A72059	conserved hypother	223	27	73.0	1369	2	T32338	hypothetical prote
151	27	73.0	323	2	H84564	CT476 hypother	224	27	73.0	1404	2	T19277	hypothetical prote
152	27	73.0	329	2	F70156	conserved hypother	225	27	73.0	1435	2	C82898	hypothetical prote
153	27	73.0	330	2	T27086	hypothetical prote	226	27	73.0	1442	2	S59384	DNA polymerase III
154	27	73.0	330	2	B97343	ABC-type MDR trans	227	27	73.0	1490	2	F88311	protein T06D8.10 [
155	27	73.0	331	2	T15458	hypothetical prote	228	27	73.0	1490	2	T24502	hypothetical prote
156	27	73.0	347	2	A99989	cyclin B (imported	229	27	73.0	1518	2	PQ0221	polyprotein - plum
157	27	73.0	358	2	I45532	protein co-factor	230	27	73.0	1815	2	S73021	polyketide synthas
158	27	73.0	361	2	G83879	hypothetical prote	231	27	73.0	1822	2	F87203	polyketide synthas
159	27	73.0	363	2	T37630	protein disulfide-	232	27	73.0	1855	2	S41649	DNA polymerase - m
160	27	73.0	380	2	AF1131	ATP-binding protei	233	27	73.0	1997	2	F71607	DNA helicase II BR
161	27	73.0	382	2	H70144	conserved hypother	234	27	73.0	3125	1	GNVSPP	genome polyprotein
162	27	73.0	382	2	AF1491	conserved hypother	235	27	73.0	3140	1	GNVSRA	genome polyprotein
163	27	73.0	387	2	T22511	hypothetical prote	236	27	73.0	3140	2	S47508	genome polyprotein
164	27	73.0	387	2	E90533	nitrogen fixation	237	27	73.0	3141	1	GNVSPD	genome polyprotein
165	27	73.0	398	2	A95848	probable replicati	238	27	73.0	669	2	S55024	nebulin, skeletal
166	27	73.0	399	2	D86177	protein F9ip9.3 [	239	26.5	71.6	549	2	A39345	alpha-mannosidase
167	27	73.0	404	2	T32725	hypothetical prote	240	26	70.3	42	2	E82801	hypothetical prote
168	27	73.0	406	2	F70019	nifs protein homol	241	26	70.3	69	2	A64527	hypothetical prote
169	27	73.0	412	2	S66925	hypothetical prote	242	26	70.3	69	2	C71980	hypothetical prote
170	27	73.0	413	2	D89857	hypothetical prote	243	26	70.3	80	2	G70013	hypothetical prote
171	27	73.0	415	2	E84397	Nifs protein, clas	244	26	70.3	84	2	T44006	ig kappa chain v r
172	27	73.0	420	2	AH2117	hypothetical prote	245	26	70.3	86	2	S26459	ig kappa chain v r
173	27	73.0	421	2	T33523	hypothetical prote	246	26	70.3	86	2	S29587	ig kappa chain v r
174	27	73.0	422	1	SYECFG	tetrahydrofolylpol	247	26	70.3	98	2	S26342	ig kappa chain v r
175	27	73.0	422	2	AC0802	dihydrofolate synt	248	26	70.3	101	2	S59640	ig light chain v r

249	26	70.3	102	2	S29584	Ig kappa chain V r	322	26	70.3	409	2	S76126	hypothetical prote
250	26	70.3	104	2	S29592	Ig kappa chain V r	323	26	70.3	415	2	PL0165	hemocyanin chain b
251	26	70.3	104	2	S28475	Ig kappa chain V r	324	26	70.3	425	2	C72744	hypothetical prote
252	26	70.3	108	1	KVMS54	Ig kappa chain V r	325	26	70.3	425	2	T41683	hypothetical prote
253	26	70.3	108	2	S29581	Ig kappa chain V r	326	26	70.3	428	2	T15966	hypothetical prote
254	26	70.3	111	1	S09963	Ig kappa chain V-J	327	26	70.3	429	1	T38146	dihydrofolate redu
255	26	70.3	116	1	AlHUTU	Ig heavy chain V-I	328	26	70.3	434	2	S21324	probable beta-gluc
256	26	70.3	134	2	B84246	cytidine aminohydr	329	26	70.3	443	2	C89863	glucose-6-phosphat
257	26	70.3	137	2	AB0263	conserved hypothet	330	26	70.3	457	2	E81739	oxygen-independent
258	26	70.3	148	2	T37002	hypothetical prote	331	26	70.3	457	2	T39846	hypothetical prote
259	26	70.3	151	2	C86352	protein T26P17.12	332	26	70.3	459	2	T11202	NADH2 dehydrogenas
260	26	70.3	176	1	I64161	cytochrome c bioge	333	26	70.3	460	2	T11296	NADH2 dehydrogenas
261	26	70.3	180	2	S37891	hypothetical prote	334	26	70.3	471	2	S61029	hypothetical prote
262	26	70.3	191	2	S50618	SPR6 protein - yea	335	26	70.3	485	2	P85512	aminoacyl-histidin
263	26	70.3	196	2	G72063	15 kDa cysteine-r1	336	26	70.3	485	2	H90661	aminoacyl-histidin
264	26	70.3	201	2	H86559	zinc finger protei	337	26	70.3	489	2	B85022	x-His dipeptidase
265	26	70.3	201	2	I57505	zinc finger protei	338	26	70.3	489	2	B85022	probable DNA-bind
266	26	70.3	205	2	T15517	hypothetical prote	339	26	70.3	496	2	AF2305	serine/threonine k
267	26	70.3	210	2	S36394	alpha-actinin 2, s	340	26	70.3	509	2	T30861	traf protein - Sal
268	26	70.3	210	2	S50582	hypothetical prote	341	26	70.3	523	2	T15649	hypothetical prote
269	26	70.3	215	2	G85849	probable transcript	342	26	70.3	548	2	T49948	hypothetical prote
270	26	70.3	215	2	F91005	probable transcript	343	26	70.3	550	2	AB2319	two-component sens
271	26	70.3	218	1	A40181	23K integral membr	344	26	70.3	564	2	AF2351	serine/threonine k
272	26	70.3	219	2	A42526	B2R protein - vacc	345	26	70.3	566	2	T33042	hypothetical prote
273	26	70.3	219	2	JQ1796	B2R protein - vacc	346	26	70.3	577	2	I50731	Ig heavy chain - n
274	26	70.3	224	2	S77828	probable transcript	347	26	70.3	597	2	C82367	aminopeptidase P V
275	26	70.3	233	2	T28914	hypothetical prote	348	26	70.3	598	2	D95207	oligoendopeptidase
276	26	70.3	240	2	AD3584	23S ribosomal RNA m	349	26	70.3	598	2	D98072	oligoendopeptidase
277	26	70.3	240	2	E84390	24-sterol C-methyl	350	26	70.3	603	2	H69121	hypothetical prote
278	26	70.3	243	2	F64980	hypothetical trans	351	26	70.3	607	2	H88065	protein T16A1.1 f1
279	26	70.3	244	2	T41861	ACMNPV orf124 - Bo	352	26	70.3	617	2	T02121	hypothetical prote
280	26	70.3	244	2	A96806	hypothetical prote	353	26	70.3	631	2	T48255	hypothetical prote
281	26	70.3	247	2	F65074	hypothetical oxido	354	26	70.3	634	2	C81652	ATP-dependent heli
282	26	70.3	247	2	H69493	phosphoesterase-re	355	26	70.3	634	2	D71493	probable DNA helic
283	26	70.3	247	2	E90144	conserved hypothet	356	26	70.3	638	1	E22930	DNA topoisomerase
284	26	70.3	248	2	T20060	hypothetical prote	357	26	70.3	639	2	T50148	probable ser/chr p
285	26	70.3	256	2	A96588	hypothetical prote	358	26	70.3	644	1	A40585	DNA topoisomerase
286	26	70.3	256	2	S74928	hypothetical prote	359	26	70.3	644	2	E89758	DNA gyrase subunit
287	26	70.3	263	2	B75361	WD-repeat family p	360	26	70.3	657	2	A39526	probable protein k
288	26	70.3	268	2	S57542	hypothetical prote	361	26	70.3	661	2	T46364	hypothetical prote
289	26	70.3	268	2	A12212	hypothetical prote	362	26	70.3	663	2	S67259	MNE1 protein - yea
290	26	70.3	272	2	T27062	hypothetical prote	363	26	70.3	698	2	C84836	hypothetical prote
291	26	70.3	276	2	A97787	hypothetical prote	364	26	70.3	702	2	T39483	probable transmemb
292	26	70.3	276	2	E71705	hypothetical prote	365	26	70.3	710	2	S35674	phosphoprotein pho
293	26	70.3	285	2	S05714	phycocyanin linker	366	26	70.3	724	1	JQ1622	glycoprotein H pre
294	26	70.3	297	2	S23737	proline-rich prote	367	26	70.3	754	2	T50803	hypothetical prote
295	26	70.3	299	2	F95294	probable LysR-type	368	26	70.3	759	2	S53922	PMT6 protein - yea
296	26	70.3	304	2	T23588	hypothetical prote	369	26	70.3	765	2	T35719	chitinase - Strept
297	26	70.3	305	2	T20685	hypothetical prote	370	26	70.3	788	1	S28302	ribonucleoside-dip
298	26	70.3	315	2	S59779	probable membrane	371	26	70.3	793	2	B85113	hypothetical outer
299	26	70.3	323	2	T07734	homeotic protein v	372	26	70.3	816	2	T51813	ribonucleoside-dip
300	26	70.3	328	2	T41521	hypothetical prote	373	26	70.3	816	2	B84605	hypothetical prote
301	26	70.3	329	2	T18615	hypothetical prote	374	26	70.3	817	2	T03852	protein phosphatas
302	26	70.3	329	2	A84529	hypothetical prote	375	26	70.3	823	2	C81739	conserved hypothet
303	26	70.3	332	2	H84443	homeodomain transc	376	26	70.3	825	2	T32130	hypothetical prote
304	26	70.3	333	2	A49405	protein kinase Pkn	377	26	70.3	828	2	JC5706	1-phosphatidylinos
305	26	70.3	336	2	T25440	hypothetical prote	378	26	70.3	839	2	T41826	P95 orf83 - Bombyx
306	26	70.3	344	2	H83928	hypothetical prote	379	26	70.3	842	2	A87557	non-motile and pha
307	26	70.3	346	2	S48380	IMP2 protein - yea	380	26	70.3	842	2	S27533	histidine protein
308	26	70.3	354	2	T10496	UDPglucose 4-epine	381	26	70.3	849	2	S61962	probable membrane
309	26	70.3	359	2	S35157	Delta6 fatty acid	382	26	70.3	853	2	S34682	probable transport
310	26	70.3	363	2	T19165	hypothetical prote	383	26	70.3	892	2	T15760	hypothetical prote
311	26	70.3	369	2	H75345	hypothetical prote	384	26	70.3	910	2	T22050	hypothetical prote
312	26	70.3	379	2	A95130	glycogen biosynthe	385	26	70.3	919	2	T05746	hypothetical prote
313	26	70.3	379	2	G98000	required for glyco	386	26	70.3	924	2	T32044	hypothetical prote
314	26	70.3	386	2	F70058	hypothetical prote	387	26	70.3	929	2	I51027	type XII collagen
315	26	70.3	389	2	T30068	hypothetical prote	388	26	70.3	939	2	E90558	topoisomerase iv a
316	26	70.3	391	2	T20752	hypothetical prote	389	26	70.3	939	2	AF2503	hypothetical prote
317	26	70.3	400	2	T18060	molybdenum formylm	390	26	70.3	967	2	H86334	T2OH2.10 protein -
318	26	70.3	400	2	H69222	hypothetical prote	391	26	70.3	1097	2	T40678	hypothetical prote
319	26	70.3	402	2	T25001	hypothetical prote	392	26	70.3	1138	2	G71554	probable transmemb
320	26	70.3	403	2	T02003	probable DNA-bind	393	26	70.3	1174	2	A39927	RNA-directed RNA p
321	26	70.3	407	2	I39152	zinc finger protei	394	26	70.3	1234	2	B36186	I factor protein 2

395	26	70.3	1289	2	S69689	hypothetical prote	468	25	67.6	244	2	T08941	hypothetical prote
396	26	70.3	1298	2	A64157	hypothetical prote	469	25	67.6	244	2	T45046	hypothetical prote
397	26	70.3	1341	2	S66835	probable membrane	470	25	67.6	248	2	H84555	hypothetical prote
398	26	70.3	1356	2	S51389	ROM2 protein - yea	471	25	67.6	249	2	G96952	glycerophosphoryl
399	26	70.3	1356	2	T16718	hypothetical prote	472	25	67.6	249	2	H90048	hypothetical prote
400	26	70.3	1366	2	C85077	probable polyprote	473	25	67.6	250	2	T02392	hypothetical prote
401	26	70.3	1445	2	T15212	hypothetical prote	474	25	67.6	255	2	A36935	N-acetylmuranoyl-L
402	26	70.3	1447	2	G86474	probable protein g	475	25	67.6	258	1	W2BE35	gene 35 protein -
403	26	70.3	1451	1	JQ1719	E2 glycoprotein pr	476	25	67.6	268	2	F81327	probable ribonucle
404	26	70.3	1483	2	T19751	hypothetical prote	477	25	67.6	269	2	E81747	2-dehydro-3-deoxy
405	26	70.3	1645	2	AG1897	hypothetical prote	478	25	67.6	269	2	D96957	uncharacterized me
406	26	70.3	1735	2	A57607	two-component hybr	479	25	67.6	270	2	S36699	hypothetical prote
407	26	70.3	1735	2	G86152	Munc13-1 - rat	480	25	67.6	274	2	S51832	phytohemagglutinin
408	26	70.3	1895	2	T15881	T7123.15 protein -	481	25	67.6	275	2	A22826	phytohemagglutinin
409	26	70.3	1969	2	T38495	hypothetical prote	482	25	67.6	277	2	T30180	hypothetical prote
410	26	70.3	2731	1	VFIHJH	genome polyprotein	483	25	67.6	277	2	A34783	homeotic protein N
411	26	70.3	2733	2	S15760	genome polyprotein	484	25	67.6	278	2	C83625	hypothetical prote
412	26	70.3	3034	2	T14119	seven-pass transme	485	25	67.6	280	2	F97785	invasion protein h
413	26	70.3	3110	2	AC0116	probable virulence	486	25	67.6	281	2	S18245	xylyl protein - Pee
414	26	70.3	3175	1	RRWEV	genome polyprotein	487	25	67.6	286	2	T17028	cycloidea protein
415	26	70.3	4868	2	B54161	ryanodine-binding	488	25	67.6	287	2	A84181	hypothetical prote
416	26	70.3	5107	2	T29144	partial CDS - Caen	489	25	67.6	288	2	D90524	multiple sugar ABC
417	25	67.6	52	2	B81423	very hypothetical	490	25	67.6	289	2	T44599	oligopeptide trans
418	25	67.6	62	2	D95110	hypothetical prote	491	25	67.6	289	2	S50765	RNA-binding protei
419	25	67.6	62	2	B97979	hypothetical prote	492	25	67.6	297	2	T21368	hypothetical prote
420	25	67.6	80	2	AF1860	hypothetical prote	493	25	67.6	304	2	AC1931	hypothetical prote
421	25	67.6	82	2	B97884	hypothetical prote	494	25	67.6	309	1	E89347	conserved hypothet
422	25	67.6	94	2	G96786	protein F10A5.9 [i	495	25	67.6	310	2	AE3558	transcription regu
423	25	67.6	95	2	G95012	bacteriocin, proba	496	25	67.6	310	2	T43147	hypothetical prote
424	25	67.6	113	2	D69481	transcription regu	497	25	67.6	312	2	T21992	hypothetical prote
425	25	67.6	115	2	AG0688	probable bacteriop	498	25	67.6	313	2	H71646	hypothetical prote
426	25	67.6	119	2	H90082	hypothetical prote	499	25	67.6	314	2	T24704	hypothetical prote
427	25	67.6	130	2	AD3526	5-carboxymethyl-2-	500	25	67.6	314	2	T30523	dihydrocitrate deh
428	25	67.6	132	2	H96708	hypothetical prote	501	25	67.6	318	2	A45522	variant surface gl
429	25	67.6	134	2	B64062	opacity-associated	502	25	67.6	323	2	S16318	homeotic protein H
430	25	67.6	137	2	S28705	hypothetical prote	503	25	67.6	325	1	VMU17	VSG expression sit
431	25	67.6	142	1	R80BHM	RNA-directed DNA p	504	25	67.6	325	2	T38308	hypothetical prote
432	25	67.6	144	2	G81043	hypothetical prote	505	25	67.6	326	2	T04055	hypothetical prote
433	25	67.6	155	2	T10014	hypothetical prote	506	25	67.6	330	2	E70017	hypothetical prote
434	25	67.6	156	2	T12815	hypothetical prote	507	25	67.6	331	1	TVHUUN	transcription fact
435	25	67.6	162	2	T37435	probable 18.8K pro	508	25	67.6	332	2	G86182	hypothetical prote
436	25	67.6	162	2	A42522	A49R protein - vac	509	25	67.6	332	2	G84920	hypothetical prote
437	25	67.6	162	2	JQ1787	SalP12R protein -	510	25	67.6	334	2	A82443	D-alanine-D-alanin
438	25	67.6	162	2	H72170	K3R protein - vari	511	25	67.6	334	2	G96980	probable transpos
439	25	67.6	162	2	T28594	25R protein - vari	512	25	67.6	335	2	T43627	hypothetical prote
440	25	67.6	162	2	S46843	J3R protein - vari	513	25	67.6	337	2	AF2438	glyceraldhyde-3-p
441	25	67.6	170	2	T40747	probable transmemb	514	25	67.6	338	2	F84262	hypothetical prote
442	25	67.6	172	2	JE0130	scytalone dehydrat	515	25	67.6	339	2	D89930	maltose operon tra
443	25	67.6	175	2	C90227	DNA repair protein	516	25	67.6	341	2	F69789	hypothetical prote
444	25	67.6	178	2	D64036	hypothetical prote	517	25	67.6	351	2	H72360	divalent cation tr
445	25	67.6	181	2	T49104	hypothetical prote	518	25	67.6	351	2	E57131	N-acetylmuramidase
446	25	67.6	186	2	A30832	hypothetical prote	519	25	67.6	353	2	B83744	two-component sens
447	25	67.6	186	2	AC3229	protein 6a [import	520	25	67.6	357	2	T01607	hypothetical prote
448	25	67.6	186	2	T29117	hypothetical prote	521	25	67.6	357	2	T13829	probable triacylg
449	25	67.6	187	2	T46287	hypothetical prote	522	25	67.6	359	2	JC4224	alpha-N-acetylneur
450	25	67.6	189	2	JC7107	development relate	523	25	67.6	362	2	T33502	hypothetical prote
451	25	67.6	190	2	C83087	conserved hypothet	524	25	67.6	362	2	G35937	probable murinap
452	25	67.6	199	2	S78540	inducible T-cell c	525	25	67.6	364	2	T05989	hypothetical prote
453	25	67.6	202	2	D85058	hypothetical prote	526	25	67.6	365	2	C72308	conserved hypothet
454	25	67.6	209	2	D59091	hypothetical prote	527	25	67.6	365	2	C90098	hypothetical prote
455	25	67.6	211	2	JC7353	fibroblast growth	528	25	67.6	370	1	OWASG	ornithine carbamoy
456	25	67.6	212	2	JC7511	fibroblast growth	529	25	67.6	370	2	S15013	wnt-1 protein - ze
457	25	67.6	214	2	AH0308	conserved hypothet	530	25	67.6	372	2	S32694	wnt-1 protein - Ca
458	25	67.6	218	1	A43522	23K integral membr	531	25	67.6	372	2	T44318	transposase homolo
459	25	67.6	222	2	S07280	para protein - Agr	532	25	67.6	375	2	T47973	hypothetical prote
460	25	67.6	224	2	AD1114	thiamin biosynthes	533	25	67.6	375	2	T19038	hypothetical prote
461	25	67.6	233	2	T09468	hypothetical prote	534	25	67.6	377	2	T34272	hypothetical prote
462	25	67.6	238	2	F90368	hypothetical prote	535	25	67.6	381	2	E59862	hypothetical prote
463	25	67.6	238	2	S73858	arginine deiminase	536	25	67.6	383	2	E50285	hypothetical prote
464	25	67.6	239	2	E97210	extracellular neut	537	25	67.6	387	2	JU0461	sarcosine oxidase
465	25	67.6	240	2	S61110	hypothetical prote	538	25	67.6	395	2	S36029	hypothetical prote
466	25	67.6	241	2	T05479	hypothetical prote	539	25	67.6	400	2	AD0604	D-alanyl-D-alanin
467	25	67.6	244	2	B90542	hypothetical prote	540	25	67.6	400	2	S76066	hypothetical prote

541	25	67.6	400	2	S31142	probable transposase	614	25	67.6	532	2	H83993	two-component sens
542	25	67.6	402	2	D90034	hypothetical prote	615	25	67.6	542	2	T01124	probable phosphate
543	25	67.6	402	2	B99514	hypothetical prote	616	25	67.6	542	2	T23869	hypothetical prote
544	25	67.6	405	2	A84007	hypothetical prote	617	25	67.6	542	2	B56205	transcription fact
545	25	67.6	406	2	JT0357	Rep protein - Clos	618	25	67.6	543	2	S29353	Photinus-luciferin
546	25	67.6	406	2	AC2007	transposase all160	619	25	67.6	543	2	S29352	Photinus-luciferin
547	25	67.6	406	2	A12497	transposase all1716	620	25	67.6	543	2	S29354	Photinus-luciferin
548	25	67.6	408	2	E72353	extracellular poly	621	25	67.6	543	2	S29355	Photinus-luciferin
549	25	67.6	409	2	I40489	hypothetical prote	622	25	67.6	550	2	A87050	arginyl-tRNA synth
550	25	67.6	409	2	G90481	dehydrogenase, pro	623	25	67.6	550	2	T21326	hypothetical prote
551	25	67.6	411	2	T17653	hypothetical prote	624	25	67.6	555	2	AE2398	phosphodiesterase/
552	25	67.6	412	2	T27202	hypothetical prote	625	25	67.6	556	2	D69676	extracellular neut
553	25	67.6	416	2	T14021	hypothetical prote	626	25	67.6	557	2	D97210	chromatin assembly
554	25	67.6	416	2	S22611	transcription fact	627	25	67.6	559	2	B56731	HD superfamily hyd
555	25	67.6	424	2	G96742	unknown protein Fl	628	25	67.6	560	2	B97005	env polypeptid
556	25	67.6	424	2	S13934	protein kinase (EC	629	25	67.6	563	1	VCWMV7	leucyl aminopeptid
557	25	67.6	426	2	A40440	endothelin 1 and 2	630	25	67.6	566	2	T07850	conserved hypotet
558	25	67.6	426	2	E96581	hypothetical prote	631	25	67.6	569	2	E90554	conserved hypotet
559	25	67.6	427	2	D82197	hypothetical prote	632	25	67.6	571	2	F70040	sulfite reductase
560	25	67.6	431	1	UKHU	u-plasminogen acti	633	25	67.6	571	2	T07849	leucyl aminopeptid
561	25	67.6	433	2	H83444	probable cytochrom	634	25	67.6	571	2	T07047	leucyl aminopeptid
562	25	67.6	433	2	S46668	MTH1 protein - yea	635	25	67.6	572	2	C86779	conserved hypotet
563	25	67.6	433	2	T17654	hypothetical prote	636	25	67.6	574	2	T29137	hypothetical prote
564	25	67.6	435	2	T45199	probable mrp prote	637	25	67.6	575	1	HNNZ39	hemagglutinin-neur
565	25	67.6	436	2	B84845	probable AP2 domai	638	25	67.6	575	1	HNNZSH	hemagglutinin-neur
566	25	67.6	439	2	T31124	hypothetical prote	639	25	67.6	575	1	HNNZSZ	hemagglutinin-neur
567	25	67.6	440	2	T19807	hypothetical prote	640	25	67.6	575	2	S14532	hemagglutinin-neur
568	25	67.6	445	2	T01214	hypothetical prote	641	25	67.6	575	2	A43487	hemagglutinin-neur
569	25	67.6	446	2	A55021	beta-cell E-box tr	642	25	67.6	575	2	S12135	hemagglutinin-neur
570	25	67.6	448	2	H86895	glucose-6-phosphat	643	25	67.6	576	1	HNNZS	hemagglutinin-neur
571	25	67.6	449	1	NURBSA	glucose-6-phosphat	644	25	67.6	579	2	A72367	oligopeptide ABC t
572	25	67.6	449	2	T51720	glucose-6-phosphat	645	25	67.6	586	2	A71136	acylase homolog 1m
573	25	67.6	449	2	D95242	glucose-6-phosphat	646	25	67.6	593	2	A55931	Munc18-2 - rat
574	25	67.6	449	2	G98106	glucose-6-phosphat	647	25	67.6	594	2	A57022	unc-18 protein hom
575	25	67.6	450	1	WZBEE4	49.2K membrane pro	648	25	67.6	594	2	A53455	unc-18 protein hom
576	25	67.6	450	2	H97229	glucose-6-phosphat	649	25	67.6	594	2	S39346	unc-18 protein hom
577	25	67.6	450	2	G84067	glucose-6-phosphat	650	25	67.6	594	2	S39345	hypothetical prote
578	25	67.6	450	2	AG1370	glucose-6-phosphat	651	25	67.6	594	2	S00961	hypothetical prote
579	25	67.6	450	2	AE1740	glucose-6-phosphat	652	25	67.6	595	2	T15862	rop protein - frui
580	25	67.6	450	2	S15675	globulin-2 precurs	653	25	67.6	597	2	S33578	hypothetical aeri
581	25	67.6	450	2	T42595	envelope protein 5	654	25	67.6	601	2	T37872	threonine-tRNA lig
582	25	67.6	450	2	T23528	hypothetical prote	655	25	67.6	612	2	G71972	threonine-tRNA lig
583	25	67.6	452	2	AH0708	PTS system, cellob	656	25	67.6	612	2	C84535	probable adenylate
584	25	67.6	457	2	T08861	hypothetical prote	657	25	67.6	614	2	C71320	hypothetical prote
585	25	67.6	461	2	T28006	hypothetical prote	658	25	67.6	615	2	H96620	hypothetical prote
586	25	67.6	462	2	D81251	NADH2 dehydrogenas	659	25	67.6	619	2	G71861	primosomal protein
587	25	67.6	463	2	H70922	hypothetical prote	660	25	67.6	619	2	C64568	primosomal protein
588	25	67.6	463	2	T16835	hypothetical prote	661	25	67.6	620	2	T21449	hypothetical prote
589	25	67.6	466	2	H64904	hypothetical prote	662	25	67.6	627	2	A02161	alkaline phosphata
590	25	67.6	466	2	D90893	hypothetical prote	663	25	67.6	629	2	S68986	transferrin - fles
591	25	67.6	466	2	E85724	hypothetical prote	664	25	67.6	632	2	B69310	mRNA 3'-end proces
592	25	67.6	470	2	AE2155	RNA-directed RNA p	665	25	67.6	636	2	A55428	ferroxidase precu
593	25	67.6	470	2	JN0431	RNA-directed RNA p	666	25	67.6	638	2	T43018	snA41 protein - fi
594	25	67.6	473	2	S53119	hypothetical prote	667	25	67.6	639	2	H86362	hypothetical prote
595	25	67.6	474	2	H84210	hypothetical prote	668	25	67.6	650	2	T22002	hypothetical prote
596	25	67.6	476	2	S64953	hypothetical prote	669	25	67.6	653	2	S35493	site-specific DNA-
597	25	67.6	490	2	I50708	basic helix-loop-h	670	25	67.6	657	2	B84791	hypothetical prote
598	25	67.6	491	2	A86824	sensor protein kin	671	25	67.6	666	2	E71565	probable glycogen
599	25	67.6	495	2	T05388	hypothetical prote	672	25	67.6	672	2	T37763	inner centromere p
600	25	67.6	500	2	G70104	hypothetical prote	673	25	67.6	676	2	S61977	transcription fact
601	25	67.6	501	2	A42030	alpha-globin trans	674	25	67.6	679	2	H36806	probable infected
602	25	67.6	502	2	A23547	keratin, type II c	675	25	67.6	680	2	T42923	infected cell prot
603	25	67.6	502	2	C56205	transcription fact	676	25	67.6	680	2	T03106	probable transport
604	25	67.6	502	2	B42030	alpha-globin trans	677	25	67.6	680	2	H90093	guanine nucleotide
605	25	67.6	504	2	A56205	transcription fact	678	25	67.6	682	2	A42121	transcription fact
606	25	67.6	504	2	I49257	NF2d9 - mouse	679	25	67.6	682	2	C45020	basic-helix-loop-h
607	25	67.6	507	2	A71622	hypothetical proté	680	25	67.6	682	2	F83228	hypothetical prote
608	25	67.6	513	2	C81736	60 kDa chaperonin,	681	25	67.6	682	2	T18847	hypothetical prote
609	25	67.6	518	2	T13652	hypothetical prote	682	25	67.6	687	2	T09994	arginine-tRNA liga
610	25	67.6	520	2	T41709	BRCT domain contai	683	25	67.6	697	2	H84508	hypothetical prote
611	25	67.6	522	2	H64060	apolipoprotein N-a	684	25	67.6	706	2	S19958	basic helix-loop-h
612	25	67.6	528	2	G70854	probable serA prot	685	25	67.6	706	2	A48084	SR11 protein kina
613	25	67.6	528	2	T45418	phosphoglycerate d	686	25	67.6	707	2	A46691	E-box-binding prot

687	25	67.6	708	2	S53411	hypothetical prote	760	25	67.6	1325	2	T25753	hypothetical prote
688	25	67.6	708	2	T25725	hypothetical prote	761	25	67.6	1338	2	T40933	protein kinase cek
689	25	67.6	711	2	A86424	unknown protein, 3	762	25	67.6	1339	2	A84683	probable SNF2 subf
690	25	67.6	714	2	G86844	hypothetical prote	763	25	67.6	1422	2	B71437	probable resistanc
691	25	67.6	715	2	S77439	hypothetical prote	764	25	67.6	1429	2	T13720	gene expanded prot
692	25	67.6	718	2	S64024	STT3 protein precu	765	25	67.6	1446	2	T13018	hypothetical prote
693	25	67.6	730	2	T16455	hypothetical prote	766	25	67.6	1472	2	S67195	probable membrane
694	25	67.6	735	2	AC1946	adenylate cyclase	767	25	67.6	1490	2	T20513	hypothetical prote
695	25	67.6	736	2	T00023	transcription fact	768	25	67.6	1517	2	T38912	hypothetical integ
696	25	67.6	742	2	H97302	ribonucleotide red	769	25	67.6	1553	2	T09361	hypothetical prote
697	25	67.6	744	2	A32905	plakoglobin, desmo	770	25	67.6	1556	2	S59393	probable membrane
698	25	67.6	754	2	G87767	protein mes-3 [imp	771	25	67.6	1644	2	P91286	hypothetical prote
699	25	67.6	754	2	S60464	mes-3 protein - Ca	772	25	67.6	1644	2	B86128	hypothetical prote
700	25	67.6	762	2	T01444	proteinase homolog	773	25	67.6	1648	2	S61654	probable membrane
701	25	67.6	763	2	AC1344	ribonucleoside-dip	774	25	67.6	1658	2	S55101	hypothetical prote
702	25	67.6	763	2	AG1714	ribonucleoside-dip	775	25	67.6	1690	2	S41467	hypothetical prote
703	25	67.6	767	2	T41344	probable zinc-fing	776	25	67.6	2179	1	GNNYH4	DNA-directed RNA p
704	25	67.6	773	2	I59351	carnitine O-palmit	777	25	67.6	2302	2	T14328	genome polypeptin
705	25	67.6	801	1	D70309	ribonucleoside-dip	778	25	67.6	2314	2	T28698	hypothetical prote
706	25	67.6	803	2	T40036	hypothetical prote	779	25	67.6	2336	2	S37077	genome polypeptin
707	25	67.6	830	2	C82710	ribonucleoside-dip	780	25	67.6	2473	1	S38040	i-phosphatidylinos
708	25	67.6	833	2	T28385	ORF MSV224 probabl	781	25	67.6	2524	2	A35844	Xotch protein - Af
709	25	67.6	839	2	S35319	nucleoporin-intera	782	25	67.6	2700	2	D88450	protein p21H11.2 [
710	25	67.6	847	2	D72860	viral capsid assoc	783	25	67.6	2708	2	T09079	probable chloroqui
711	25	67.6	887	2	A54832	villin homolog qua	784	25	67.6	2819	2	T09080	probable chloroqui
712	25	67.6	899	2	D96594	unknown protein, 7	785	25	67.6	3097	2	T28635	glutamate synthase
713	25	67.6	905	2	H71731	DNA gyrase chain A	786	25	67.6	3871	2	T22812	hypothetical prote
714	25	67.6	906	2	T23556	hypothetical prote	787	25	67.6	4550	2	T18440	hypothetical prote
715	25	67.6	915	2	D96617	probable xylan end	788	24	64.9	70	2	B33172	C-ORF-G protein -
716	25	67.6	917	2	T52467	hypothetical prote	789	24	64.9	73	2	D97088	probable membrane
717	25	67.6	918	2	G85545	protein F59B2.12 [	790	24	64.9	75	2	A38646	osteopontin-relate
718	25	67.6	919	1	RNVZCA	DNA-directed RNA p	791	24	64.9	78	2	C31976	hypothetical prote
719	25	67.6	919	1	T29581	hypothetical prote	792	24	64.9	79	2	G34510	homeotic protein H
720	25	67.6	928	1	S38001	probable serine/th	793	24	64.9	86	2	S15229	hypothetical prote
721	25	67.6	936	2	B64567	cytochrome c bioge	794	24	64.9	87	2	C84494	hypothetical prote
722	25	67.6	936	2	H71862	probable cytochrom	795	24	64.9	91	2	F42529	B-ORF-E protein -
723	25	67.6	943	2	S31132	hypothetical prote	796	24	64.9	92	2	F70213	hypothetical prote
724	25	67.6	952	2	E86147	TiN6.4 protein - A	797	24	64.9	93	2	H81994	hypothetical prote
725	25	67.6	958	2	AC0204	probable integral	798	24	64.9	93	2	C81783	hypothetical prote
726	25	67.6	962	2	AC0865	protease III precu	799	24	64.9	98	2	PH1067	Ig light chain V r
727	25	67.6	982	2	T19526	hypothetical prote	800	24	64.9	98	2	PH1066	Ig light chain V r
728	25	67.6	1009	2	S64734	retrovirus-relate	801	24	64.9	98	2	PH1061	Ig light chain V r
729	25	67.6	1014	2	A55260	cytotoxic necrotiz	802	24	64.9	100	2	S77030	hypothetical prote
730	25	67.6	1019	1	S29509	insulysin (EC 3.4.	803	24	64.9	105	2	T00597	hypothetical prote
731	25	67.6	1019	1	SNHUIN	insulysin (EC 3.4.	804	24	64.9	106	2	S03303	Ig kappa chain V r
732	25	67.6	1029	2	S36666	membrane-associate	805	24	64.9	106	2	G90356	Ig kappa chain V-J
733	25	67.6	1036	2	H64245	hypothetical prote	806	24	64.9	107	2	S09968	Ig kappa chain V-I
734	25	67.6	1046	2	S56026	hypothetical prote	807	24	64.9	108	1	K1HUOU	Ig kappa chain V-I
735	25	67.6	1052	2	T00067	hypothetical prote	808	24	64.9	109	2	D72602	hypothetical nucle
736	25	67.6	1056	1	G02157	kinesin-like spind	809	24	64.9	110	2	B48562	hypothetical prote
737	25	67.6	1060	1	A40264	kinesin-related pr	810	24	64.9	111	2	S84460	hypothetical prote
738	25	67.6	1061	2	A57620	steroid receptor c	811	24	64.9	113	1	S5BY1E	ribosomal protein
739	25	67.6	1063	2	T03743	bifocal protein -	812	24	64.9	113	2	S55962	ribosomal protein
740	25	67.6	1067	2	S33417	kinesin-like prote	813	24	64.9	114	2	A84618	hypothetical prote
741	25	67.6	1068	2	T42382	guanylate cyclase	814	24	64.9	115	2	B71141	hypothetical prote
742	25	67.6	1073	2	F89467	protein R09H3.1 [i	815	24	64.9	115	2	B26667	hit-like protein (
743	25	67.6	1102	2	JH0717	guanylate cyclase	816	24	64.9	116	2	H90512	hypothetical prote
744	25	67.6	1103	2	JCS581	guanylate cyclase	817	24	64.9	117	2	S03364	hypothetical prote
745	25	67.6	1108	2	AH1633	DNA polymerase III	818	24	64.9	117	2	T13210	minor capsid prote
746	25	67.6	1108	2	I59385	guanylate cyclase	819	24	64.9	119	2	PQ0067	T-cell receptor be
747	25	67.6	1108	2	A55915	guanylate cyclase	820	24	64.9	119	2	E84580	60S ribosomal prot
748	25	67.6	1108	2	B55915	guanylate cyclase	821	24	64.9	119	2	T06007	ribosomal protein
749	25	67.6	1110	1	S55279	G protein-coupled	822	24	64.9	120	2	F71115	vsar protein - Sal
750	25	67.6	1115	2	S40241	Eph receptor tyros	823	24	64.9	120	2	F71115	hypothetical prote
751	25	67.6	1122	2	T42400	probable amine tra	824	24	64.9	122	2	S08039	hypothetical prote
752	25	67.6	1138	2	H71615	hypothetical prote	825	24	64.9	123	2	T46307	thioredoxin (impor
753	25	67.6	1141	2	T23185	luk6 protein kinase	826	24	64.9	130	2	C87136	hypothetical prote
754	25	67.6	1150	2	T13824	calcium-activated	827	24	64.9	132	2	G97768	finger protein (cl
755	25	67.6	1162	2	T49191	hypothetical prote	828	24	64.9	136	2	S06571	hypothetical prote
756	25	67.6	1184	2	I49017	calcium-activated	829	24	64.9	140	2	S73701	hypothetical prote
757	25	67.6	1188	2	S50434	hypothetical prote	830	24	64.9	141	2	A34043	hypothetical prote
758	25	67.6	1224	2	E71611	hypothetical prote	831	24	64.9	143	2	S68226	growth-blocking pe
759	25	67.6	1252	2	D71810	probable type II D	832	24	64.9	144	2	S34150	Ig mu chain - axol

833	24	64.9	145	2	A96817	P9K20.17 (imported	906	24	64.9	280	2	T48434	hypothetical prote
834	24	64.9	145	2	A12869	NTP pyrophosphohyd	907	24	64.9	282	2	T03906	cytochrome B561 ho
835	24	64.9	147	2	C97646	hypothetical prote	908	24	64.9	283	2	T15659	hypothetical prote
836	24	64.9	148	2	F84758	hypothetical prote	909	24	64.9	284	2	B90190	conserved hypothet
837	24	64.9	150	2	A69289	conserved hypothet	910	24	64.9	285	2	F65035	hypothetical prote
838	24	64.9	151	2	AF2103	hypothetical prote	911	24	64.9	285	2	G81059	probable enzyme (f
839	24	64.9	154	2	T19903	hypothetical prote	912	24	64.9	285	2	G85903	probable enzyme yf
840	24	64.9	154	2	T18808	hypothetical prote	913	24	64.9	285	2	T26325	hypothetical prote
841	24	64.9	160	2	E72529	hypothetical prote	914	24	64.9	287	2	S12738	T-cell alloantigen
842	24	64.9	161	2	AE0357	conserved hypothet	915	24	64.9	291	2	S66770	probable membrane
843	24	64.9	167	2	AH0747	ferritin-like prot	916	24	64.9	291	2	S75654	hypothetical prote
844	24	64.9	167	2	G85803	ferritin-like prot	917	24	64.9	293	1	RGY554	translation activa
845	24	64.9	167	2	B90955	ferritin-like prot	918	24	64.9	293	2	AH1221	ethanolamine ammon
846	24	64.9	167	2	F64953	ferritin-like prot	919	24	64.9	293	2	AC1575	probable transmembr
847	24	64.9	168	2	AE0175	probable cell divi	920	24	64.9	295	2	C81369	hypothetical prote
848	24	64.9	169	2	AE0217	ferritin (imported	921	24	64.9	295	2	T23989	hypothetical prote
849	24	64.9	172	2	T38708	hypothetical prote	922	24	64.9	297	2	AG0143	probable lyase-fam1
850	24	64.9	175	2	A17680	cytochrome C (cyto	923	24	64.9	297	2	AB2879	hypothetical prote
851	24	64.9	176	2	AH0781	trypsin inhibitor	924	24	64.9	298	2	S45898	probable membrane
852	24	64.9	176	2	D72668	hypothetical prote	925	24	64.9	298	2	P82532	isopentenyl monoph
853	24	64.9	178	1	TVRTBM	transforming prote	926	24	64.9	299	2	B92623	aspartate carbamoy
854	24	64.9	180	2	AC2198	hypothetical prote	927	24	64.9	299	2	F96828	hypothetical prote
855	24	64.9	182	2	A64121	nonheme ferritin h	928	24	64.9	300	1	D64823	ribosomal protein
856	24	64.9	182	2	AC0545	hypothetical prote	929	24	64.9	300	2	H85595	ribosomal protein
857	24	64.9	186	2	T07977	protoporphyrin IX	930	24	64.9	300	2	AH0605	ribosomal protein
858	24	64.9	193	2	T40922	hypothetical prote	931	24	64.9	300	2	D90745	ribosomal protein
859	24	64.9	194	2	B87442	orotate phosphorib	932	24	64.9	301	2	H70890	hypothetical prote
860	24	64.9	196	2	T49023	hypothetical prote	933	24	64.9	301	2	D82997	ribosomal protein
861	24	64.9	196	2	S54050	hypothetical prote	934	24	64.9	301	2	E82096	ribosomal protein
862	24	64.9	197	2	S23240	hypothetical prote	935	24	64.9	303	2	T17774	hypothetical prote
863	24	64.9	201	2	JC5562	trypsin inhibitor	936	24	64.9	305	2	H86245	bifunctional nucle
864	24	64.9	202	2	D63342	hypothetical prote	937	24	64.9	308	2	AC1867	hypothetical prote
865	24	64.9	203	2	T06277	MADS box protein A	938	24	64.9	309	2	D97126	tRNA Delta(2)-isop
866	24	64.9	204	2	T32902	hypothetical prote	939	24	64.9	310	2	B47050	glut 3'-region hyp
867	24	64.9	206	2	AF0498	hypothetical prote	940	24	64.9	312	2	D97655	hemin-binding per1
868	24	64.9	207	2	G97226	uncharacterized me	941	24	64.9	314	2	T15045	spermidine synthas
869	24	64.9	209	2	S47068	finger protein H2F	942	24	64.9	314	2	E72287	hypothetical prote
870	24	64.9	215	2	H81314	probable leucyl/ph	943	24	64.9	316	2	T08694	hypothetical prote
871	24	64.9	216	2	D86564	yagB family (impor	944	24	64.9	317	2	T20302	hypothetical prote
872	24	64.9	216	2	G72060	yage family - Chla	945	24	64.9	317	2	T42645	hypothetical prote
873	24	64.9	217	2	A19506	alpha-amylase (EC	946	24	64.9	317	2	E95922	probable glycosylc
874	24	64.9	222	2	I39192	gene HOXA1 protein	947	24	64.9	319	2	S59416	hypothetical prote
875	24	64.9	225	2	A86462	AIIG1-like protein,	948	24	64.9	321	1	D69112	2-phosphoglycerate
876	24	64.9	227	2	D84943	hypothetical protei	949	24	64.9	321	2	H89869	transcription regu
877	24	64.9	233	2	E89976	conserved hypothet	950	24	64.9	321	2	T42591	gene 48 protein -
878	24	64.9	236	2	C81253	probable peptide A	951	24	64.9	321	2	D97836	tetraacyl-disacchar
879	24	64.9	236	2	A70808	hypothetical prote	952	24	64.9	321	2	H71924	hypothetical prote
880	24	64.9	240	2	T02180	probable aquamosa-	953	24	64.9	321	2	B64589	hypothetical prote
881	24	64.9	243	2	F63725	tRNA methyltransfe	954	24	64.9	321	2	T24773	hypothetical prote
882	24	64.9	244	2	T04700	hypothetical prote	955	24	64.9	322	2	E89496	porphobilinogen sy
883	24	64.9	245	2	AD2205	hypothetical prote	956	24	64.9	322	2	T07724	hypothetical prote
884	24	64.9	248	2	A44547	receptor tyrosine	957	24	64.9	323	2	A44504	suhk protein - Rhl
885	24	64.9	250	2	D69470	conserved hypothet	958	24	64.9	323	2	T04826	hypothetical prote
886	24	64.9	251	1	QCQVP2	coat protein - pot	959	24	64.9	324	2	G81330	probable phosphata
887	24	64.9	251	2	AD1131	hypothetical prote	960	24	64.9	325	2	A97482	hypothetical prote
888	24	64.9	253	2	C81670	undecaprenyl pyrop	961	24	64.9	325	2	A12699	conserved hypothet
889	24	64.9	253	2	A90558	hypothetical prote	962	24	64.9	326	1	S74570	alkaline phosphata
890	24	64.9	254	2	T45264	cobalt transport p	963	24	64.9	326	2	G89835	conserved hypothet
891	24	64.9	256	2	T25707	hypothetical prote	964	24	64.9	329	2	G81299	phosphoribosylform
892	24	64.9	260	1	CRH01D	carbonate dehydrat	965	24	64.9	329	2	T18622	hypothetical prote
893	24	64.9	261	1	CRH01	carbonate dehydrat	966	24	64.9	330	2	T22293	hypothetical prote
894	24	64.9	261	2	JN08336	carbonate dehydrat	967	24	64.9	333	1	DEMSG	glyceraldehyde-3-p
895	24	64.9	261	2	JN08335	carbonate dehydrat	968	24	64.9	333	1	DEMTG	glyceraldehyde-3-p
896	24	64.9	261	2	B86643	carbonyl reductase	969	24	64.9	333	2	F85035	hypothetical prote
897	24	64.9	264	2	A81668	conserved hypothet	970	24	64.9	334	2	I39843	iron-uptake system
898	24	64.9	264	2	E71509	hypothetical prote	971	24	64.9	335	2	S58997	NAH2 dehydrogenas
899	24	64.9	265	2	T15486	hypothetical prote	972	24	64.9	335	2	B71693	integrase/recombin
900	24	64.9	268	2	AD2377	ATP-binding protei	973	24	64.9	335	2	T39033	hypothetical prote
901	24	64.9	268	2	T06020	hypothetical prote	974	24	64.9	335	2	S35542	replication-associ
902	24	64.9	278	2	T00923	hypothetical prote	975	24	64.9	335	2	G01448	homeobox protein H
903	24	64.9	278	1	DCS70S	orotidine-5'-phosp	976	24	64.9	337	1	D5SKG	glyceraldehyde-3-p
904	24	64.9	279	2	T37216	beta-galactoside-b	977	24	64.9	338	2	S50339	NAH2 dehydrogenas
905	24	64.9	280	2	S73916	MG103 homolog K04_	978	24	64.9	338	2	F71690	hypothetical prote



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979      24      64.9      340      2      G69628      glyceraldhyde-3-p
980      24      64.9      341      2      AS7136      class I histocomp
981      24      64.9      342      2      T27410      hypothetical prote
982      24      64.9      343      2      T27410      phosphoribosylform
983      24      64.9      344      1      AJBSCL      D-alanine-D-alanin
984      24      64.9      347      2      B64612      D-alanine-D-alanin
985      24      64.9      347      2      A71903      hypothetical prote
986      24      64.9      349      2      T18981      hypothetical prote
987      24      64.9      349      2      T30952      hypothetical prote
988      24      64.9      350      2      S07222      outer membrane pro
989      24      64.9      351      2      JCS904      major capsid prote
990      24      64.9      352      2      S37873      hypothetical prote
991      24      64.9      356      2      E90013      conserved hypothet
992      24      64.9      359      1      A31425      uracil-DNA glycosy
993      24      64.9      360      2      D71888      lipid-a-disacchari
994      24      64.9      360      2      A56066      basic helix-loop-h
995      24      64.9      361      2      F97068      histidinol-phospha
996      24      64.9      364      2      H87184      5'-phosphoribosyl-
997      24      64.9      364      2      A70809      probable 5'-phosph
998      24      64.9      364      2      A81331      probable pyridoxal
999      24      64.9      367      2      C93590      TPA-induced protei
1000     24      64.9      367      2      F64022      hypothetical prote
1000     24      64.9      368      1      G75058      probable hexosyltr

ALIGNMENTS

RESULT 1
T30122
hypothetical protein F22H10.6 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T30122
R:Langston, Y.; Hawkins, J.
submitted to the EMBL Data Library, September 1996
A:Description: The sequence of C. elegans cosmid F22H10.
A:Reference number: 220740
A:Accession: T30122
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-219 <LAN>
A:Cross-references: UNIPROT:Q94192; UNIPARC:UPI000007A670; EMBL:U70845; PIDN: AAB09103.1;
A:Experimental source: strain Bristol N2; clone F22H10
C:Genetics:
A:Gene: CESP:F22H10.6
A:Map position: X
A:Introns: 47/1; 67/1; 107/3; 135/3

Query Match      89.2%; Score 33; DB 2; Length 219;
Best Local Similarity 85.7%; Pred. No. 11;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 YSSNLHS 7
      :|||||
Db      22 FSSNLHS 28

RESULT 2
G86895
hypothetical protein yweB [imported] - Lactococcus lactis subsp. lactis (strain IL1403)
C:Species: Lactococcus lactis subsp. lactis
C>Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
C:Accession: G86895
R:Boletini, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarms, K.; Weissensbach, J.; Ehrlich
Genome Res. 11, 731-753, 2001
A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis se
A:Reference number: A86625; MUID:21235186; PMID:11337471
A:Accession: G86895
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-368 <STO>
A:Cross-references: UNIPROT:O9CD01; UNIPARC:UPI00000D4EBC; GB:AE005176; PID:g1272528; F
A:Experimental source: strain IL1403
```

```
C:Genetics:
A:Gene: yweB

Query Match      89.2%; Score 33; DB 2; Length 368;
Best Local Similarity 85.7%; Pred. No. 19;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 YSSNLHS 7
      :|||||
Db      121 FSSNLHS 127

RESULT 3
S61447
cellulase (EC 3.2.1.4) CX3 - pepper (fragment)
C:Species: Capsicum annuum (pepper)
C>Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
C:Accession: S61447
R:Ferrarese, L.; Trainotti, L.; Moretto, P.; Polverino de Laureto, P.; Rascio, N.; Casad
Plant Mol. Biol. 29, 735-747, 1995
A:Title: Differential ethylene-inducible expression of cellulase in pepper plants.
A:Reference number: S61445; MUID:96128016; PMID:8541500
A:Accession: S61447
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-324 <FER>
A:Cross-references: UNIPROT:Q43751; UNIPARC:UPI0000179794; EMBL:X83711
C:Superfamily: Arabidopsis membrane-anchored cellulase KOR
C:Keywords: glycosidase; hydrolase

Query Match      86.5%; Score 33; DB 2; Length 324;
Best Local Similarity 85.7%; Pred. No. 28;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 YSSNLHS 7
      :|||||
Db      144 YSSSLHS 150

RESULT 4
T06350
cellulase (EC 3.2.1.4) Cel2 precursor - tomato
N:Alternate names: endo-1,4-beta-glucanase
C:Species: Lycopersicon esculentum (tomato)
C>Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 09-Jul-2004
C:Accession: T06350
R:Laehbrook, C.C.; Gonzalez-Bosch, C.; Bennett, A.B.
Plant Cell 6, 1485-1493, 1994
A:Title: Two divergent endo-beta-1,4-glucanase genes exhibit overlapping expression in r
A:Reference number: Z15614; MUID:95086382; PMID:7994180
A:Accession: T06350
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-489 <LAS>
A:Cross-references: UNIPROT:Q42872; UNIPARC:UPI000009DCDA; EMBL:U13055; NID:g531904; PID
A:Experimental source: strain Castlemart; tissue-type pericarp
C:Genetics:
A:Gene: Cel2
C:Function:
A:Description: hydrolysis of 1,4-beta-D-glucosidic linkages in beta-D-glucans such as ce
A:Pathway: cellulose degradation
C:Superfamily: Arabidopsis membrane-anchored cellulase KOR
C:Keywords: glycosidase; hydrolase; polysaccharide degradation
F:1-23/Domain: signal sequence #status predicted <Sig>
F:24-489/Product: cellulase 2 #status predicted <Mat>

Query Match      86.5%; Score 32; DB 2; Length 489;
Best Local Similarity 85.7%; Pred. No. 43;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 YSSNLHS 7
      :|||||
Db      216 YSSSLHS 222
```



RESULT 5  
A48677

Ig kappa chain V-J region (48) - mouse (fragment)  
 A:Species: Mus musculus (house mouse)  
 C:Date: 19-May-1994 #sequence\_revision 19-May-1994 #text\_change 21-Jan-2000  
 C:Accession: A48677  
 R:Rasignion, J.; Brait, M.; Jamila, I.; Urbain, J.; Gottlieb, P.; Brown, A.; Hasemann, C.  
 Proc. Natl. Acad. Sci. U.S.A. 90, 9508-9512, 1993  
 A:Title: Molecular characterization of monoclonal CRI-A-positive anti-arsonate antibodies  
 A:Reference number: A48677; MUID:94022404; PMID:8415731  
 A:Accession: A48677  
 A:Status: preliminary; not compared with conceptual translation  
 A:Molecule type: mRNA  
 A:Residues: 1-107 <TAS>  
 A:Cross-references: UNIPARC:UPI0000176CB8  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: immunoglobulin  
 F16-90/Domain: immunoglobulin homology <IMM>

Query Match 83.8%; Score 31; DB 2; Length 107;  
 Best Local Similarity 85.7%; Pred. No. 14;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSNLHS 7  
 ||| |||  
 DB 50 YSSRLHS 56

RESULT 6  
A81198

conserved hypothetical protein NMB0455 [imported] - Neisseria meningitidis (strain MC58  
 C:Species: Neisseria meningitidis  
 C:Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 09-Jul-2004  
 C:Accession: A81198  
 R:Tetelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.  
 Hickey, E.K.; Haft, D.H.; Salzberg, S.B.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;  
 xi, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masiugnani, V.; Pizzza, M.  
 Science 287, 1809-1815, 2000  
 A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve  
 A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.  
 A:Reference number: A81000; MUID:20175755; PMID:10710307  
 A:Accession: A81198  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-380 <TET>  
 A:Cross-references: UNIPROT:Q9K0V4; UNIPARC:UPI00000C44B6; GB:AE002401; GB:AE002098; NID  
 A:Experimental source: serogroup B, strain MC58  
 C:Genetics:  
 A:Gene: NMB0455  
 C:Superfamily: Bacillus conserved hypothetical protein ypsc

Query Match 83.8%; Score 31; DB 2; Length 380;  
 Best Local Similarity 71.4%; Pred. No. 54;  
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLHS 7  
 ||| |||  
 DB 48 YAANLHS 54

RESULT 7  
A81833

conserved hypothetical protein NMA2030 [imported] - Neisseria meningitidis (strain Z2491  
 C:Species: Neisseria meningitidis  
 C:Date: 05-May-2000 #sequence\_revision 05-May-2000 #text\_change 09-Jul-2004  
 C:Accession: A81833  
 R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel  
 i; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,  
 Nature 404, 502-506, 2000  
 A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.  
 A:Reference number: A81775; MUID:20222556; PMID:10761919

A:Accession: A81833  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-380 <PAR>  
 A:Cross-references: UNIPROT:Q9R0W4; UNIPARC:UPI00000C2213; GB:AL162757; GB:AL157959; NID  
 A:Experimental source: serogroup A, strain Z2491  
 C:Genetics:  
 A:Gene: NMA2030  
 C:Superfamily: Bacillus conserved hypothetical protein ypsC

Query Match 83.8%; Score 31; DB 2; Length 380;  
 Best Local Similarity 71.4%; Pred. No. 54;  
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLHS 7  
 ||| |||  
 DB 48 YAANLHS 54

RESULT 8  
AF0777

probable transcription regulator STY2390 [imported] - Salmonella enterica subsp. enteric  
 C:Species: Salmonella enterica subsp. enterica serovar Typhi  
 A:Note: this species has also been called Salmonella typhi  
 C:Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 18-Nov-2002  
 C:Accession: AF0777  
 R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,  
 th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,  
 . S.; Moule, S.; O'Gaora, P.  
 Nature 413, 848-852, 2001  
 A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;  
 A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov  
 A:Reference number: AB0502; MUID:21534947; PMID:11677608  
 A:Accession: AF0777  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-243 <PAR>  
 A:Cross-references: UNIPARC:UPI00000598F1; GB:AL513382; PIDN:CAD02540.1; PID:g16503401;  
 C:Genetics:  
 A:Gene: STY2390  
 C:Superfamily: probable transcription regulator ycgE

Query Match 81.1%; Score 30; DB 2; Length 243;  
 Best Local Similarity 100.0%; Pred. No. 55;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SSNLHS 7  
 ||| |||  
 DB 94 SSNLHS 99

RESULT 9  
AI2054

hypothetical protein all1991 [imported] - Nostoc sp. (strain PCC 7120)  
 C:Species: Nostoc sp. PCC 7120  
 A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120  
 C:Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 09-Jul-2004  
 C:Accession: AI2054  
 R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi  
 Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S  
 DNA Res. 8, 205-213, 2001  
 A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana  
 A:Reference number: AB1807; MUID:21595285; PMID:11759840  
 A:Accession: AI2054  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-290 <KUR>  
 A:Cross-references: UNIPROT:Q8YV17; UNIPARC:UPI00000CE29D; GB:BA000019; PIDN:BA073690.1;  
 A:Experimental source: strain PCC 7120  
 C:Genetics:  
 A:Gene: all1991

Query Match 81.1%; Score 30; DB 2; Length 290;

Best Local Similarity 83.3%; Pred. No. 67;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSSNLH 6  
Db 190 YSSNLH 195  
||:||||

RESULT 10  
T48439  
probable RNA-binding protein - Arabidopsis thaliana  
N:Alternate names: protein T32M21.30  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 09-Jul-2004  
C:Accession: T48439  
R:Bevan, M.; Terry, N.; Ardiles, W.; Buysshaert, C.; Dasseville, R.; De Clerck, R.; De  
ewes, H.W.; Rudd, S.; Lemcke, K.; Mayer, K.F.X.  
submitted to the Protein Sequence Database, March 2000  
A:Reference number: Z24487  
A:Accession: T48439  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-313 <BEV>  
A:Cross-references: UNIPROT:Q9L282; UNIPARC:UPI00000AC0F2; EMBL:AL162875  
A:Experimental source: cultivar Columbia; BAC clone T32M21  
C:Genetics:  
A:Map position: 5  
A:Introns: 29/1; 108/3; 144/2; 209/1; 229/3; 261/3; 282/2  
A:Note: T32M21.30

Query Match 81.1%; Score 30; DB 2; Length 313;  
Best Local Similarity 71.4%; Pred. No. 73;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YSSNLH 7  
Db 197 YSQNVHS 203  
||:||||

RESULT 11  
S72617  
alcohol dehydrogenase homolog bli-4 [imported] - Neurospora crassa  
N:Alternate names: protein B24M22.250  
C:Species: Neurospora crassa  
C:Date: 24-Jul-1998 #sequence\_revision 24-Jul-1998 #text\_change 09-Jul-2004  
C:Accession: S72617; T51229  
R:Bruchez, J.J.P.; Eberle, J.; Kohler, W.; Kruft, V.; Radford, A.; Russo, V.E.A.  
Mol. Gen. Genet. 252, 223-229, 1996  
A:Title: bli-4, a gene that is rapidly induced by blue light, encodes a novel mitochondr  
A:Reference number: S72617; MUID:96439828; PMID:8842141  
A:Accession: S72617  
A:Molecule type: mRNA  
A:Residues: 1-412 <BRU>  
A:Cross-references: UNIPROT:Q2247; UNIPARC:UPI00001269F2; EMBL:g1620434; PI  
A:Experimental source: mycelium, strain Sca  
C:Genetics: BRU1  
R:Schulte, U.; Aign, V.; Hohisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura,  
submitted to the Protein Sequence Database, July 2000  
A:Reference number: Z25286  
A:Accession: T51229  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-412 <SCH>  
A:Cross-references: UNIPARC:UPI00001269F2; EMBL:AL390354; PIDN:CAB99393.1; GSPDB:GN00116  
A:Experimental source: strain OR74A  
C:Genetics: SCH1  
A:Gene: bli-4  
A:Map position: II  
C:Genetics: <SCH1>  
A:Gene: B24M22.250  
A:Map position: 6  
A:Introns: 67/3; 320/2

C:Function:  
A:Description: may play a role as an (NAD+)-dependent alcohol dehydrogenase in mitochondrion  
A:Note: induced by blue light  
C:Keywords: mitochondrion

Query Match 81.1%; Score 30; DB 2; Length 412;  
Best Local Similarity 100.0%; Pred. No. 98;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SSNLHS 7  
Db 240 SSNLHS 245  
|||||

RESULT 12  
C86247  
hypothetical protein [imported] - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004  
C:Accession: C86247  
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,  
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Dewar, K.;  
ansen, N.F.; Hughes, B.; Huizar, L.  
Nature 408, 816-820, 2000  
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.;  
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,  
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,  
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A:Reference number: A86141; MUID:21016719; PMID:11130712  
A:Accession: C86247  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-424 <STO>  
A:Cross-references: UNIPROT:Q9SXB7; UNIPARC:UPI000000C716; GB:AE005172; NID:G5734725; PI  
C:Genetics:  
A:Map position: 1

Query Match 81.1%; Score 30; DB 2; Length 424;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SSNLHS 7  
Db 277 SSNLHS 282  
|||||

RESULT 13  
T23954  
hypothetical protein R06B9.1 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 31-Dec-2004  
C:Accession: T23954  
R:Baynes, C.  
submitted to the EMBL Data Library, December 1996  
A:Reference number: Z19823  
A:Accession: T23954  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-427 <WIL>  
A:Cross-references: UNIPROT:O17981; UNIPARC:UPI000000CF3B; EMBL:Z83237; PIDN:CAB05786.1;  
A:Experimental source: clone R06B9  
C:Genetics:  
A:Gene: CESP:R06B9.1  
A:Map position: 2  
A:Introns: 62/2; 97/3; 156/1; 380/1

Query Match 81.1%; Score 30; DB 2; Length 427;  
Best Local Similarity 83.3%; Pred. No. 1e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSSNLH 6

Db 77 YSSNVH 82  
 |||||:  
 RESULT 14  
 F97296  
 UDP-N-acetylmuramate-alanine ligase [imported] - Clostridium acetobutylicum  
 C:Species: Clostridium acetobutylicum  
 C:Date: 14-Sep-2001 #sequence\_revision 14-Sep-2001 #text\_change 09-Jul-2004  
 C:Accession: F97296  
 R:Noelling, J.; Bretton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,  
 ; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.  
 J. Bacteriol. 183, 4823-4838, 2001  
 A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo  
 A:Reference number: A96900; MUID:21359325; PMID:21359325  
 A:Accession: F97296  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-458 <KUR>  
 A:CROSS-references: UNIPROT:Q97E89; UNIPARC:UPI000012F959; GB:AE001437; PIDN:AAK81161.1;  
 A:Experimental source: Clostridium acetobutylicum ATCC824  
 C:Genetics:  
 A:Gene: CAC3225  
 C:Superfamily: UDP-N-acetylmuramate-alanine ligase  
 Query Match 81.1%; Score 30; DB 2; Length 458;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 SSNLHS 7  
 |||||  
 Db 417 SSNLHS 422  
 |||||  
 RESULT 15  
 AF2847  
 two component sensor kinase envZ [imported] - Agrobacterium tumefaciens (strain C58, Dup  
 C:Species: Agrobacterium tumefaciens  
 C:Date: 11-Jan-2002 #sequence\_revision 11-Jan-2002 #text\_change 09-Jul-2004  
 C:Accession: AF2847  
 R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I  
 erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClell  
 ; Karp, P.; Romero, P.; Zhang, S.  
 Science 294, 2317-2323, 2001  
 A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,  
 ster, E.W.  
 A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.  
 A:Reference number: AB2577; MUID:21608550; PMID:11743193  
 A:Accession: AF2847  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-459 <KUR>  
 A:CROSS-references: UNIPROT:Q8UDC0; UNIPARC:UPI00000D1E04; GB:AE008688; PIDN:AAL43196.1;  
 A:Experimental source: strain C58 (Dupont)  
 C:Genetics:  
 A:Gene: envZ  
 A:Map position: circular chromosome  
 Query Match 81.1%; Score 30; DB 2; Length 459;  
 Best Local Similarity 83.3%; Pred. No. 1.1e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YSSNLH 6  
 |||||  
 Db 371 YASNLH 376  
 |||||  
 RESULT 16  
 E97624  
 osmolarity sensor protein envZ (envZ) rp426 [imported] - Agrobacterium tumefaciens (stra  
 C:Species: Agrobacterium tumefaciens  
 C:Date: 30-Sep-2001 #sequence\_revision 30-Sep-2001 #text\_change 09-Jul-2004  
 C:Accession: E97624

R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quorollo, B.; Goldman,  
 A.; Liu, F.; Wollam, C.; Allinger, M.; Dougherty, D.; Scott, C.; Lappas, C.; Markeltz, B.,  
 Science 294, 2323-2328, 2001  
 A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum  
 A:Reference number: A97359; MUID:21608551; PMID:11743194  
 A:Accession: E97624  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-459 <KUR>  
 A:CROSS-references: UNIPROT:Q8UDC0; UNIPARC:UPI00000D1E04; GB:AE007869; PIDN:AAK87950.1;  
 C:Genetics:  
 A:Gene: AGR\_C 4011  
 A:Map position: circular chromosome  
 Query Match 81.1%; Score 30; DB 2; Length 459;  
 Best Local Similarity 83.3%; Pred. No. 1.1e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YSSNLH 6  
 |||||  
 Db 371 YASNLH 376  
 |||||  
 RESULT 17  
 AD2532  
 hypothetical protein alr7543 [imported] - Nostoc sp. (strain PCC 7120) plasmid pCC7120bse  
 C:Species: Nostoc sp. PCC 7120  
 A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120  
 C:Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 09-Jul-2004  
 C:Accession: AD2532  
 R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi  
 Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.  
 DNA Res. 8, 205-213, 2001  
 A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana  
 A:Reference number: AB1807; MUID:21595285; PMID:11759840  
 A:Accession: AD2532  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-472 <KUR>  
 A:CROSS-references: UNIPROT:Q8ZSG7; UNIPARC:UPI00000CCD6C; GB:AP003602; PIDN:BA877186.1;  
 A:Experimental source: strain PCC 7120  
 C:Genetics:  
 A:Gene: alr7543  
 A:Genome: plasmid  
 Query Match 81.1%; Score 30; DB 2; Length 472;  
 Best Local Similarity 83.3%; Pred. No. 1.1e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YSSNLH 6  
 |||||  
 Db 170 YSTNLH 175  
 |||||  
 RESULT 18  
 T17257  
 hypothetical protein DKFZp586P1422.1 - human  
 C:Species: Homo sapiens (man)  
 C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
 C:Accession: T17257  
 R:Koshner, K.; Beyer, A.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.  
 submitted to the Protein Sequence Database, September 1999  
 A:Reference number: Z18722  
 A:Accession: T17257  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-816 <KOE>  
 A:CROSS-references: UNIPROT:Q9UFT2; UNIPARC:UPI0000070259; EMBL:AL117472  
 A:Experimental source: adult uterus; clone DKFZp586P1422  
 C:Genetics:  
 A:Note: DKFZp586P1422.1  
 Query Match 81.1%; Score 30; DB 2; Length 816;

Best Local Similarity 71.4%; Pred. No. 2e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSNLHS 7  
|||||  
Db 492 YSSNFEHA 498

RESULT 19  
B83136  
evolved beta-D-galactosidase usher protein PA4084 [imported] - Pseudomonas aeruginosa (B83136)  
C:Species: Pseudomonas aeruginosa  
C:Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 09-Jul-2004  
C:Accession: B83136  
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warriner, P.; Hickey, M.J.; Boman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V.  
Nature 406, 959-964, 2000  
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen  
A:Reference number: A82950; MUID:20437337; PMID:10984043  
A:Accession: B83136  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-844 <STO>  
A:Cross-references: UNIPROT:Q9HWU4; UNIPARC:UPI00000C5BFE; GB:AE0040824; GB:AE004091; NID:10984043  
A:Experimental source: strain PA01  
C:Genetics:  
A:Gene: PA4084  
C:Superfamily: outer membrane usher protein f1mD

Query Match 81.1%; Score 30; DB 2; Length 844;  
Best Local Similarity 83.3%; Pred. No. 2.1e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLH 6  
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Db 169 YNSNLH 174

RESULT 20  
GBCE  
beta-galactosidase (EC 3.2.1.23) alpha chain - Escherichia coli (strain K-12)  
N:Alternate names: beta-D-galactoside galactohydrolase; lactase; phospho-beta-D-galactose  
C:Species: Escherichia coli  
C:Date: 30-Sep-1987 #sequence\_revision 05-Dec-1997 #text\_change 09-Jul-2004  
C:Accession: A65096; A25751; S09206  
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cohen, A.; Rose, D.J.; Mau, B.; Shao, Y.  
Science 277, 1453-1462, 1997  
A:Title: The complete genome sequence of Escherichia coli K-12.  
A:Reference number: A64720; MUID:97426617; PMID:9278503  
A:Accession: A65096  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-1042 <BLAT>  
A:Cross-references: UNIPROT:P06864; UNIPROT:Q471170; UNIPARC:UPI000016818E; GB:AE000389; A:Experimental source: strain K-12, substrain MG1655  
R:Stokes, H.W.; Betts, P.W.; Hall, B.G.  
Mol. Biol. Evol. 2, 469-477, 1985  
A:Title: Sequence of the ebgA gene of Escherichia coli: comparison with the lacZ gene.  
A:Reference number: A93056; MUID:88216133; PMID:3939707  
A:Accession: A25751  
A:Molecule type: DNA  
A:Residues: 80-476,'R', 478-651,'S', 653-660,'P', 662-674,'CRSWTPAKRS', 685-724,'KCA5V', 730-739,'R', 740-749,'R', 750-759,'R', 760-769,'R', 770-779,'R', 780-789,'R', 790-799,'R', 800-809,'R', 810-819,'R', 820-829,'R', 830-839,'R', 840-849,'R', 850-859,'R', 860-869,'R', 870-879,'R', 880-889,'R', 890-899,'R', 900-909,'R', 910-919,'R', 920-929,'R', 930-939,'R', 940-949,'R', 950-959,'R', 960-969,'R', 970-979,'R', 980-989,'R', 990-999,'R', 1000-1009,'R', 1010-1019,'R', 1020-1029,'R', 1030-1039,'R', 1040-1049,'R', 1050-1059,'R', 1060-1069,'R', 1070-1079,'R', 1080-1089,'R', 1090-1099,'R', 1100-1109,'R', 1110-1119,'R', 1120-1129,'R', 1130-1139,'R', 1140-1149,'R', 1150-1159,'R', 1160-1169,'R', 1170-1179,'R', 1180-1189,'R', 1190-1199,'R', 1200-1209,'R', 1210-1219,'R', 1220-1229,'R', 1230-1239,'R', 1240-1249,'R', 1250-1259,'R', 1260-1269,'R', 1270-1279,'R', 1280-1289,'R', 1290-1299,'R', 1300-1309,'R', 1310-1319,'R', 1320-1329,'R', 1330-1339,'R', 1340-1349,'R', 1350-1359,'R', 1360-1369,'R', 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C:Superfamily: beta-galactosidase

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Query Match      81.1%; Score 30; DB 2; Length 1042;
Best Local Similarity 71.4%; Pred. No. 2.6e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 YSSNLHS 7
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Db       1032 FSTNLHS 1038
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RESULT 23
H86557
polymorphic membrane protein B Family [imported] - Chlamydothrix pneumoniae (strain J138)
C;Species: Chlamydothrix pneumoniae, Chlamydia pneumoniae
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: H86557
R;Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Isai,
Nucleic Acids Res. 28, 2311-2314, 2000
A;Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
A;Reference number: A86491; MUID:20330349; PMID:10871362
A;Accession: H86557
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1723 <STO>
A;Cross-references: UNIPROT:Q92812; UNIPARC:UPI00000047BE; GB:BA000008; NID:G9978911; PT:
A;Experimental source: strain J138
C;Genetics:
A;Gene: pmp 20

```

Query Match	81.1%	Score 30;	DB 2;	Length 1723;
Best Local Similarity	100.0%;	Pred. No. 4.5e+02;		
Matches 6;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy 2 SSNLHS 7  
db 105 SSNLHS 110

RESULT 24  
E72067  
polymorphic membrane protein B family - Chlamydophila pneumoniae (strain CWL029)  
C/Species: Chlamydophila pneumoniae, Chlamydia pneumoniae  
C/Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 09-Jul-2004  
C/Accession: E72067  
R/Kalman, S.; Mitchell, W.; Mazatke, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.;  
Nature Genet. 21, 385-389, 1999  
A/Title: Comparative Genomes of Chlamydia pneumoniae and C. trachomatis.  
A/Reference number: A72000; MUID:99206606; PMID:10192388  
A/Accession: E72067  
A/Status: Preliminary  
A/Molecule type: DNA  
A/Residues: 1-1723 <ARN>  
A/Cross-references: UNIPROT:Q92812; UNIPARC:UPI00000470AB; GB:AE001363; NITD  
A/Experimental source: strain CWL029  
C/Genetics:  
A/Gene: pmp 20

Query Match	81.1%	Score 30	DB 2	Length 1723
Best Local Similarity	100.0%	Pred. No. 4.5e+02		
Matches	6	Conservative	0	Mismatches 0
				Indels 0
				Gaps 0

```
QY      2 SSNLHS 7  
        |||||  
Db     105 SSNLHS 110
```

RESULT 25

C81601

polymorphic membrane protein B/c family CP0212 [imported] - Chlamydophila pneumoniae (seq  
C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae  
C;Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 11-May-2000  
C;Accession: C81601

R:Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, Nucleic Acids Res. 28, 1397-1406, 2000  
A:Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.  
A:Reference number: AB1500; MUID:20150255; PMID:10684935  
A:Accession: CB1601  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1732 <REA>  
A:Cross-references: UNIPARC:UPI00001655P4; GB:AE002182; GB:AE002161; NID:G7189140; PIDN:  
A:Experimental source: strain AR39, HL cells  
C:Genetics:  
A:Gene: CP0212

C; Accession: H8657  
Nucleic Acids Res. 28, 2311-2314, 2000  
A; Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.  
A; Reference number: A86491; PMID:20330349; PMID:10871362  
C; Species: Chlamydophila pneumoniae, Chlamydia pneumoniae  
C; Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004  
C; Accession: H8657

A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-1723 <STO>  
A;Cross-references: UNIPROT:Q92812; UNIPARC:UPI0000047BE; GS:BA000008; NID:G8978911; PT:  
A;Experimental source: strain J138  
C;Genetics:  
A;Gene: bmd 20

Query Match	81.1%	Score 30;	DB 2;	Length 1723;
Best Local Similarity	100.0%;	Pred. No. 4.5e+02;		
Matches 6;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy 2 SSNLHS 7  
db 105 SSNLHS 110

RESULT 24  
E72067  
polymorphic membrane protein B family - Chlamydophila pneumoniae (strain CWL029)  
C/Species: Chlamydophila pneumoniae, Chlamydia pneumoniae  
C/Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 09-Jul-2004  
C/Accession: E72067  
R/Kalman, S.; Mitchell, W.; Mazatke, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.;  
Nature Genet. 21, 385-389, 1999  
A/Title: Comparative Genomes of Chlamydia pneumoniae and C. trachomatis.  
A/Reference number: A72000; MUID:99206606; PMID:10192388  
A/Accession: E72067  
A/Status: Preliminary  
A/Molecule type: DNA  
A/Residues: 1-1723 <ARN>  
A/Cross-references: UNIPROT:Q92812; UNIPARC:UPI00000470AB; GB:AE001363; NITD  
A/Experimental source: strain CWL029  
C/Genetics:  
A/Gene: pmp 20

Query Match	81.1%	Score 30	DB 2	Length 1723
Best Local Similarity	100.0%	Pred. No. 4.5e+02		
Matches	6	Conservative	0	Mismatches 0
				Indels 0
				Gaps 0

Qy            2 SSNLHS 7  
               |  
               |||  
Db          105 SSNLHS 110

RESULT 25  
C81S01  
polymorphic membrane protein B/C family CP0212 [imported] - Chlamydophila pneumoniae (seq  
C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae  
C;Date: 31-Mar-2000 #sequence revision 31-Mar-2000 #text change 11-May-2000

```

Query Match      81.1%; Score 30; DB 2; Length 1732;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 SSNLS 7
        |||||
Db      114 SSNLS 119

RESULT 26
KVMS73
I9 Kappa chain V region (MOPC 173) - mouse (tentative sequence)
C:Species: Mus musculus (house mouse)
C:Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 09-Jul-2004
C:Accession: A01926

```

Eur. J. Biochem. 59, 525-537, 1975  
A:Title: Determination of the primary structure of a mouse IgG2a immunoglobulin. Amino-acid sequence of the heavy chain.  
A:Reference number: A01936; PMID:812696  
A:Accession number: M01936

A: Molecule type: protein  
 A: Residues: 1-108 <SCH>  
 A: Cross-references: UNIPROT: P01543; UNIPARC: UPI000002A0C4  
 C: Comment: This chain was isolated from a myeloma protein.  
 C: Comment: An immunoglobulin heterotetramer subunit consists of two identical light (Kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into a C: Superfamily: immunoglobulin V region; immunoglobulin homology  
 C: Keywords: heterotetramer  
 F: 16-90/Domain: immunoglobulin homology <IMM>  
 F: 23-88/Disulfide bonds: #status predicted

Query Match	78.4%	Score 29;	DB 1;	Length 108;
Best Local Similarity	71.4%	Prod. No. 38;		
Matches 5;	Conservative	2;	Mismatches	0;
Indels	0;	Gaps	0;	

Qy	1	YSSNLHS	7
		: :	
Db	50	YTSSLHS	56

RESULT 27  
G38740  
Ig kappa chain V region (Py69) - mouse  
C/Species: Mus musculus (house mouse)  
C/Date: 18-Oct-1991 #sequence\_revision 18-Oct-1991 #text\_change 09-Jul-2004  
C/Accession: G38740  
R/Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.  
J. Biol. Chem. 266, 6507-6613, 1991  
A/Title: Heavy and light chain variable region sequences and antibody properties of anti  
A/Reference number: A38740; MUID:91177923; PMID:1706720  
A/Accession: G38740

A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-111 <RUF>  
A:Cross-references: UNIPROT:Q91WS9; UNIPARC:UPI0000176CDA  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:19-93/Domain: immunoglobulin homology <IMM>

```
Query Match      78.4%; Score 29; DB 2; Length 111;
Best Local Similarity 71.4%; Pred. No. 39;
Matches 5; Conservative 2; Mismatches 0; Gaps 0;

QY      1 YSSNLHS 7
       |:|:|
Db      53 YTSSLHS 59

RESULT 28
A38740
Ig kappa chain V region (Py20) - mouse
C:Species: Mus musculus (house mouse)
C>Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 09-Jul-2004
C:Accession: A38740
R:Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.
J. Biol. Chem. 266, 6607-6613, 1991
A:Title: Heavy and light chain variable region sequences and antibody properties of anti
A:Reference number: A38740; MUID:91177923; PMID:1706720
A:Accession: A38740
A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A:Molecule type: mRNA
A:Residues: 1-111 <RUF>
A:Cross-references: UNIPROT:Q91WS9; UNIPARC:UPI0000176CD9
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:19-93/Domain: immunoglobulin homology <IMM>

Query Match      78.4%; Score 29; DB 2; Length 111;
Best Local Similarity 71.4%; Pred. No. 39;
Matches 5; Conservative 2; Mismatches 0; Gaps 0;

QY      1 YSSNLHS 7
       |:|:|
Db      53 YTSSLHS 59

RESULT 29
E38740
Ig kappa chain V region (Py54) - mouse
C:Species: Mus musculus (house mouse)
C>Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 09-Jul-2004
C:Accession: E38740
R:Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.
J. Biol. Chem. 266, 6607-6613, 1991
A:Title: Heavy and light chain variable region sequences and antibody properties of anti
A:Reference number: A38740; MUID:91177923; PMID:1706720
A:Accession: E38740
A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A:Molecule type: mRNA
A:Residues: 1-111 <RUF>
A:Cross-references: UNIPROT:Q91WS9; UNIPARC:UPI0000176CD8
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:19-93/Domain: immunoglobulin homology <IMM>

Query Match      78.4%; Score 29; DB 2; Length 111;
Best Local Similarity 71.4%; Pred. No. 39;
Matches 5; Conservative 2; Mismatches 0; Gaps 0;

QY      1 YSSNLHS 7
       |:|:|
Db      53 YTSSLHS 59

RESULT 30
C38740
Ig kappa chain V region (Py2) - mouse
C:Species: Mus musculus (house mouse)
C>Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 09-Jul-2004
C:Accession: C38740
R:Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.
J. Biol. Chem. 266, 6607-6613, 1991
```

```
A:Title: Heavy and light chain variable region sequences and antibody properties of anti
A:Reference number: A38740; MUID:91177923; PMID:1706720
A:Accession: C38740
A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A:Molecule type: mRNA
A:Residues: 1-111 <RUF>
A:Cross-references: UNIPROT:Q91WS9; UNIPARC:UPI0000176CD8
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:19-93/Domain: immunoglobulin homology <IMM>

Query Match      78.4%; Score 29; DB 2; Length 111;
Best Local Similarity 71.4%; Pred. No. 39;
Matches 5; Conservative 2; Mismatches 0; Gaps 0;

QY      1 YSSNLHS 7
       |:|:|
Db      53 YTSSLHS 59

RESULT 31
T11242
ribosomal protein S3, mitochondrial - red alga (Porphyra purpurea) mitochondrial
C:Species: mitochondrial Porphyra purpurea
C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C:Accession: T11242
R:Burger, G.; Saint-Louis, D.; Gray, M.W.; Lang, B.F.
submitted to the EMBL Data Library, December 1998
A:Description: Complete sequence of the mitochondrial DNA of the red alga, Porphyra purp
A:Reference number: Z17255
A:Accession: T11242
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-227 <BUR>
A:Cross-references: UNIPROT:O99993; UNIPARC:UPI0000092B96; EMBL:AF114794; MUID:94106927;
C:Genetics:
A:Gene: rps3
A:Genome: mitochondrion
C:Function:
A:Pathway: protein biosynthesis
C:Keywords: mitochondrion; protein biosynthesis; ribosome

Query Match      78.4%; Score 29; DB 2; Length 227;
Best Local Similarity 71.4%; Pred. No. 85;
Matches 5; Conservative 2; Mismatches 0; Gaps 0;

QY      1 YSSNLHS 7
       |:|:|
Db      205 YSSSLHT 211

RESULT 32
G89567
protein T08A9.2 [imported] - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Nov-2001
C:Accession: G89567
R:anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog
A:Reference number: A75000; MUID:99069613; PMID:9851916
A:Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_ele
A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A:Accession: G89567
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-243 <STO>
A:Cross-references: UNIPARC:UPI000017CB93; GB:chr_X; PIDN:AAA81419.1; PID:gi0655500; GSPD
A:Note: similar to C. elegans protein C40H1.5
C:Genetics:
A:Gene: T08A9.2
A:Map position: X
```

Query Match 78.4%; Score 29; DB 2; Length 243;  
 Best Local Similarity 83.3%; Pred. No. 91;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSNLH 6  
 |||||  
 Db 150 YSSNFH 155

RESULT 33  
 TVMSJA  
 N:Alternate names: fos-associated 39K protein; protein PE1; transcription factor, TGACT  
 C:Species: Mus musculus (house mouse)  
 C>Date: 31-Dec-1989 #sequence\_revision 31-Dec-1989 #text\_change 09-Jul-2004  
 C:Accession: A31345; MUID:89042204; PMID:3186736  
 R:Ryder, K.; Nathans, D.  
 Proc. Natl. Acad. Sci. U.S.A. 85, 8464-8467, 1988  
 A:Title: Induction of protooncogene c-jun by serum growth factors.  
 A:Reference number: A31345; MUID:89042204; PMID:3186736  
 A:Accession: A31345  
 A:Molecule type: mRNA  
 A:Residues: 1-334 <RYD>  
 A:Cross-references: UNIPROT:P05627; UNIPARC:UPI0000019B4; GB:J04115; NID:gi92577; PIDN:  
 R:Lauph, W.W.; Wamsley, P.; Sassone-Corsi, P.; Verma, I.M.  
 Nature 334, 629-631, 1988  
 A:Title: Induction of protooncogene JUN/AP-1 by serum and TPA.  
 A:Reference number: S04683; MUID:88302467; PMID:2457172  
 A:Accession: S04683  
 A:Molecule type: mRNA  
 A:Residues: 1-334 <LAM>  
 A:Cross-references: UNIPARC:UPI0000019B4; EMBL:X12740; NID:G52762; PIDN:CAA31236.1; PID  
 R:Ryseck, R.P.; Hirai, S.I.; Yaniv, M.; Bravo, R.  
 Nature 334, 535-537, 1988  
 A:Title: Transcriptional activation of c-jun during the G(0)/G(1) transition in mouse fi  
 A:Reference number: S04537; MUID:88302446; PMID:3136397  
 A:Accession: S04537  
 A:Molecule type: mRNA  
 A:Residues: 1-182, 'C', 184-334 <RYS>  
 A:Cross-references: UNIPARC:UPI000016CB62; EMBL:X12761; NID:G52758; PIDN:CAA31252.1; PID  
 C:Genetics:  
 A:Gene: jun-A  
 C:Superfamily: jun transforming protein; fos/jun DNA-binding domain homology  
 C:Keywords: DNA binding; leucine zipper; phosphoprotein; proto-oncogene; transcription f  
 F:250-290/Domain: fos/jun DNA-binding domain homology <FJD>  
 F:283-311/Region: leucine zipper motif

Query Match 78.4%; Score 29; DB 1; Length 334;  
 Best Local Similarity 71.4%; Pred. No. 1.3e+02;  
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLH 7  
 |||||  
 Db 159 YSASLH 165

RESULT 34  
 S12742  
 N:Alternate names: transcription factor AP-1 - rat  
 C:Species: Rattus norvegicus (Norway rat)  
 C>Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 09-Jul-2004  
 C:Accession: S12742; S20028; A37381  
 R:Kitabayashi, I.; Saka, F.; Gachelin, G.; Yokoyama, K.  
 Nucleic Acids Res. 18, 3400, 1990  
 A:Title: Nucleotide sequence of rat c-jun protooncogene.  
 A:Reference number: S12742; MUID:90287724; PMID:2113275  
 A:Accession: S12742  
 A:Molecule type: DNA  
 A:Residues: 1-334 <KIT>  
 A:Cross-references: UNIPROT:P17325; UNIPARC:UPI0000125BBE; EMBL:X17215; NID:G57079; PIDN  
 R:Kitabayashi, I.; Kawakami, Z.; Chiu, R.; Ozawa, K.; Matsuo, T.; Toyoshima, S.; Unesc  
 EMBO J. 11, 167-175, 1992

A:Title: Transcriptional regulation of the c-jun gene by retinoic acid and E1a during di  
 A:Reference number: S20028; MUID:92155155; PMID:1310930  
 A:Accession: S20028  
 A:Status: translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-334 <K12>  
 A:Cross-references: UNIPARC:UPI0000125BBE; EMBL:X17215; NID:G57079; PIDN:CAA35084.1; PID  
 R:Sakai, M.; Okuda, A.; Hatayama, I.; Sato, K.; Nishi, S.; Muramatsu, M.  
 Cancer Res. 49, 5633-5637, 1989  
 A:Title: Structure and expression of the rat c-jun messenger RNA: tissue distribution an  
 A:Reference number: A37381; MUID:90002916; PMID:2507134  
 A:Accession: A37381  
 A:Molecule type: mRNA  
 A:Residues: 1-334 <SAK>  
 A:Cross-references: UNIPARC:UPI0000125BBE; GB:X17163; NID:G57819; PIDN:CAA35041.1; PID:G  
 C:Genetics:  
 A:Gene: jun  
 C:Function:  
 A:Description: transcription factor  
 C:Superfamily: jun transforming protein; fos/jun DNA-binding domain homology  
 C:Keywords: DNA binding; leucine zipper; nucleus; phosphoprotein; transcription factor;  
 F:250-290/Domain: fos/jun DNA-binding domain homology <FJD>  
 F:283-311/Region: leucine zipper motif

Query Match 78.4%; Score 29; DB 2; Length 334;  
 Best Local Similarity 71.4%; Pred. No. 1.3e+02;  
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLH 7  
 |||||  
 Db 159 YSASLH 165

RESULT 35  
 T25192  
 N:Alternate names: hypochetrical protein T23G11.2 - Caenorhabditis elegans  
 C:Species: Caenorhabditis elegans  
 C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
 C:Accession: T25192  
 R:Gardner, A.  
 submitted to the EMBL Data Library, October 1996  
 A:Reference number: Z19993  
 A:Accession: T25192  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-347 <WIL>  
 A:Cross-references: UNIPROT:O45811; UNIPARC:UPI0000077DB9; EMBL:Z81130; PIDN:CA03416.1,  
 C:Genetics:  
 A:Gene: CESP:T23G11.2  
 A:Map position: 1  
 A:Introns: 74/2; 128/3; 250/2

Query Match 78.4%; Score 29; DB 2; Length 347;  
 Best Local Similarity 83.3%; Pred. No. 1.3e+02;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSNLH 6  
 |||||  
 Db 151 YSKNLH 156

RESULT 36  
 T38822  
 N:Alternate names: hypochetrical protein SPAC4F10.18 - fission yeast (Schizosaccharomyces pombe)  
 C:Species: Schizosaccharomyces pombe  
 C>Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004  
 C:Accession: T38822  
 R:Connor, R.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, V.  
 submitted to the EMBL Data Library, September 1997  
 A:Reference number: Z21813  
 A:Accession: T38822  
 A:Status: preliminary; translated from GB/EMBL/DBJ



A;Molecule type: DNA  
A;Residues: 1-391 <CONS>  
A;Cross-references: UNIPROT:Q36030; UNIPARC:UPI000006A744; EMBL:Z98980; PIDN:CAB11721.1;  
A;Experimental source: strain 972h-; cosmid c4f10  
C;Genetics:  
A;Gene: SPDB:SPAC4F10.18  
A;Map position: 1  
A;Introns: 9/2; 35/1  
C;Superfamily: Schizosaccharomyces pombe hypothetical protein SPAC4F10.18

Query Match 78.4%; Score 29; DB 2; Length 391;  
Best Local Similarity 83.3%; Pred. No. 1.5e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSNLH 6  
|||  
DB 81 YSENLH 86

RESULT 37  
B69675  
glucose-6-phosphate isomerase pgI - Bacillus subtilis  
C;Species: Bacillus subtilis  
C;Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 09-Jul-2004  
C;Accession: B69675  
R;Kunst, P.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berte  
C.; Bron, S.; Brouillet, S.; Bruschli, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch  
A.; Ehrlich, S.D.; Emerson, P.T.; Entlan, K.D.; Errington, J.; Fabret, C.; Ferrari, E.  
Nature 390, 249-256, 1997  
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gall  
iech, J.; Harwood, C.R.; Hensaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.  
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,  
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle  
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,  
A;Authors: Schleich, S.; Schroeder, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror  
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpsstra, P.; Tognoni, A.; Tosato, V.; Uchiyama  
T.; Winters, P.; Wipac, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K  
A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Banchin, A.  
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.  
A;Reference number: A69580; MUID:98044033; PMID:9384377  
C;Accession: B69675  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-451 <KUN>  
A;Cross-references: UNIPROT:P80860; UNIPARC:UPI0000060991; GB:Z99120; GB:AL009126; NID:9  
A;Experimental source: strain 168  
C;Genetics:  
A;Gene: pgI  
C;Superfamily: glucose-6-phosphate isomerase

Query Match 78.4%; Score 29; DB 2; Length 451;  
Best Local Similarity 71.4%; Pred. No. 1.8e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLHS 7  
||:|  
DB 307 YSTDLSH 313

RESULT 38  
G36655  
unknown protein, 29405-27288 [imported] - Arabidopsis thaliana  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004  
C;Accession: G36655  
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,  
ansen, N.F.; Hughes, B.; Huizar, L.  
Nature 408, 816-820, 2000  
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.  
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziali,  
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,  
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A;Reference number: A86141; MUID:21016719; PMID:11130712  
A;Accession: G36655  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-465 <STO>  
A;Cross-references: UNIPROT:Q9CAN8; UNIPARC:UPI0000004B2D6; GB:AE005173; NID:G6598844; PI  
C;Genetics:  
A;Gene: F16M19.14  
A;Map position: 1

Query Match 78.4%; Score 29; DB 2; Length 465;  
Best Local Similarity 83.3%; Pred. No. 1.8e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLH 6  
:||||  
DB 63 FSSNLH 68

RESULT 39  
T33061  
hypothetical protein F56C3.2 - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 31-Dec-2004  
C;Accession: T33061  
R;Stoneking, T.  
submitted to the EMBL Data Library, May 1998  
A;Description: The sequence of C. elegans cosmid F56C3.  
A;Reference number: 221276  
A;Accession: T33061  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-516 <STO>  
A;Cross-references: UNIPROT:O61758; UNIPARC:UPI000007E18A; EMBL:AF067214; PIDN:AAC17005  
A;Experimental source: strain Bristol N2; clone F56C3  
C;Genetics:  
A;Gene: CESP:F56C3.2  
A;Map position: X  
A;Introns: 69/2; 144/3; 230/2; 446/3

Query Match 78.4%; Score 29; DB 2; Length 516;  
Best Local Similarity 83.3%; Pred. No. 2e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSNLH 6  
:||||  
DB 257 YQSNLH 262

RESULT 40  
F90407  
molybdopterin biosynthesis protein (moeA-2) [imported] - Sulfolobus solfataricus  
C;Species: Sulfolobus solfataricus  
C;Date: 24-May-2001 #sequence\_revision 24-May-2001 #text\_change 05-Oct-2004  
C;Accession: F90407  
R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-  
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P.  
arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.  
submitted to GenBank, April 2001  
A;Description: Sulfolobus solfataricus complete genome.  
A;Reference number: A99139  
A;Accession: F90407  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-550 <KUR>  
A;Cross-references: UNIPROT:Q97W71; UNIPARC:UPI0000064713; GB:AE006661; NID:G13815669; P

C;Superfamily: molybdenum cofactor molybdenum incorporation protein MoeA with molybdate-



Query Match 78.4%; Score 29; DB 2; Length 550;  
 Best Local Similarity 83.3%; Pred. No. 2.2e+02; Mismatches 1; Indels 0; Gaps 0;  
 Matches 5; Conservative 0;

QY 1 YSSNLH 6  
 I I I I I  
 DB 208 YESNLH 213

RESULT 41  
 T51525  
 hypothetical protein T20K14\_80 - Arabidopsis thaliana  
 C:Species: Arabidopsis thaliana (mouse-ear cress)  
 C>Date: 18-Aug-2000 #sequence\_revision 18-Aug-2000 #text\_change 09-Jul-2004  
 C:Accession: T51525  
 R:Sato, S.; Nakamura, Y.; Kaneko, T.; Kato, T.; Asamizu, E.; Kotani, H.; Tabata, S.; Mew  
 submitted to the Protein Sequence Database, August 2000  
 A:Reference number: Z25394  
 A:Accession: T51525  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-572 <SAT>  
 A:CROSS-references: UNIPROT:Q9LF35; UNIPARC:UPI00000A4196; EMBL:AL391143  
 A:Experimental source: cultivar Columbia; BAC clone T20K14  
 C:Genetics:  
 A:Map position: 5  
 A:introns: 43/2; 114/1; 129/3; 181/3; 378/3; 479/3  
 A:Note: T20K14\_80

Query Match 78.4%; Score 29; DB 2; Length 572;  
 Best Local Similarity 71.4%; Pred. No. 2.3e+02; Mismatches 1; Indels 0; Gaps 0;  
 Matches 5; Conservative 1;

QY 1 YSSNLH 7  
 I I I I I  
 DB 222 YSSNAH 228

RESULT 42  
 A12158  
 hypothetical protein alr2824 [imported] - Nostoc sp. (strain PCC 7120)  
 C:Species: Nostoc sp. PCC 7120  
 A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120  
 C>Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 09-Jul-2004  
 C:Accession: A12158  
 R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Itiguchi  
 Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Tabata, S.  
 DNA Res. 8, 205-213, 2001  
 A>Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana  
 A:Reference number: AB1807; MUID:21595285; PMID:11759840  
 A:Accession: A12158  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-732 <KUR>  
 A:CROSS-references: UNIPROT:Q8Y7A0; UNIPARC:UPI00000CE58C; GB:BA0000019; PIDN:BA074523.1;  
 A:Experimental source: strain PCC 7120  
 C:Genetics:  
 A:Gene: alr2824

Query Match 78.4%; Score 29; DB 2; Length 732;  
 Best Local Similarity 71.4%; Pred. No. 3e+02; Mismatches 2; Indels 0; Gaps 0;  
 Matches 5; Conservative 2;

QY 1 YSSNLH 7  
 I I I I I  
 DB 321 YSNHLH 327

RESULT 43  
 S74219  
 alpha-galactosidase (EC 3.2.1.22) II precursor - fungus (Trichoderma reesei)  
 C:Species: Trichoderma reesei  
 C>Date: 04-Dec-1997 #sequence\_revision 12-Dec-1997 #text\_change 09-Jul-2004

Query Match 78.4%; Score 29; DB 2; Length 550;  
 Best Local Similarity 83.3%; Pred. No. 2.2e+02; Mismatches 1; Indels 0; Gaps 0;  
 Matches 5; Conservative 0;

QY 1 YSSNLH 6  
 I I I I I  
 DB 208 YESNLH 213

RESULT 41  
 T51525  
 hypothetical protein T20K14\_80 - Arabidopsis thaliana  
 C:Species: Arabidopsis thaliana (mouse-ear cress)  
 C>Date: 18-Aug-2000 #sequence\_revision 18-Aug-2000 #text\_change 09-Jul-2004  
 C:Accession: T51525  
 R:Sato, S.; Nakamura, Y.; Kaneko, T.; Kato, T.; Asamizu, E.; Kotani, H.; Tabata, S.; Mew  
 submitted to the Protein Sequence Database, August 2000  
 A:Reference number: Z25394  
 A:Accession: T51525  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-572 <SAT>  
 A:CROSS-references: UNIPROT:Q9LF35; UNIPARC:UPI00000A4196; EMBL:AL391143  
 A:Experimental source: cultivar Columbia; BAC clone T20K14  
 C:Genetics:  
 A:Map position: 5  
 A:introns: 43/2; 114/1; 129/3; 181/3; 378/3; 479/3  
 A:Note: T20K14\_80

Query Match 78.4%; Score 29; DB 2; Length 746;  
 Best Local Similarity 71.4%; Pred. No. 3e+02; Mismatches 2; Indels 0; Gaps 0;  
 Matches 5; Conservative 2;

QY 1 YSSNLH 7  
 I I I I I  
 DB 239 YSSHLN 245

RESULT 44  
 T00798  
 hypothetical protein At2g32700 [imported] - Arabidopsis thaliana  
 N:Alternate names: hypothetical protein F24L7.16  
 C:Species: Arabidopsis thaliana (mouse-ear cress)  
 C>Date: 12-Feb-1999 #sequence\_revision 12-Feb-1999 #text\_change 09-Jul-2004  
 C:Accession: T00798; D84736  
 R:Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaul  
 submitted to the EMBL Data Library, February 1998  
 A:Description: Arabidopsis thaliana chromosome II BAC F24L7 genomic sequence.  
 A:Reference number: Z14204  
 A:Accession: T00798  
 A:Status: translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-787 <ROU>  
 A:CROSS-references: UNIPROT:O48847; UNIPARC:UPI00000AC3D4; EMBL:AC003974; NID:92914688;  
 A:Experimental source: cultivar Columbia  
 R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;  
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.  
 euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.  
 Nature 402, 761-768, 1999  
 A>Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
 A:Reference number: A84420; MUID:20083487; PMID:10617197  
 A:Accession: D84736  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-787 <STO>  
 A:CROSS-references: UNIPARC:UPI00000AC3D4; GB:AS002093; NID:92914703; PIDN:AAC04493.1;  
 C:Genetics:  
 A:Gene: At2g32700; F24L7.16  
 A:Map position: 2  
 A:introns: 11/2; 44/1; 80/3; 174/2; 200/3; 238/1; 254/3; 347/3; 372/3; 448/3; 497/1; 533

Query Match 78.4%; Score 29; DB 2; Length 787;  
 Best Local Similarity 71.4%; Pred. No. 3.2e+02; Mismatches 2; Indels 0; Gaps 0;  
 Matches 5; Conservative 2;

QY 1 YSSNLH 7  
 I I I I I  
 DB 676 HSSNVH 692

RESULT 45  
 T14777  
 hypothetical protein DKF7p434N061.1 - human (fragment)  
 C:Species: Homo sapiens (man)

C;Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 09-Jul-2004  
C;Accession: T14777  
R;Poustka, A.; Klein, M.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.  
submitted to the Protein Sequence Database, August 1999  
A;Reference number: Z18183  
A;Accession: T14777  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-867 <POU>  
A;Cross-references: UNIPROT:Q9URX9; UNIPARC:UPI0000071384; EMBL:AL110249  
A;Experimental source: adult testis; clone DKFZp434N061  
C;Genetics:  
A;Note: DKFZp434N061.1

Query Match 78.4%; Score 29; DB 2; Length 867;  
Best Local Similarity 85.7%; Pred. No. 3.6e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YSSNLHS 7  
|||||  
Db 239 YSSNLQS 245

RESULT 46  
G86420  
probable receptor-like serine/threonine kinase [imported] - Arabidopsis thaliana  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 31-Dec-2004  
C;Accession: G86420  
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,  
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;  
ansen, N.F.; Hughes, B.; Huizar, L.  
Nature 408, 816-820, 2000  
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.  
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziali,  
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,  
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A;Reference number: A86141; MUID:21016719; PMID:11130712  
A;Accession: G86420  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-947 <STO>  
A;Cross-references: UNIPROT:Q9FXF0; UNIPARC:UPI000009FC7B; GB:AB005172; NID:g9972371; PI  
C;Genetics:  
A;Map position: 1  
C;Superfamily: Receptor-like protein kinase

Query Match 78.4%; Score 29; DB 2; Length 947;  
Best Local Similarity 83.3%; Pred. No. 3.9e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YSSNLH 6  
|||||  
Db 905 YSDNLH 910

RESULT 47  
T18968  
probable serine-type carboxypeptidase (EC 3.4.16.-) Y16B4A.2 - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C;Accession: T18968; T23145; T26477  
R;Thomas, K.  
submitted to the EMBL Data Library, March 1996  
A;Reference number: Z19053  
A;Accession: T18968  
A;Status: preliminary; translated from GB/EMBL/DBDJ  
A;Molecule type: DNA  
A;Residues: 1-2105 <WIL>  
A;Cross-references: UNIPROT:Q17679; UNIPARC:UPI0000060EBB; EMBL:Z70203; PIDN:CAA94110.1;  
A;Experimental source: clone C05G5

R;Lloyd, C.  
submitted to the EMBL Data Library, March 1997  
A;Reference number: Z19697  
A;Accession: T23145  
A;Status: preliminary; translated from GB/EMBL/DBDJ  
A;Molecule type: DNA  
A;Residues: 1-2105 <W12>  
A;Cross-references: UNIPARC:UPI0000060EBB; EMBL:Z93339; PIDN:CAB07544.1; GSPDB:GN000028;  
A;Experimental source: clone H40D05

R;Wallis, J.  
submitted to the EMBL Data Library, June 1998  
A;Reference number: Z20220  
A;Accession: T26477  
A;Status: preliminary; translated from GB/EMBL/DBDJ  
A;Molecule type: DNA  
A;Residues: 1-2105 <W13>  
A;Cross-references: UNIPARC:UPI0000060EBB; EMBL:AL023825; PIDN:CAA19443.1; GSPDB:GN000028  
A;Experimental source: clone Y16B4A

C;Comment: This protein has 4 repeats of sequence homologous to serine carboxypeptidase.  
C;Genetics:  
A;Gene: CESP:Y16B4A.2  
A;Map position: X  
A;Introns: 43/3; 67/2; 179/1; 208/3; 239/2; 281/2; 296/3; 346/2; 444/3; 503/3; 588/3; 68  
1664/3; 1752/2; 1794/3; 1834/3; 1882/2; 1905/2; 1942/3; 1982/3  
C;Keywords: duplication; hydrolase; serine carboxypeptidase

Query Match 78.4%; Score 29; DB 2; Length 2105;  
Best Local Similarity 83.3%; Pred. No. 9.2e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YSSNLH 6  
|||||  
Db 434 YSSNFH 439

RESULT 48  
T43063  
RAD51 protein, long isoform - Caenorhabditis elegans (fragment)  
C;Species: Caenorhabditis elegans  
C;Date: 11-Jan-2000 #sequence\_revision 11-Jan-2000 #text\_change 09-Jul-2004  
C;Accession: T43063  
R;Rinaldo, C.; Ederle, S.; Rocco, V.; La Volpe, A.  
Mol. Gen. Genet. 260, 289-294, 1998  
A;Title: The Caenorhabditis elegans RAD51 homolog is transcribed into two alternative mRNAs.  
A;Reference number: Z22307; MUID:99077299; PMID:9862483  
A;Accession: T43063  
A;Status: preliminary; translated from GB/EMBL/DBDJ  
A;Molecule type: mRNA  
A;Residues: 1-48 <RIN>

A;Cross-references: UNIPROT:Q9XTK2; UNIPARC:UPI000007C050; EMBL:AF061202; NID:g3786403;  
C;Genetics:  
A;Gene: rad51  
C;Superfamily: yeast DNA repair protein RAD51

Query Match 75.7%; Score 28; DB 2; Length 48;  
Best Local Similarity 71.4%; Pred. No. 26;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YSSNLHS 7  
|||||  
Db 22 YNLNLHS 28

RESULT 49  
S38466  
hypothetical protein - Desulfurococcus mobilis  
C;Species: Desulfurococcus mobilis  
C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 09-Jul-2004  
C;Accession: S38466  
R;Ceccarelli, E.  
submitted to the EMBL Data Library, June 1993  
A;Reference number: S38463  
A;Accession: S38466

A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-79 <CEC>  
A:Cross-references: UNIPROT:Q46514; UNIPARC:UPI0000062448; EMBL:X73582; NID:G410438; PID

Query Match 75.7%; Score 28; DB 2; Length 79;  
Best Local Similarity 71.4%; Pred. No. 45;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSNLHS 7  
Db 18 HGSNLHS 24

RESULT 50  
S38564  
Ig kappa chain V region (ASWU1) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 21-Jan-2000  
C:Accession: S38564  
R:Monestier, M.; Losman, L.J.; Novick, K.E.; Aris, J.P.  
submitted to the EMBL Data Library, September 1993  
A:Description: Molecular analysis of mercury-induced anti-nucleolar antibodies in H-2s M  
A:Reference number: S38559  
A:Accession: S38564  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-93 <MON>  
A:Cross-references: UNIPARC:UPI00001161CA; EMBL:X75105; NID:G414153; PIDN:CAA52996.1; PI  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: immunoglobulin  
F16-90/Domain: immunoglobulin homology <IMM>

Query Match 75.7%; Score 28; DB 2; Length 93;  
Best Local Similarity 71.4%; Pred. No. 53;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSNLHS 7  
Db 50 YTSRLHS 56

Search completed: April 6, 2006, 08:58:02  
Job time : 21 secs

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GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: April 6, 2006, 08:55:21 ; Search time 46.5085 Seconds  
(without alignments)  
106.189 Million cell updates/sec

**Title:** US-10-089-500-7

Perfect score: 37

Sequence: 1 YSSNLHS 7

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Minimum DB seq length: 0  
Maximum DB seq length: 20000000

Post-processing: Minimum Match 0%

**Post-processing:** Minimum Match 0%  
Maximum Match 100%

Maximum match 100%  
Listing first 1000 summaries

Database : Uniprot 05.80:\*

```
Database : DIFFROT_03:80:
1: uniprot sprout:*
```

```
1: uniprot_prot:
2: uniprot_trembl:
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match		Length	DB	ID	Description
		Score	Match				
1	37	100.0	4780	2	Q8IE54	PLAF7	Q8IE54 plasmodium
2	35	94.6	423	2	Q4JB8	SULAC	Q4JB8 sulfolobus
3	34	91.9	112	2	Q5ND44	MOUSE	Q5ND44 mus musculus
4	34	91.9	404	2	Q7RIQ6	PLAYO	Q7RIQ6 plasmodium
5	34	91.9	446	2	Q5XIU8	RAT	Q5XIU8 rattus norv
6	34	91.9	468	1	SKIP	MOUSE	Q8C516 mus musculus
7	34	91.9	468	2	Q5ND43	MOUSE	Q5ND43 mus musculus
8	34	91.9	642	2	Q9FC03	STRCO	Q9FC03 streptomyces
9	34	91.9	744	2	Q62788	RAT	Q62788 rattus norv
10	33	89.2	177	2	Q4RJ14	TESTNG	Q4RJ14 tetraodon n
11	33	89.2	219	2	Q94192	CABEL	Q94192 caenorhabdi
12	33	89.2	219	2	Q504E5	BRARE	Q504E5 brachydanio
13	33	89.2	368	2	Q9CDQ1	LACLA	Q9CDQ1 lactococcus
14	33	89.2	391	2	Q8RR04	9SPHI	Q8RR04 capnocytoph
15	33	89.2	423	2	Q4LL46	9FLAO	Q4LL46 capnocytoph
16	33	89.2	470	2	Q845X4	9FLAO	Q845X4 cellulophag
17	33	89.2	474	2	Q9PAV9	CYTLY	Q9PAV9 cytophaga 1
18	33	89.2	474	2	Q9FIY9	9FLAO	Q9FIY9 tenacibacul
19	33	89.2	474	2	Q9AIU9	9BACT	Q9AIU9 marine cfb-
20	33	89.2	474	2	Q9FAM2	CYTLY	Q9FAM2 cytophaga 1
21	33	89.2	474	2	Q9FAM1	CYTLY	Q9FAM1 cytophaga 1
22	33	89.2	474	2	Q9FI20	9FLAO	Q9FI20 tenacibacul
23	33	89.2	474	2	Q9FIY8	9FLAO	Q9FIY8 tenacibacul
24	33	89.2	474	2	Q9PAV1	9FLAO	Q9PAV1 psychroflex
25	33	89.2	474	2	Q9FAM0	CYTLY	Q9FAM0 cytophaga 1
26	33	89.2	474	2	Q9ETS8	9FLAO	Q9ETS8 tenacibacul
27	33	89.2	474	2	Q9ETV9	CYTLY	Q9ETV9 cytophaga 1
28	33	89.2	480	2	Q9FAM4	9FLAO	Q9FAM4 capnocytoph
29	33	89.2	817	2	Q7PX57	ANOGA	Q7PX57 anopheles g
30	32	86.5	169	2	Q9S950	LYCES	Q9S950 lycopersico
31	32	86.5	172	2	Q7OY33	LYCES	Q7OY33 lycopersico

105	30	81.1	196	2	Q93251_ARATH	Q93251_arabidopsis	178	30	81.1	455	2	Q95DG3_9ROSI	Q95dg3_quercus ali
106	30	81.1	202	2	Q5GT69_WOLTR	Q5gt69_wolbachia s	179	30	81.1	455	2	Q95DG4_9ROSI	Q95dg4_quercus ali
107	30	81.1	207	2	Q7JH05_WOLPM	Q7jh05_wolbachia p	180	30	81.1	455	2	Q95DG5_9ROSI	Q95dg5_quercus acu
108	30	81.1	207	2	Q5WMH7_LEGFL	Q5wmh7_legionella	181	30	81.1	455	2	Q95DG6_9ROSI	Q95dg6_quercus den
109	30	81.1	207	2	Q5X513_LEGPA	Q5x513_legionella	182	30	81.1	455	2	Q95DG8_9ROSI	Q95dg8_quercus aea
110	30	81.1	210	2	Q6AZ17_XENLA	Q6az17_xenopus lae	183	30	81.1	455	2	Q95DG9_9ROSI	Q95dg9_quercus aea
111	30	81.1	211	2	Q5ZV90_LEGPH	Q5zv90_legionella	184	30	81.1	455	2	Q95DH0_9ROSI	Q95dh0_quercus gil
112	30	81.1	243	1	MLRA_SALTY	P58398_salmonella	185	30	81.1	455	2	Q95DH2_9ROSI	Q95dh2_quercus phi
113	30	81.1	243	1	Q57MH9_SALCH	P57mh9_salmonella	186	30	81.1	455	2	Q95DH3_9ROSI	Q95dh3_quercus myr
114	30	81.1	243	2	Q5FJ39_SALPA	Q5fj39_salmonella	187	30	81.1	455	2	Q95DH4_9ROSI	Q95dh4_quercus gla
115	30	81.1	243	2	Q825B9_SALTI	Q825b9_salmonella	188	30	81.1	455	2	Q95DH5_9ROSI	Q95dh5_quercus sal
116	30	81.1	243	2	Q4TGL3_TETNG	Q4tgl3_tetradon n	189	30	81.1	455	2	Q95DH9_FAGJA	Q95dh9_fagus japon
117	30	81.1	290	2	Q8YV17_ANASP	Q8yv17_anabaena sp	190	30	81.1	455	2	Q95DI0_CASCR	Q95di0_castanea cr
118	30	81.1	294	1	PET54_SACBA	O13364_saccharomyc	191	30	81.1	455	2	Q95DI1_9ROSI	Q95di1_castanopsis
119	30	81.1	313	2	Q9LZ82_ARATH	Q9lzm2_arabidopsis	192	30	81.1	455	2	Q95DI2_9ROSI	Q95di2_castanopsis
120	30	81.1	337	2	Q5FFM6_EHRRG	Q5ffm6_ehrlichia r	193	30	81.1	458	1	MURC_CLOAB	Q97e89_clostridium
121	30	81.1	361	2	Q5DY69_VIBF1	Q5dy69_vibrio fusc	194	30	81.1	458	1	ZN239_HUMAN	Q16600_homo sapien
122	30	81.1	361	2	Q502N4_BRARE	Q502n4_brachydanio	195	30	81.1	459	2	Q8UDC0_AGRIT5	Q8udc0_agrobacteri
123	30	81.1	374	2	Q6MPB2_BDRBA	Q6mpb2_bdellovibri	196	30	81.1	461	2	Q95DG7_QUEAC	Q95dg7_quercus acu
124	30	81.1	391	2	Q8RR13_9SPHI	Q8rr13_cytophaga s	197	30	81.1	461	2	Q95DH1_9ROSI	Q95dh1_quercus var
125	30	81.1	391	2	Q8RQX8_9SPHI	Q8rx8_cytophaga s	198	30	81.1	464	2	Q76DY9_CASCR	Q76dy9_castanea cr
126	30	81.1	391	2	Q8RQY2_9SPHI	Q8ry2_cytophaga s	199	30	81.1	464	2	Q76E03_9ROSI	Q76e03_quercus mon
127	30	81.1	391	2	Q8RR16_9SPHI	Q8rr16_cytophaga s	200	30	81.1	464	2	Q76E06_9ROSI	Q76e06_quercus mon
128	30	81.1	391	2	Q8RQY4_9SPHI	Q8ry4_cytophaga s	201	30	81.1	464	2	Q76E07_9ROSI	Q76e07_quercus mon
129	30	81.1	391	2	Q8RR08_9SPHI	Q8rr08_cytophaga s	202	30	81.1	472	2	Q8ZSG7_ANASP	Q8zsg7_anabaena ep
130	30	81.1	391	2	Q8RQZ6_9SPHI	Q8rz6_cytophaga s	203	30	81.1	473	2	Q8UCJ0_9ERIC	Q8ucj0_androstoma
131	30	81.1	391	2	Q8RQZ1_9SPHI	Q8rz1_cytophaga s	204	30	81.1	474	2	Q9AJK7_9BACT	Q9ajk7_marine cfb-
132	30	81.1	391	2	Q8RR11_9SPHI	Q8rr11_cytophaga s	205	30	81.1	474	2	Q9AJH9_9SPHI	Q9ajh9_cytophaga s
133	30	81.1	391	2	Q8RR10_9SPHI	Q8rr10_cytophaga s	206	30	81.1	474	2	Q9AJH4_9BACT	Q9ajh4_marine cfb-
134	30	81.1	391	2	Q8RQW3_9SPHI	Q8rw3_cytophaga s	207	30	81.1	474	2	Q9AJJ6_9BACT	Q9ajj6_marine cfb-
135	30	81.1	391	2	Q8RR12_9SPHI	Q8rr12_cytophaga s	208	30	81.1	474	2	Q9AJI5_9BACT	Q9aji5_marine cfb-
136	30	81.1	391	2	Q8RQY6_9SPHI	Q8ry6_cytophaga s	209	30	81.1	474	2	Q9AJH6_9SPHI	Q9ajh6_cytophaga s
137	30	81.1	391	2	Q8RQX6_9SPHI	Q8rx6_cytophaga s	210	30	81.1	474	2	Q9AJH8_9SPHI	Q9ajh8_cytophaga s
138	30	81.1	391	2	Q8RR05_9SPHI	Q8rr05_cytophaga s	211	30	81.1	474	2	Q9FAV6_9FLAO	Q9fav6_leeuwenhoek
139	30	81.1	391	2	Q8RQZ0_9SPHI	Q8rz0_cytophaga s	212	30	81.1	474	2	Q9FAW3_9BACT	Q9faw3_marine cfb-
140	30	81.1	391	2	Q8RQX7_9SPHI	Q8rx7_cytophaga s	213	30	81.1	474	2	Q9AJK3_9BACT	Q9ajk3_marine cfb-
141	30	81.1	391	2	Q8RQ07_9SPHI	Q8rr07_cytophaga s	214	30	81.1	474	2	Q9AJI3_9BACT	Q9aji3_marine cfb-
142	30	81.1	391	2	Q8RR15_9SPHI	Q8rr15_cytophaga s	215	30	81.1	474	2	Q9AJJ7_9BACT	Q9ajj7_marine cfb-
143	30	81.1	391	2	Q8RR09_9SPHI	Q8rr09_cytophaga s	216	30	81.1	474	2	Q9AJJ5_9BACT	Q9ajj5_marine cfb-
144	30	81.1	391	2	Q8RQY9_9SPHI	Q8ry9_cytophaga s	217	30	81.1	474	2	Q9AJK1_9BACT	Q9ajk1_marine cfb-
145	30	81.1	391	2	Q8RQY5_9SPHI	Q8ry5_cytophaga s	218	30	81.1	474	2	Q9AJL0_9SPHI	Q9ajl0_cytophaga s
146	30	81.1	391	2	Q8RR06_9SPHI	Q8rr06_cytophaga s	219	30	81.1	474	2	Q9AJK9_9SPHI	Q9ajk9_cytophaga s
147	30	81.1	391	2	Q8RQZ7_9SPHI	Q8rz7_cytophaga s	220	30	81.1	474	2	Q9AJJ3_9BACT	Q9ajj3_marine cfb-
148	30	81.1	391	2	Q8RQY0_9SPHI	Q8ry0_cytophaga s	221	30	81.1	474	2	Q9AJK2_9BACT	Q9ajk2_marine cfb-
149	30	81.1	391	2	Q8RQY9_9SPHI	Q8ry9_cytophaga s	222	30	81.1	474	2	Q9AJL1_9BACT	Q9ajl1_marine cfb-
150	30	81.1	391	2	Q8RQZ4_9SPHI	Q8rz4_cytophaga s	223	30	81.1	474	2	Q9AJJ9_9BACT	Q9ajj9_marine cfb-
151	30	81.1	391	2	Q8RQY3_9BACT	Q8ry3_cfb-group b	224	30	81.1	474	2	Q9AJI8_9BACT	Q9aji8_marine cfb-
152	30	81.1	391	2	Q8RQY6_9SPHI	Q8ry6_cytophaga s	225	30	81.1	474	2	Q9F205_9FLAO	Q9f205_tenacibacul
153	30	81.1	391	2	Q8RQW4_9SPHI	Q8rw4_cytophaga s	226	30	81.1	474	2	Q9AJK5_9BACT	Q9ajk5_marine cfb-
154	30	81.1	391	2	Q8RQY1_9SPHI	Q8ry1_cytophaga s	227	30	81.1	474	2	Q9AJH5_9SPHI	Q9ajh5_cytophaga s
155	30	81.1	391	2	Q8RQZ3_9SPHI	Q8rz3_cytophaga s	228	30	81.1	474	2	Q9AJJ0_9BACT	Q9ajj0_marine cfb-
156	30	81.1	391	2	Q8RR14_9SPHI	Q8rr14_cytophaga s	229	30	81.1	474	2	Q9FAU7_9FLAO	Q9fau7_polaribacte
157	30	81.1	391	2	Q8RQZ2_9SPHI	Q8rz2_cytophaga s	230	30	81.1	474	2	Q9FAV4_9FLAO	Q9fav4_stanierella
158	30	81.1	391	2	Q8RQY7_9SPHI	Q8ry7_cytophaga s	231	30	81.1	474	2	Q9AJJ2_9BACT	Q9ajj2_marine cfb-
159	30	81.1	393	2	Q6CGE2_YARLI	Q6cge2_varrowia li	232	30	81.1	474	2	Q9AJI9_9BACT	Q9aji9_marine cfb-
160	30	81.1	399	2	Q597M5_9ROSI	Q597m5_quercus mul	233	30	81.1	474	2	Q9FAV3_9FLAO	Q9fav3_zobellia ul
161	30	81.1	403	2	Q8MZG6_DROME	Q8mzg6_drosophila	234	30	81.1	474	2	Q9AJK0_9BACT	Q9ajk0_marine cfb-
162	30	81.1	403	2	Q9VCZ2_DROME	Q9vcz2_drosophila	235	30	81.1	474	2	Q845X1_9FLAO	Q845x1_polaribacte
163	30	81.1	403	2	Q597M7_9ROSI	Q597m7_castanea se	236	30	81.1	474	2	Q845X3_9FLAO	Q845x3_cytophaga s
164	30	81.1	408	2	Q597M6_9ROSI	Q597m6_castanopsis	237	30	81.1	475	2	Q9AJH7_9SPHI	Q9ajh7_cytophaga s
165	30	81.1	412	1	BLI4_NEUCR	Q92247_neurospora	238	30	81.1	475	2	Q845X3_9FLAO	Q845x3_cytophaga s
166	30	81.1	420	2	Q4UE35_THEAN	Q4ue35_thaieria a	239	30	81.1	476	2	Q9LCL1_9FLAO	Q9lcl1_weeksella v
167	30	81.1	422	2	Q4NSF6_THEPA	Q4nsf6_thaieria p	240	30	81.1	478	2	Q9FAU5_9SPHI	Q9fau5_flexibacter
168	30	81.1	423	2	Q17981_CAEEL	Q17981_caenorhabdi	241	30	81.1	479	2	Q5JNT6_ORYSA	Q5jnt6_oryza sativ
169	30	81.1	424	2	Q9SKB7_ARATH	Q9skb7_arabidopsis	242	30	81.1	479	2	Q9LAW7_FLECA	Q9law7_flexibacter
170	30	81.1	426	1	ATG23_KLULA	Q6cwa7_kluyveromyc	243	30	81.1	479	2	Q9LCK3_PEDHE	Q9lck3_pedobacter
171	30	81.1	429	2	Q8A7F1_BACTN	Q8a7f1_bacteroides	244	30	81.1	480	2	Q9EV2_9SPHI	Q9ev2_bradyrhizob
172	30	81.1	441	2	Q54W25_DICDI	Q54w25_dictyosteli	245	30	81.1	481	2	Q9FAX4_CAPOC	Q9fax4_capnocytoph
173	30	81.1	445	2	Q6BSJ4_DEBHA	Q6bsj4_debaryomyce	246	30	81.1	482	2	Q9LGZ2_ORYSA	Q9lgz2_oryza sativ
174	30	81.1	446	2	Q6F8V2_ACTAD	Q6f8v2_acinetobact	247	30	81.1	482	2	Q9LGF2_ORYSA	Q9lgef2_oryza sativ
175	30	81.1	455	2	Q95DF9_9ROSI	Q95df9_quercus miy	248	30	81.1	484	2	Q88EF8_PSEPK	Q88ef8_pseudomonas
176	30	81.1	455	2	Q95DGI_9ROSI	Q95dgi_quercus mon	249	30	81.1	486	2	Q4W9P1_ASPFU	Q4w9p1_aspergillus
177	30	81.1	455	2	Q95DG2_9ROSI	Q95dgi2_quercus hon	250	30	81.1	504	1	MATK_FAGCR	Q8w8e6_fagus crena

251	30	81.1	504	1	MATK_FAGHA	Q8wke6	fagus hayat	324	29	78.4	109	2	Q8EX83	LEPIN	Q8EX83	leptospira
252	30	81.1	504	1	MATK_FAGJA	Q8wke7	fagus japon	325	29	78.4	129	2	Q7PAPA	RICSI	Q7PAPA	ricketsia
253	30	81.1	504	1	MATK_QUECE	Q75vb5	quercus cer	326	29	78.4	135	2	Q5CTP9	CRYPV	Q5CTP9	cryptospori
254	30	81.1	504	1	MATK_QUECO	Q75vb4	quercus coc	327	29	78.4	141	2	Q4MYK8	THEPA	Q4MYK8	theileria p
255	30	81.1	504	1	MATK_QUEGA	Q75vb3	quercus gam	328	29	78.4	142	2	Q8D226	STRA5	Q8D226	streptococ
256	30	81.1	504	1	MATK_QUEIL	Q75vb2	quercus ile	329	29	78.4	145	2	Q93P82	9SPHI	Q93P82	microscilla
257	30	81.1	504	1	MATK_QUELY	Q75vb1	quercus lyr	330	29	78.4	147	2	Q4LED0	9CREN	Q4LED0	uncultured
258	30	81.1	504	1	MATK_QUEPA	Q75va9	quercus pal	331	29	78.4	148	2	Q8E4N2	STRA3	Q8E4N2	streptococ
259	30	81.1	504	1	MATK_QUEPE	Q75va8	quercus pec	332	29	78.4	201	2	Q68A49	9UROC	Q68A49	olkopleura
260	30	81.1	504	1	MATK_QUERO	Q8m920	quercus rob	333	29	78.4	205	2	Q55U14	CRYN	Q55U14	cryptococ
261	30	81.1	504	1	MATK_QUERU	Q7ym14	quercus rub	334	29	78.4	215	2	Q8NH00	HUMAN	Q8NH00	homo sapien
262	30	81.1	504	1	MATK_QUESU	Q75va5	quercus sub	335	29	78.4	224	2	Q5CRH61	CRYPV	Q5CR61	cryptospori
263	30	81.1	504	2	Q75VA7_QUERO	Q75xc8	oryza sativ	336	29	78.4	227	2	Q99993	PORPU	Q99993	porphyra pu
264	30	81.1	504	2	Q75VA7_QUERO	Q75va7	quercus rob	337	29	78.4	228	2	Q5CM03	CRYHO	Q5CM03	cryptospori
265	30	81.1	504	2	Q75VB0_9ROSI	Q75vb0	quercus oia	338	29	78.4	230	2	Q8CQ59	PSEAE	Q8CQ59	pseudomonas
266	30	81.1	504	2	Q75VB6_9ROSI	Q75vb6	quercus arg	339	29	78.4	235	2	Q6D6M2	ERWCT	Q6D6M2	erwinia car
267	30	81.1	504	2	Q75VB7_9ROSI	Q75vb7	lithocarpus	340	29	78.4	250	2	Q6D6M2	ERWCT	Q6D6M2	erwinia car
268	30	81.1	504	2	Q75VB8_9ROSI	Q75vb8	lithocarpus	341	29	78.4	266	2	Q7Q8B8	ANOCA	Q7Q8B8	anopheles g
269	30	81.1	504	2	Q75VB9_9ROSI	Q75vb9	lithocarpus	342	29	78.4	268	2	Q5XPY0	9CALI	Q5XPY0	norovirus h
270	30	81.1	504	2	Q75VC0_9ROSI	Q75vc0	castanopsis	343	29	78.4	271	2	Q4YAY0	PLABE	Q4YAY0	plasmodium
271	30	81.1	504	2	Q75VC1_9ROSI	Q75vc1	castanopsis	344	29	78.4	279	1	EFTS_BORGA		Q6avh9	borrelia ga
272	30	81.1	504	2	Q8MGF5_9ROSI	Q8mgp5	trigonobala	345	29	78.4	294	2	Q6AVH9	ORYSA	Q6AVH9	oryza sativ
273	30	81.1	504	2	Q8MGF6_9ROSI	Q8mgp6	trigonobala	346	29	78.4	304	2	Q6D898	ERWCT	Q6D898	erwinia car
274	30	81.1	504	2	Q8MGF7_9ROSI	Q8mgp7	trigonobala	347	29	78.4	323	2	Q7VXS1	BORPE	Q7VXS1	borderella
275	30	81.1	504	2	Q8WKE5_FAGSY	Q8wke5	fagus sylv	348	29	78.4	334	1	API_MOUSE		P05627	mus musculu
276	30	81.1	515	2	Q8T108_BOKMO	Q8t108	bombyx mori	349	29	78.4	334	1	API_MOUSE		P17325	mus musculu
277	30	81.1	523	2	Q54B87_DICDI	Q54b87	dictyosteli	350	29	78.4	334	2	Q52L79	MOUSE	Q52L79	rattus norv
278	30	81.1	541	2	Q60D40_SOLTU	Q60d40	solanum tub	351	29	78.4	347	2	Q45811	CAEEL	Q45811	caenorhabdi
279	30	81.1	548	2	Q6M2Y5_HUMAN	Q6m2y5	homo sapien	352	29	78.4	358	2	Q9D4E7	MOUSE	Q9D4E7	mus musculu
280	30	81.1	556	2	Q4SSV7_TETNG	Q4ssv7	tetraodon n	353	29	78.4	371	2	Q41272	GIBZE	Q41272	gibberella
281	30	81.1	573	2	Q4HM08_CAMLA	Q4hm08	campylobact	354	29	78.4	391	2	Q36030	SCHPO	Q36030	schizosacch
282	30	81.1	613	2	Q8IDF3_PLAF7	Q8idf3	plasmodium	355	29	78.4	391	2	Q8RQZ9	9SPHI	Q8RQZ9	cytophaga s
283	30	81.1	662	2	Q823K2_CHLCV	Q823k2	chlamydogphi	356	29	78.4	391	2	Q8RR02	9SPHI	Q8RR02	cytophaga s
284	30	81.1	671	2	Q4WT68_ASFPV	Q4wt68	aspergillus	357	29	78.4	391	2	Q8RR02	9SPHI	Q8RR02	cytophaga s
285	30	81.1	677	2	Q4ID14_GIBZE	Q4id14	gibberella	358	29	78.4	391	2	Q8RQZ8	9SPHI	Q8RQZ8	cytophaga s
286	30	81.1	684	2	Q5T928_HUMAN	Q5t928	homo sapien	359	29	78.4	391	2	Q8RR03	9SPHI	Q8RR03	cytophaga s
287	30	81.1	692	2	Q627E9_CABER	Q627e9	caenorhabdi	360	29	78.4	391	2	Q8RR01	9SPHI	Q8RR01	cytophaga s
288	30	81.1	706	2	Q7Y275_PLACH	Q7y275	plasmodium	361	29	78.4	396	2	Q55DS3	DICDI	Q55DS3	dictyosteli
289	30	81.1	736	2	Q6L417_SOLDE	Q6l417	solanum dem	362	29	78.4	405	2	Q9L9K5	PASMU	Q9L9K5	pasteurella
290	30	81.1	742	2	Q4Y207_PLACH	Q4y207	plasmodium	363	29	78.4	408	2	Q85454	PASMU	Q85454	pasteurella
291	30	81.1	749	2	Q5RDH3_PONPY	Q5rdh3	pongo pygma	364	29	78.4	408	2	Q9CMP3	PASMU	Q9CMP3	pasteurella
292	30	81.1	781	2	Q5T930_HUMAN	Q5t930	homo sapien	365	29	78.4	412	2	Q7PMH0	ANOCA	Q7PMH0	anopheles g
293	30	81.1	786	2	Q9C2E8_NEUCR	Q9c2e8	neurospora	366	29	78.4	420	2	Q87MP3	VIBPA	Q87MP3	vibrio para
294	30	81.1	806	2	Q5ED38_DICDI	Q55d38	dictyosteli	367	29	78.4	430	2	Q7ZXV5	XENLA	Q7ZXV5	xenopus lae
295	30	81.1	811	2	Q5T932_HUMAN	Q5t932	homo sapien	368	29	78.4	450	1	G6PI_BACSU		P80860	bacillus su
296	30	81.1	816	2	Q5T923_HUMAN	Q5t923	homo sapien	369	29	78.4	451	2	Q5JS39	HUMAN	Q5JS39	homo sapien
297	30	81.1	816	2	Q5RF56_PONPY	Q5rf56	pongo pygma	370	29	78.4	457	2	Q61758	CAEEL	Q61758	caenorhabdi
298	30	81.1	844	2	Q9HMU4_PSEAE	Q9hm4	pseudomonas	371	29	78.4	457	2	Q9LN83	ARATH	Q9LN83	arabidopsis
299	30	81.1	905	2	Q5T929_HUMAN	Q5t929	homo sapien	372	29	78.4	461	2	Q852L2	ORYSA	Q852L2	oryza sativ
300	30	81.1	1004	2	Q5T927_HUMAN	Q5t927	homo sapien	373	29	78.4	462	2	Q8RWH4	ARATH	Q8RWH4	arabidopsis
301	30	81.1	1014	2	Q5PAL5_ANAMM	Q5pal5	anaplasma m	374	29	78.4	465	2	Q9CAN8	ARATH	Q9CAN8	arabidopsis
302	30	81.1	1020	2	Q6BX81_DEBHA	Q6bx81	debaryomyce	375	29	78.4	470	2	Q8L8I0	ORYSA	Q8L8I0	oryza sativ
303	30	81.1	1028	2	Q83Q39_SHIFL	Q83q39	shigella fl	376	29	78.4	474	2	Q9FAV0	9FLAO	Q9FAV0	salegentiba
304	30	81.1	1030	1	BGA2_ECOLI	P06864	escherichia	377	29	78.4	474	2	Q9AJK8	9BACT	Q9AJK8	marine cfb-
305	30	81.1	1042	2	Q8XAM9_ECOS7	Q8xam9	escherichia	378	29	78.4	474	2	Q9AJK6	9BACT	Q9AJK6	marine cfb-
306	30	81.1	1089	2	Q8FDF0_ECOL6	Q8fdf0	escherichia	379	29	78.4	474	2	Q9AJK6	9BACT	Q9AJK6	marine cfb-
307	30	81.1	1138	2	Q5BAJ4_EMENI	Q5bj4	aspergillus	380	29	78.4	474	2	Q9AJH3	9BACT	Q9AJH3	marine cfb-
308	30	81.1	1151	2	Q5T931_HUMAN	Q5t931	homo sapien	381	29	78.4	474	2	Q9AJI4	9BACT	Q9AJI4	marine cfb-
309	30	81.1	1290	1	SRBS1_MOUSE	Q62417	mus musculu	382	29	78.4	474	2	Q9AJI7	9BACT	Q9AJI7	marine cfb-
310	30	81.1	1292	1	SRBS1_MOUSE	Q9bx66	homo sapien	383	29	78.4	474	2	Q9AJK4	9BACT	Q9AJK4	marine cfb-
311	30	81.1	1292	2	Q5T924_HUMAN	Q5t924	homo sapien	384	29	78.4	474	2	Q9AJJ1	9BACT	Q9AJJ1	marine cfb-
312	30	81.1	1329	2	Q54TH7_DICDI	Q54th7	dictyosteli	385	29	78.4	474	2	Q9AJJ1	9BACT	Q9AJJ1	marine cfb-
313	30	81.1	1420	2	Q8I185_PLAF7	Q8i185	plasmodium	386	29	78.4	474	2	Q9AJJ4	9BACT	Q9AJJ4	marine cfb-
314	30	81.1	1723	1	PMP20_CHLPL	Q92812	chlamydia p	387	29	78.4	474	2	Q9AJI2	9BACT	Q9AJI2	marine cfb-
315	30	81.1	2115	2	Q8IE55_PLAF7	Q8ie55	plasmodium	388	29	78.4	474	2	Q9AJJ8	9BACT	Q9AJJ8	marine cfb-
316	30	81.1	2125	2	Q61PD5_CABER	Q6lpd5	caenorhabdi	389	29	78.4	480	2	Q8J050	GVCF	Q8J050	choriostoneu
317	30	81.1	2475	2	Q4WN65_USTPA	Q4wn65	aspergillus	390	29	78.4	486	2	Q6J130	BAROU	Q6J130	bartonella
318	30	81.1	5431	2	Q4PAT5_ASFPV	Q4pat5	ustilago ma	391	29	78.4	486	2	Q7ZWR5	XENLA	Q7ZWR5	xenopus lae
319	29	78.4	70	2	Q4YGM8_PLABE	Q4ygm8	plasmodium	392	29	78.4	496	2	Q5HL88	STAEQ	Q5HL88	staphylococ
320	29	78.4	84	2	Q4NVV3_9DBLT	Q4nvv3	anaeromyxob	393	29	78.4	496	2	Q8CR47	STAEQ	Q8CR47	staphylococ
321	29	78.4	102	2	Q5BGR1_9HIV1	Q5bgr1	human immun	394	29	78.4	497	2	Q652F9	ORYSA	Q652F9	oryza sativ
322	29	78.4	108	1	KV5J_MOUSE	P01543	mus musculu	395	29	78.4	502	2	Q4SRB8	TETNG	Q4SRB8	tetraodon n
323	29	78.4	109	2	Q75FE2_LEPIC	Q75fe2	leptospira	396	29	78.4	508	2	Q4XUG1	PLACH	Q4XUG1	plasmodium

397	29	78.4	510	2	Q9MAB8_ARATH	Q9mab8 arabidopsis	470	28	75.7	72	2	Q80ZP2_MOUSE	Q80zp2 mus musculus
398	29	78.4	512	2	Q697G6_9HEMI	Q697g6 neomaekelli	471	28	75.7	75	2	Q5C084_SCHJA	Q5c084 schistosoma
399	29	78.4	517	2	Q5B897_EMENI	Q5b897 aspergillus	472	28	75.7	75	2	Q4N4R7_THERP	Q4n4r7 theileria p
400	29	78.4	532	2	Q8GWT1_ARATH	Q8gwt1 arabidopsis	473	28	75.7	79	2	Q46514_DESMA	Q46514 desulfofuroco
401	29	78.4	533	2	Q96Z47_SULTO	Q96z47 sulfobolus	474	28	75.7	85	2	Q6MAY7_PARACH	Q6may7 parachlamyd
402	29	78.4	538	1	TTU11_HUMAN	Q8nhh1 homo sapien	475	28	75.7	87	2	Q6YMR1_9HEMI	Q6ymr1 acizzia hol
403	29	78.4	547	2	Q812K3_BACCR	Q812k3 bacillus ce	476	28	75.7	98	2	Q831H7_ENTFA	Q831h7 enterococcu
404	29	78.4	550	2	Q97W71_SULSO	Q97w71 sulfobolus	477	28	75.7	108	2	Q1K5K_MOUSE	Q1k5k mus musculus
405	29	78.4	565	2	Q81I51_PLAF7	Q81i51 plasmodium	478	28	75.7	108	1	Q1K5L_MOUSE	Q1k5l mus musculus
406	29	78.4	572	2	Q9YF35_ARATH	Q9yf35 arabidopsis	479	28	75.7	108	1	Q1K5M_MOUSE	Q1k5m mus musculus
407	29	78.4	597	2	Q4YXZ0_PLABE	Q4yxz0 plasmodium	480	28	75.7	108	1	Q1K5N_MOUSE	Q1k5n mus musculus
408	29	78.4	607	2	Q6FLG0_CANGA	Q6flg0 candida gla	481	28	75.7	108	1	Q1K5O_MOUSE	Q1k5o mus musculus
409	29	78.4	612	2	Q4WUN5_ASPPU	Q4wun5 aspergillus	482	28	75.7	108	1	Q1K5U_MOUSE	Q1k5u mus musculus
410	29	78.4	640	2	Q4SKL5_TETNG	Q4skl5 tetraodon n	483	28	75.7	112	2	Q8H4F6_ORYSA	Q8h4f6 oryza sativ
411	29	78.4	644	2	Q9R166_MOUSE	Q9r166 mus musculus	484	28	75.7	119	1	RLI8_DESVH	Q72c94 deulfovibr
412	29	78.4	645	2	Q5CNF0_CRYHO	Q5cnf0 cryptospori	485	28	75.7	125	2	Q7UGH3_RHOBA	Q7ugh3 rhodopirell
413	29	78.4	663	2	Q87Z98_PSESM	Q87z98 pseudomonas	486	28	75.7	128	2	Q76YU4_9CAUD	Q76yu4 bacteriopho
414	29	78.4	666	2	Q5L7N2_BACFN	Q5l7n2 bacteroides	487	28	75.7	129	2	Q5C566_SCHJA	Q5c566 schistosoma
415	29	78.4	666	2	Q64MVL_BACFR	Q64mvl bacteroides	488	28	75.7	129	2	Q9SA59_ARATH	Q9sa59 arabidopsis
416	29	78.4	682	2	Q84G19_STRHY	Q84g19 streptomyce	489	28	75.7	130	2	Q7P4W4_FUSNV	Q7p4w4 fusobacteri
417	29	78.4	683	2	Q8JYC6_9GAMA	Q8jyc6 porcine lym	490	28	75.7	130	2	Q8R6Z6_FUSNV	Q8r6z6 fusobacteri
418	29	78.4	718	1	ILVB_CRYNE	Q5kpfj3 cryptococcu	491	28	75.7	141	2	Q6KHS8_MYCMO	Q6khs8 mycoplasma
419	29	78.4	718	1	ILVB_CRYNE	Q5kpfj3 cryptococcu	492	28	75.7	145	1	GTCA_LISIN	Q927u4 listeria in
420	29	78.4	718	2	Q96VZ6_CRYNE	Q96vz6 cryptococcu	493	28	75.7	146	2	Q688D7_ORYSA	Q688d7 oryza sativ
421	29	78.4	718	2	Q560J9_CRYNE	Q560j9 cryptococcu	494	28	75.7	149	2	Q4W1V1_ASPPU	Q4w1v1 aspergillus
422	29	78.4	725	2	Q4XLY8_PLACH	Q4xly8 plasmodium	495	28	75.7	151	2	Q9Q1Z3_PICO	Q9q1z3 foot-and-mo
423	29	78.4	732	2	Q8YTA0_ANASP	Q8yta0 anabaena sp	496	28	75.7	154	2	Q8U2F4_PRFU	Q8u2f4 pyrococcus
424	29	78.4	732	2	Q7RJ15_PLAYO	Q7rj15 plasmodium	497	28	75.7	154	2	Q6TS18_CULQU	Q6ts18 culex quinq
425	29	78.4	736	2	Q4VYV2_PLABE	Q4vyv2 plasmodium	498	28	75.7	183	2	Q8K0W6_MOUSE	Q8k0w6 mus musculus
426	29	78.4	744	2	Q4ILV5_GIBZE	Q4ilv5 gibberella	499	28	75.7	186	2	Q8E1U9_STRAS	Q8e1u9 streptococc
427	29	78.4	746	2	Q92457_TRIRE	Q92457 trichoderma	500	28	75.7	186	2	Q8E7B0_STRAJ	Q8e7b0 streptococc
428	29	78.4	747	1	AGALC_8SPNG	Q9auz4 aspergillus	501	28	75.7	186	2	Q8ENF5_OCEIH	Q8enf5 oceanobacil
429	29	78.4	750	2	Q5AU92_EMENI	Q5au92 aspergillus	502	28	75.7	190	2	Q4R9X3_TETNG	Q4r9x3 tetraodon n
430	29	78.4	787	2	Q48847_ARATH	Q48847 arabidopsis	503	28	75.7	198	2	Q6YL49_HUMAN	Q6yl49 homo sapien
431	29	78.4	788	2	Q73FZ8_WOLPM	Q73fz8 wolbachia p	504	28	75.7	205	2	Q7QZB5_GIALA	Q7qzb5 giardia lam
432	29	78.4	832	2	Q6BID2_DEBHA	Q6bid2 debaryomyce	505	28	75.7	213	2	Q8LHNS_ORYSA	Q8lhn5 oryza sativ
433	29	78.4	867	2	Q9UFX9_HUMAN	Q9ufx9 homo sapien	506	28	75.7	217	2	Q9VHA2_DROSOPH	Q9vha2 drosophila
434	29	78.4	871	2	Q8IDZ7_PLAF7	Q8idz7 plasmodium	507	28	75.7	219	2	Q8CGR8_MOUSE	Q8cgr8 mus musculus
435	29	78.4	881	2	Q5LYS7_MAGGR	Q5lys7 magnaporthe	508	28	75.7	222	2	Q4XT44_PLACH	Q4xt44 plasmodium
436	29	78.4	903	2	Q7RNY8_PLAYO	Q7rny8 plasmodium	509	28	75.7	222	2	Q721Q6_LISMF	Q721q6 listeria mo
437	29	78.4	906	2	Q6ORU4_CAEHR	Q6oru4 caenorhabdi	510	28	75.7	224	2	Q8Y8J4_LISMO	Q8y8j4 listeria mo
438	29	78.4	909	2	Q4TNK9_9SPHN	Q4tnk9 erythrobract	511	28	75.7	224	2	Q92DA9_LISIN	Q92da9 listeria in
439	29	78.4	932	2	Q7RCN5_PLAYO	Q7rcn5 plasmodium	512	28	75.7	227	2	Q8XA54_ECO57	Q8xa54 escherichia
440	29	78.4	932	2	Q8DRZ1_STRMU	Q8drz1 streptococc	513	28	75.7	234	2	Q4Z9D2_9CAUD	Q4z9d2 staphylococ
441	29	78.4	940	2	Q5C6G4_ARATH	Q5c6g4 arabidopsis	514	28	75.7	240	2	Q63ZL4_XENLA	Q63zl4 xenopus lae
442	29	78.4	947	2	Q9FXF0_ARATH	Q9fxf0 arabidopsis	515	28	75.7	245	2	Q5HBES_BHRWR	Q5hbes ehrlichia r
443	29	78.4	969	2	Q4RBZ7_TETNG	Q4rbz7 tetraodon n	516	28	75.7	250	2	Q98PG7_VIBF1	Q98pg7 mycoplasma
444	29	78.4	975	2	Q54CT6_DICDI	Q54ct6 dictyosteli	517	28	75.7	252	2	Q5E687_VIBF1	Q5e687 vibrio fisc
445	29	78.4	988	2	Q815B0_PLAF7	Q815b0 plasmodium	518	28	75.7	261	2	Q9LM15_ARATH	Q9lm15 arabidopsis
446	29	78.4	1048	2	Q4RBZ6_TETNG	Q4rbz6 tetraodon n	519	28	75.7	261	2	Q4ZVH1_PSESVM	Q4zvhl pseudomonas
447	29	78.4	1078	2	Q7QOU7_ANOGA	Q7qou7 anopheles g	520	28	75.7	261	2	Q87YX1_PSESVM	Q87yx1 pseudomonas
448	29	78.4	1171	2	Q4Q9T1_LETMA	Q4q9t1 leishmania	521	28	75.7	264	2	Q9JG87_9VIRU	Q9jg87 torque teno
449	29	78.4	1177	2	Q5TEA3_HUMAN	Q5tea3 homo sapien	522	28	75.7	267	2	Q7QX16_GIALA	Q7qx16 giardia lam
450	29	78.4	1221	2	Q9BIW9_CAEEL	Q9biw9 caenorhabdi	523	28	75.7	267	2	Q8NT67_CORGL	Q8nt67 corynebacte
451	29	78.4	1221	2	Q9N5Z3_CAEEL	Q9n5z3 caenorhabdi	524	28	75.7	268	2	Q4N836_THERP	Q4n836 theileria p
452	29	78.4	1251	2	Q9DFT9_BRARE	Q9dft9 brachydanio	525	28	75.7	269	2	Q9DAG2_MOUSE	Q9dag2 mus musculus
453	29	78.4	1314	2	Q5CW82_CRYPV	Q5cw82 cryptospori	526	28	75.7	270	1	NUP1_PENCI	Q9qag2 penicillium
454	29	78.4	1433	2	Q8A043_BACTN	Q8a043 bacteroides	527	28	75.7	270	1	NUP3_PENSQ	P24504 penicillium
455	29	78.4	1437	2	Q91BP7_9VIRU	Q91bp7 sugarcane s	528	28	75.7	271	1	SDRI_PICAN	Q86332 picea abies
456	29	78.4	2105	2	Q17679_CAEEL	Q17679 caenorhabdi	529	28	75.7	273	2	Q5L5W8_CHLAB	Q5l5w8 chlamydomyc
457	29	78.4	2146	2	Q4T7A2_TETNG	Q4t7a2 tetraodon n	530	28	75.7	277	2	Q06109_YEAST	Q06109 saccharomyc
458	29	78.4	2298	2	Q4SQ70_TETNG	Q4sq70 tetraodon n	531	28	75.7	277	2	Q4HRY3_CAMUP	Q4hry3 campylobact
459	29	78.4	2328	2	Q6PMX8_9PICO	Q6pmx8 foot-and-mo	532	28	75.7	278	2	Q6ND11_RHOPA	Q6nd11 rhodopseudo
460	29	78.4	2331	2	Q6PN26_9PICO	Q6pn26 foot-and-mo	533	28	75.7	280	2	Q7U966_SINPX	Q7u966 synecococc
461	29	78.4	2332	2	Q6PMW3_9PICO	Q6pmw3 foot-and-mo	534	28	75.7	281	2	Q811V6_RAT	Q811v6 rattus norv
462	29	78.4	2332	2	Q6PMZ7_9PICO	Q6pmz7 foot-and-mo	535	28	75.7	282	2	Q9IC83_HRV8	Q9ic83 human herpe
463	29	78.4	2335	2	Q902N9_9PICO	Q902n9 foot-and-mo	536	28	75.7	283	2	Q8CC37_MOUSE	Q8cc37 mus musculus
464	29	78.4	2340	2	Q6PMU2_9PICO	Q6pmu2 foot-and-mo	537	28	75.7	285	2	Q51H86_ENTHI	Q51h86 entamoeba h
465	29	78.4	2837	2	Q5SCN6_DICDI	Q5scn6 dictyosteli	538	28	75.7	286	1	SPEE_BUCAP	Q8k9t5 buchnera ap
466	29	78.4	3193	2	Q81590_PLAF7	Q81590 plasmodium	539	28	75.7	287	2	Q4W9G2_ASPPU	Q4w9g2 aspergillus
467	29	78.4	3713	2	Q4UFD1_THEAN	Q4ufd1 theileria a	540	28	75.7	287	2	Q9VHA1_DROME	Q9vha1 drosophila
468	29	78.4	3913	2	Q4U919_THEAN	Q4u919 theileria a	541	28	75.7	289	2	Q81EB8_BACCR	Q81eb8 bacillus ce
469	29	75.7	48	2	Q9XTK2_CAEEL	Q9xtk2 caenorhabdi	542	28	75.7	295	2	Q4MRL6_BACCR	Q4mrl6 bacillus ce



543	28	75.7	295	2	06HJ29_BACHK	06hjp9 bacillus th	616	28	75.7	489	2	05KU22_GEOKA	05kuz2 geobacillus
544	28	75.7	295	2	081RG6_BACAN	Q81rg6 bacillus an	617	28	75.7	501	2	07PV90_ANOGA	Q7pv90 anopheles g
545	28	75.7	295	2	063C88_BACCZ	Q63c88 bacillus ce	618	28	75.7	501	2	Q7RJ08_PLAYO	Q7rj08 plasmodium
546	28	75.7	299	2	086P04_DROME	Q86p04 drosophila	619	28	75.7	506	2	062975_9ERIC	Q62975 rhododendro
547	28	75.7	300	2	096LJ0_HUMAN	Q96lj0 homo sapien	620	28	75.7	506	2	Q8ME36_9ERIC	Q8me36 vaccinium p
548	28	75.7	303	2	04J4C7_AZOVI	Q4j4c7 azotobacter	621	28	75.7	506	2	Q8ME40_9ERIC	Q8me40 vaccinium e
549	28	75.7	306	2	09CUD9_MOUSE	Q9cud9 mus musculu	622	28	75.7	506	2	Q8WIL1_9ERIC	Q8wil1 vaccinium h
550	28	75.7	309	2	04UH5_THEAN	Q4uh5 theileria a	623	28	75.7	506	2	Q8WINO_9ERIC	Q8win0 chemistocle
551	28	75.7	309	2	08DIE7_SYNEL	Q8die7 synectococc	624	28	75.7	508	2	082233_ORISA	Q82233 oryza sativ
552	28	75.7	312	1	PANE_LACLA	Q9c1y8 lactococcu	625	28	75.7	512	2	082390_ARATH	Q82390 arabidopsis
553	28	75.7	312	2	07TQX6_MOUSE	Q7tcx7 mus musculu	626	28	75.7	512	2	Q8W4H0_ARATH	Q8w4h0 arabidopsis
554	28	75.7	312	2	Q7TQX6_MOUSE	Q7tcx7 mus musculu	627	28	75.7	513	2	Q4V5W6_DROME	Q4v5w6 drosophila
555	28	75.7	319	2	04YXR9_PLABE	Q4yxr9 plasmodium	628	28	75.7	514	2	064J25_9ERIC	Q64j25 rhododendro
556	28	75.7	321	2	0517K9_ENTHI	Q517k9 entamoeba h	629	28	75.7	514	2	064J26_9ERIC	Q64j26 rhododendro
557	28	75.7	327	2	0872C3_NEUCR	Q872c3 neurospora	630	28	75.7	514	2	Q84J31_9ERIC	Q84j31 rhododendro
558	28	75.7	327	2	04LSF3_9BURK	Q4lsf3 burkholderi	631	28	75.7	515	2	Q6R7H2_9HERP	Q6r7h2 ostreid her
559	28	75.7	327	2	06VNB9_MOUSE	Q6vnb9 mus musculu	632	28	75.7	515	2	064J27_9ERIC	Q64j27 rhododendro
560	28	75.7	335	2	06VNB9_MOUSE	Q6vnb9 mus musculu	633	28	75.7	516	2	064J29_9ERIC	Q64j29 rhododendro
561	28	75.7	335	2	06DV10_9HEXA	Q6dv10 onychiurus	634	28	75.7	516	2	064J30_9ERIC	Q64j30 rhododendro
562	28	75.7	339	2	Q4H947_9DETO	Q4h947 deinococcus	635	28	75.7	516	2	064J32_9ERIC	Q64j32 rhododendro
563	28	75.7	342	2	Q9NSR3_HUMAN	Q9nsr3 homo sapien	636	28	75.7	520	2	Q5SMR0_CRYNE	Q5smr0 cryptococcu
564	28	75.7	343	2	Q944B1_PRUPE	Q944b1 prunus pers	637	28	75.7	521	2	Q9N9G8_9ASCI	Q9n9g8 phallusia m
565	28	75.7	343	2	Q4T062_TETNG	Q4t062 tetraodon n	638	28	75.7	521	2	Q8RON4_MOUSE	Q8ron4 mus musculu
566	28	75.7	345	2	05LEP7_BACFN	Q5lep7 bacteroides	639	28	75.7	522	2	Q7XRT8_NEUCR	Q7xrt8 neurospora
567	28	75.7	345	2	064VN3_BACFR	Q64vn3 bacteroides	640	28	75.7	522	2	Q7Q709_ANOGA	Q7q709 anopheles g
568	28	75.7	348	2	Q4J397_9SMEG	Q4j397 poecilia sp	641	28	75.7	523	2	Q7S002_ASHGO	Q7s002 ashya gosa
569	28	75.7	367	2	05A387_CANAL	Q5a387 candida alb	642	28	75.7	526	2	Q9LQ77_ARATH	Q9lq77 arabidopsis
570	28	75.7	370	2	Q97DT2_CLOAB	Q97dt2 clostridium	643	28	75.7	527	2	Q5CDY9_CRYHO	Q5cdy9 cryptocospori
571	28	75.7	373	2	083NF8_TROW8	Q83nf8 tropheryma	644	28	75.7	527	2	Q7NAM6_MYCGA	Q7nam6 mycoplasma
572	28	75.7	373	2	Q83N12_TROWT	Q83n12 tropheryma	645	28	75.7	540	2	Q7FB20_ORYSA	Q7fb20 oryza sativ
573	28	75.7	379	2	09K1T9_CHLPN	Q9k1t9 chlamydia p	646	28	75.7	540	2	Q6ADN6_LEIFSON	Q6adn6 leifsonia x
574	28	75.7	379	2	Q80U24_MOUSE	Q80u24 mus musculu	647	28	75.7	544	2	Q6ADN6_LEIFSON	Q6adn6 leifsonia x
575	28	75.7	385	2	Q81DT2_PLAF7	Q81dt2 plasmodium	648	28	75.7	554	2	Q4IJN3_GIBZE	Q4ijn3 gibberella
576	28	75.7	395	2	Q9SQ25_CABEL	Q9sq25 caenorhabdi	649	28	75.7	557	2	Q6BVD0_DBBHA	Q6bvd0 debaryomyce
577	28	75.7	398	2	Q8H0X1_ARATH	Q8h0x1 arabidopsis	650	28	75.7	558	2	Q4RSC5_TETNG	Q4rsc5 tetraodon n
578	28	75.7	400	2	081EP7_PLAF7	Q81ep7 plasmodium	651	28	75.7	569	2	Q4T583_TETNG	Q4t583 tetraodon n
579	28	75.7	401	2	Q5XB35_CRYNE	Q5xb35 cryptococcu	652	28	75.7	570	2	Q5PP19_ARATH	Q5pp19 arabidopsis
580	28	75.7	404	2	085338_ECOLI	Q85338 escherichia	653	28	75.7	586	2	Q4RFB8_TETNG	Q4rfb8 tetraodon n
581	28	75.7	404	2	Q7DBF4_ECO57	Q7dbf4 escherichia	654	28	75.7	590	2	Q93CA0_BIFAD	Q93ca0 bifidobacte
582	28	75.7	409	1	YGJ2_SCHPO	Q9y7l4 schizosacch	655	28	75.7	596	2	Q7SGY7_NEUCR	Q7sgy7 neurospora
583	28	75.7	409	2	Q83YM1_9FLAO	Q83ym1 flavobacter	656	28	75.7	606	1	ZN214_HUMAN	Q812k8 plasmodium
584	28	75.7	410	2	Q9H7F2_HUMAN	Q9h7f2 homo sapien	657	28	75.7	609	2	Q812K8_PLAF7	Q812k8 plasmodium
585	28	75.7	410	2	Q6E842_9HEMI	Q6e842 metcalfiell	658	28	75.7	610	2	Q81I64_PLAF7	Q81i64 plasmodium
586	28	75.7	415	2	Q92739_CHLPN	Q92739 chlamydia p	659	28	75.7	610	2	Q5A170_DICDI	Q5a170 dictyosteli
587	28	75.7	422	2	Q7X7D6_ORYSA	Q7x7d6 oryza sativ	660	28	75.7	613	2	Q5A2V2_CANAL	Q5a2v2 candida alb
588	28	75.7	422	2	Q6MDJ0_PARUW	Q6mdj0 parachlamyd	661	28	75.7	614	2	Q5CYX9_CRYPY	Q5cyx9 cryptocospori
589	28	75.7	424	2	Q4XR08_PLACH	Q4xr08 plasmodium	662	28	75.7	617	2	Q5RDY8_PONPY	Q5rdy8 pongo pygma
590	28	75.7	424	2	Q8S236_DROME	Q8s236 drosophila	663	28	75.7	626	2	Q5CJ64_CRYHO	Q5cj64 cryptocospori
591	28	75.7	431	2	Q7QJPI_ANOGA	Q7qjpi anopheles g	664	28	75.7	629	2	Q4V6W4_PLACH	Q4v6w4 plasmodium
592	28	75.7	431	2	Q9VK94_DROME	Q9vk94 drosophila	665	28	75.7	632	2	Q5SRC1_CRYNE	Q5src1 cryptococcu
593	28	75.7	431	2	Q6FPE3_ACIAD	Q6ffe3 acinetobact	666	28	75.7	632	2	Q5KEV0_CRYNE	Q5kev0 cryptococcu
594	28	75.7	433	2	Q7T6X0_MIMIV	Q7t6x0 mimivirus.	667	28	75.7	639	1	SYT_CLOTE	Q891t0 clostridium
595	28	75.7	435	2	Q7TOR0_XENLA	Q7tor0 xenopus lae	668	28	75.7	649	2	Q54GJ0_DICDI	Q54gj0 dictyosteli
596	28	75.7	437	2	Q90W14_CHICK	Q90w14 gallus gall	669	28	75.7	653	2	Q6V2M9_CNPV	Q6v2m9 canarypox v
597	28	75.7	438	2	Q4UIK4_THEAN	Q4uik4 theileria a	670	28	75.7	656	2	Q7RA47_PLAYO	Q7ra47 plasmodium
598	28	75.7	440	2	Q8CA99_MOUSE	Q8ca99 mus musculu	671	28	75.7	656	2	Q80V96_MOUSE	Q80v96 mus musculu
599	28	75.7	450	2	Q4N091_THEPA	Q4n091 theileria p	672	28	75.7	661	2	Q9DDU3_BRARE	Q9ddu3 brachydanio
600	28	75.7	453	2	Q9VCT6_DROME	Q9vct6 drosophila	673	28	75.7	661	2	Q98TU2_BRARE	Q98tu2 brachydanio
601	28	75.7	453	2	Q4S5U7_TETNG	Q4s5u7 tetraodon n	674	28	75.7	664	2	Q928F5_CHLPN	Q928f5 chlamydia p
602	28	75.7	455	2	Q6CGH6_YARLI	Q6cgh6 yarowia li	675	28	75.7	666	2	Q9VC33_DROME	Q9vc33 drosophila
603	28	75.7	463	2	Q812K7_PLAF7	Q812k7 plasmodium	676	28	75.7	667	2	Q5RHU8_BRARE	Q5rhu8 brachydanio
604	28	75.7	465	2	Q4S2A7_TETNG	Q4s2a7 tetraodon n	677	28	75.7	671	2	Q5VZK4_CNPV	Q5vzk4 canarypox v
605	28	75.7	468	2	Q5UQ90_MIMIV	Q5uq90 mimivirus.	678	28	75.7	675	2	Q8DTP6_MOUSE	Q8dtp6 mus musculu
606	28	75.7	470	2	Q54MX4_DICDI	Q54mx4 dictyosteli	679	28	75.7	678	2	Q4V5A7_9VIRU	Q4v5a7 caephalia e
607	28	75.7	470	2	Q9DS11_9PICO	Q9ds11 foot-and-mo	680	28	75.7	689	2	Q4P5S0_USTMA	Q4p5s0 ustilago ma
608	28	75.7	470	2	Q84807_9PICO	Q84807 foot-and-mo	681	28	75.7	696	2	Q5A708_CANAL	Q5a708 candida alb
609	28	75.7	471	1	SEC12_YEAST	P11655 saccharomyc	682	28	75.7	699	2	Q27034_THEPA	Q27034 theileria p
610	28	75.7	471	2	Q8XVT8_RALSO	Q8xvt8 raistonia s	683	28	75.7	700	2	Q4WT57_ASPFU	Q4wt57 aspergillus
611	28	75.7	475	2	Q6BLZ5_DEBHA	Q6blz5 debaryomyce	684	28	75.7	704	2	Q7QIF8_ANOGA	Q7qif8 anopheles g
612	28	75.7	475	2	Q9LX53_ARATH	Q9lx53 arabidopsis	685	28	75.7	714	2	Q4YHM5_PLABE	Q4yhm5 plasmodium
613	28	75.7	475	2	Q94I17_CUCMA	Q94i17 cucurbita m	686	28	75.7	720	2	Q40902_PETIN	Q40902 petunia int
614	28	75.7	480	2	Q6SFG5_9BACT	Q6sf5 uncultured	687	28	75.7	734	2	Q6FQ28_CANGA	Q6fq28 candida gla
615	28	75.7	482	2	Q5SBY9_DICDI	Q5sby9 dictyosteli	688	28	75.7	734	2	Q7QYLE_GITALA	Q7qyle giardia lam

689	28	75.7	742	2	Q5WHJ7_BACSK	Q5whj7 bacillus cl	762	28	75.7	2311	2	Q6PMY9_9PICO	Q6pmY9 foot-and-mo
690	28	75.7	743	2	Q39256_9ALPH	Q39256 equid herpe	763	28	75.7	2317	2	Q5UVJ0_9PICO	Q5uvJ0 foot-and-mo
691	28	75.7	777	2	Q9B5F5_HUMAN	Q9b5f5 homo sapien	764	28	75.7	2320	2	Q39176_9PICO	Q39176 foot-and-mo
692	28	75.7	807	2	Q8IKK6_PLAF7	Q8ikk6 plasmodium	765	28	75.7	2322	2	Q68J56_9PICO	Q68J56 foot-and-mo
693	28	75.7	814	2	Q5PY52_DAUCA	Q5py52 daucus caro	766	28	75.7	2322	2	Q9WN12_9PICO	Q9wn12 foot-and-mo
694	28	75.7	824	2	Q6JK76_9NUCL	Q6jk76 neodiprion	767	28	75.7	2322	2	Q6PMV1_9PICO	Q6pmV1 foot-and-mo
695	28	75.7	830	2	Q6LFF3_PLAF7	Q6lff3 plasmodium	768	28	75.7	2322	2	Q6PMV3_9PICO	Q6pmV3 foot-and-mo
696	28	75.7	846	2	Q4S135_TETNG	Q4s135 tetraodon n	769	28	75.7	2322	2	Q6W0A7_9PICO	Q6w0A7 foot-and-mo
697	28	75.7	861	1	POLG_FMDVS	P03311 foot-and-mo	770	28	75.7	2322	2	Q9DLK1_9PICO	Q9dlK1 foot-and-mo
698	28	75.7	870	2	Q7XX72_ORYSA	Q7xx72 oryza sativ	771	28	75.7	2327	2	Q6PMX6_9PICO	Q6pmX6 foot-and-mo
699	28	75.7	875	2	Q9H706_HUMAN	Q9h706 homo sapien	772	28	75.7	2327	2	Q6PMY1_FMDVT	Q6pmY1 foot-and-mo
700	28	75.7	877	2	Q8ND03_HUMAN	Q8nd03 homo sapien	773	28	75.7	2327	2	Q6PMY2_FMDVT	Q6pmY2 foot-and-mo
701	28	75.7	901	2	Q4Z073_PLABE	Q4z073 plasmodium	774	28	75.7	2327	2	Q9E2G4_9PICO	Q9e2G4 foot-and-mo
702	28	75.7	907	2	Q84773_9PICO	Q84773 foot-and-mo	775	28	75.7	2327	2	Q9QCE3_9PICO	Q9qce3 foot-and-mo
703	28	75.7	921	2	Q4N1W8_THEPA	Q4n1w8 theileria p	776	28	75.7	2327	2	Q9QCE4_9PICO	Q9qce4 foot-and-mo
704	28	75.7	928	2	Q81NV6_DROME	Q81nv6 drosophila	777	28	75.7	2327	2	Q9QCE2_9PICO	Q9qce2 foot-and-mo
705	28	75.7	929	2	Q7R824_PLAYO	Q7r824 plasmodium	778	28	75.7	2328	2	Q9YQO5_9PICO	Q9yqq5 foot-and-mo
706	28	75.7	932	2	Q6PUB4_ANOGA	Q6pub4 anopheles g	779	28	75.7	2328	2	Q6PMY0_9PICO	Q6pmY0 foot-and-mo
707	28	75.7	940	2	Q58C18_EMENI	Q5bc18 aspergillus	780	28	75.7	2328	2	Q6PMZ1_9PICO	Q6pmZ1 foot-and-mo
708	28	75.7	959	2	Q97045_HALRO	Q97045 halocynthia	781	28	75.7	2328	2	Q9YJX0_9PICO	Q9yJx0 foot-and-mo
709	28	75.7	963	1	LOLA5_DROME	O9v5m6 drosophila	782	28	75.7	2329	2	Q5TP16_9PICO	Q5tp16 foot-and-mo
710	28	75.7	968	2	Q4X4Q9_PLACH	Q4x4q9 plasmodium	783	28	75.7	2329	2	Q6PMX7_9PICO	Q6pmX7 foot-and-mo
711	28	75.7	969	2	Q4S8D2_TETNG	Q4s8d2 tetraodon n	784	28	75.7	2329	2	Q6PMX9_9PICO	Q6pmX9 foot-and-mo
712	28	75.7	977	2	Q81GV1_DROME	Q81gv1 drosophila	785	28	75.7	2329	2	Q6PMZ0_9PICO	Q6pmZ0 foot-and-mo
713	28	75.7	1001	2	Q6NYV7_BRARE	Q6nyv7 brachydanio	786	28	75.7	2329	2	Q6I02_9PICO	Q6i02 foot-and-mo
714	28	75.7	1014	2	Q9EYH7_YERPS	Q9eyh7 yersinia ps	787	28	75.7	2330	2	Q7TDB3_9PICO	Q7tdb3 foot-and-mo
715	28	75.7	1022	2	Q4S618_TETNG	Q4s618 tetraodon n	788	28	75.7	2331	2	Q9PYF1_FMDVO	Q9pyf1 foot-and-mo
716	28	75.7	1026	2	Q61S19_BRARE	Q61s19 brachydanio	789	28	75.7	2332	1	POLG_FMDVA	P03308 f genome po
717	28	75.7	1036	2	Q805F0_BRARE	Q805f0 brachydanio	790	28	75.7	2332	1	POLG_FMDVA	P03305 f genome po
718	28	75.7	1030	2	Q90ZT4_CHICK	Q90zt4 gallus gall	791	28	75.7	2332	1	POLG_FMDVO	P03305 f genome po
719	28	75.7	1040	1	PCD10_HUMAN	Q9p2e7 homo sapien	792	28	75.7	2332	2	Q7TD06_9PICO	Q7td06 foot-and-mo
720	28	75.7	1040	2	Q4W5F6_HUMAN	Q4w5f6 homo sapien	793	28	75.7	2332	2	Q7TD07_9PICO	Q7td07 foot-and-mo
721	28	75.7	1040	2	Q9Z518_MOUSE	Q9z518 mus musculu	794	28	75.7	2332	2	Q6PMU9_9PICO	Q6pmU9 foot-and-mo
722	28	75.7	1075	1	MTMR3_MOUSE	Q8k296 mus musculu	795	28	75.7	2332	2	Q6PMV4_9PICO	Q6pmV4 foot-and-mo
723	28	75.7	1075	2	Q5NCA1_MOUSE	Q5nca1 mus musculu	796	28	75.7	2332	2	Q6PMV6_9PICO	Q6pmV6 foot-and-mo
724	28	75.7	1098	2	Q80TE2_MOUSE	Q80te2 mus musculu	797	28	75.7	2332	2	Q6PMV7_9PICO	Q6pmV7 foot-and-mo
725	28	75.7	1099	2	Q54KF6_DICDI	Q54kf6 dictyosteli	798	28	75.7	2332	2	Q6PMV8_9PICO	Q6pmV8 foot-and-mo
726	28	75.7	1107	2	Q6FIM5_CANGA	Q6fim5 candida gia	799	28	75.7	2332	2	Q6PMV9_9PICO	Q6pmV9 foot-and-mo
727	28	75.7	1110	2	Q4Z0J7_PLABE	Q4z0j7 plasmodium	800	28	75.7	2332	2	Q6PMW0_9PICO	Q6pmW0 foot-and-mo
728	28	75.7	1125	2	Q4N0Z7_THEPA	Q4n0z7 theileria p	801	28	75.7	2332	2	Q6PMW1_9PICO	Q6pmW1 foot-and-mo
729	28	75.7	1132	2	Q5Z1B2_CHICK	Q5z1b2 gallus gall	802	28	75.7	2332	2	Q6PMW2_9PICO	Q6pmW2 foot-and-mo
730	28	75.7	1134	2	Q99D22_BHV4	Q99d22 bovine herp	803	28	75.7	2332	2	Q6PMW4_9PICO	Q6pmW4 foot-and-mo
731	28	75.7	1159	2	Q5NCA2_MOUSE	Q5nca2 mus musculu	804	28	75.7	2332	2	Q6PMW5_9PICO	Q6pmW5 foot-and-mo
732	28	75.7	1159	2	Q6G145_MOUSE	Q6g145 mus musculu	805	28	75.7	2332	2	Q6PMW6_9PICO	Q6pmW6 foot-and-mo
733	28	75.7	1167	2	Q5NCA3_MOUSE	Q5nca3 mus musculu	806	28	75.7	2332	2	Q6PMW7_9PICO	Q6pmW7 foot-and-mo
734	28	75.7	1190	2	Q7S867_NEUCR	Q7s867 neurospora	807	28	75.7	2332	2	Q6PMW8_9PICO	Q6pmW8 foot-and-mo
735	28	75.7	1195	2	Q5NCA4_MOUSE	Q5nca4 mus musculu	808	28	75.7	2332	2	Q6PMW9_9PICO	Q6pmW9 foot-and-mo
736	28	75.7	1269	2	Q5B6U5_EMENI	Q5b6u5 aspergillus	809	28	75.7	2332	2	Q6PMX0_9PICO	Q6pmX0 foot-and-mo
737	28	75.7	1291	2	Q6BZ89_DEBHA	Q6bz89 debaryomyce	810	28	75.7	2332	2	Q6PMX1_9PICO	Q6pmX1 foot-and-mo
738	28	75.7	1292	2	Q5C1W4_CRYHO	Q5c1w4 cryptospori	811	28	75.7	2332	2	Q6PMX2_9PICO	Q6pmX2 foot-and-mo
739	28	75.7	1304	2	Q6FR07_CANGA	Q6fr07 candida gia	812	28	75.7	2332	2	Q6PMX4_9PICO	Q6pmX4 foot-and-mo
740	28	75.7	1308	2	Q5CVU2_CRYEV	Q5cvu2 cryptospori	813	28	75.7	2332	2	Q6PMZ4_9PICO	Q6pmZ4 foot-and-mo
741	28	75.7	1339	2	Q4XZV4_PLACH	Q4xzv4 plasmodium	814	28	75.7	2332	2	Q6PMZ7_9PICO	Q6pmZ7 foot-and-mo
742	28	75.7	1347	2	Q7RR30_PLAYO	Q7rr30 plasmodium	815	28	75.7	2332	2	Q6PN05_9PICO	Q6pn05 foot-and-mo
743	28	75.7	1376	2	Q5FIC2_LACAC	Q5fic2 lactobacill	816	28	75.7	2332	2	Q6PN06_9PICO	Q6pn06 foot-and-mo
744	28	75.7	1395	2	Q4P950_USTMA	Q4p950 usilago ma	817	28	75.7	2332	2	Q6PN07_9PICO	Q6pn07 foot-and-mo
745	28	75.7	1466	2	Q4N8P3_THEPA	Q4n8p3 theileria p	818	28	75.7	2332	2	Q6PN08_9PICO	Q6pn08 foot-and-mo
746	28	75.7	1564	1	NUIB84_SCHPO	Q9p7m8 schizosacch	819	28	75.7	2332	2	Q6PN09_9PICO	Q6pn09 foot-and-mo
747	28	75.7	1583	2	Q8YTR4_ANASP	Q8ytr4 anabaena sp	820	28	75.7	2332	2	Q6PN12_9PICO	Q6pn12 foot-and-mo
748	28	75.7	1641	2	Q9HLU6_TREAC	Q9hlu6 thermoplasma	821	28	75.7	2332	2	Q6PN15_9PICO	Q6pn15 foot-and-mo
749	28	75.7	1669	2	Q9W1A8_DROME	Q9w1a8 drosophila	822	28	75.7	2332	2	Q6PN17_9PICO	Q6pn17 foot-and-mo
750	28	75.7	1673	2	Q4PCB9_USTMA	Q4pcb9 usilago ma	823	28	75.7	2332	2	Q6PN19_9PICO	Q6pn19 foot-and-mo
751	28	75.7	1726	2	Q6NEV4_CORDI	Q6nev4 corynebacte	824	28	75.7	2332	2	Q6PN32_9PICO	Q6pn32 foot-and-mo
752	28	75.7	1749	2	Q81IG8_PLAF7	Q81ig8 plasmodium	825	28	75.7	2332	2	Q6PN35_9PICO	Q6pn35 foot-and-mo
753	28	75.7	1785	2	Q815Z0_PLAF7	Q815z0 plasmodium	826	28	75.7	2332	2	Q6Z2B7_9PICO	Q6z2b7 foot-and-mo
754	28	75.7	1892	2	Q51JA3_9VIRU	Q51ja3 apricot pse	827	28	75.7	2332	2	Q80B19_9PICO	Q80b19 foot-and-mo
755	28	75.7	1943	2	Q4P5F6_USTMA	Q4p5f6 usilago ma	828	28	75.7	2332	2	Q80B20_9PICO	Q80b20 foot-and-mo
756	28	75.7	2012	2	Q81DC5_PLAF7	Q81dc5 plasmodium	829	28	75.7	2332	2	Q80B21_9PICO	Q80b21 foot-and-mo
757	28	75.7	2028	2	Q4QHD9_LEIMA	Q4qhd9 leishmania	830	28	75.7	2332	2	Q80B22_9PICO	Q80b22 foot-and-mo
758	28	75.7	2168	2	Q4Q5W1_LEIMA	Q4q5w1 leishmania	831	28	75.7	2332	2	Q80B23_9PICO	Q80b23 foot-and-mo
759	28	75.7	2200	2	Q4SZM9_TETNG	Q4szm9 tetraodon n	832	28	75.7	2332	2	Q80B24_9PICO	Q80b24 foot-and-mo
760	28	75.7	2285	2	Q4Z5U8_PLABE	Q4z5u8 plasmodium	833	28	75.7	2332	2	Q8JR20_9PICO	Q8jR20 foot-and-mo
761	28	75.7	2305	2	Q6PMZ9_9PICO	Q6pmz9 foot-and-mo	834	28	75.7	2332	2	Q8JRE1_9PICO	Q8jRe1 foot-and-mo

835	28	75.7	2332	2	Q8JW41_9PICO	Q8Jw41	foot-and-mo	908	27	73.0	132	2	Q81LT6_BACAN	Q81lt6	bacillus an
836	28	75.7	2332	2	Q8U2C1_9PICO	Q8uzc1	foot-and-mo	909	27	73.0	138	2	Q14867_HUMAN	Q14867	homo sapien
837	28	75.7	2332	2	Q91AH4_9PICO	Q91ah4	foot-and-mo	910	27	73.0	145	2	Q6ANF5_DESPS	Q6anf5	desulfotale
838	28	75.7	2332	2	Q6EF47_9PICO	Q6ef47	foot-and-mo	911	27	73.0	145	2	Q9DVU1_9BACU	Q9dvu1	plutellia xy
839	28	75.7	2333	2	Q6PM25_9PICO	Q6pm25	foot-and-mo	912	27	73.0	147	2	Q5TQ96_ANOGA	Q5tq96	anopheles g
840	28	75.7	2333	2	Q6PN08_9PICO	Q6pn08	foot-and-mo	913	27	73.0	149	2	Q5CZD5_BACFN	Q5czd5	bacteroides
841	28	75.7	2333	2	Q6PN04_9PICO	Q6pn04	foot-and-mo	914	27	73.0	152	2	Q939G6_PSEAC	Q939g6	pseudomonas
842	28	75.7	2333	2	Q6PN11_9PICO	Q6pn11	foot-and-mo	915	27	73.0	157	2	Q4IRJ4_GIBZE	Q4irj4	gibberella
843	28	75.7	2333	2	Q6PN16_9PICO	Q6pn16	foot-and-mo	916	27	73.0	157	2	Q4VR81_CAWJE	Q4vr81	campylobact
844	28	75.7	2333	2	Q6PN18_9PICO	Q6pn18	foot-and-mo	917	27	73.0	158	2	Q5TWC0_ANOGA	Q5twc0	anopheles g
845	28	75.7	2333	2	Q6PN20_9PICO	Q6pn20	foot-and-mo	918	27	73.0	159	2	Q53356_MYCTU	Q53356	mycobacteri
846	28	75.7	2333	2	Q6PN28_9PICO	Q6pn28	foot-and-mo	919	27	73.0	159	2	Q7TWS3_MYCBO	Q7tws3	mycobacteri
847	28	75.7	2333	2	Q6PN29_9PICO	Q6pn29	foot-and-mo	920	27	73.0	160	2	Q12540_AGABI	Q12540	agaricus bi
848	28	75.7	2333	2	Q6PN30_9PICO	Q6pn30	foot-and-mo	921	27	73.0	160	2	Q5DGY5_SCHJA	Q5dgy5	schistosoma
849	28	75.7	2333	2	Q6PN31_9PICO	Q6pn31	foot-and-mo	922	27	73.0	160	2	Q8C9L2_MOUSE	Q8c9l2	mus musculus
850	28	75.7	2333	2	Q6PN33_9PICO	Q6pn33	foot-and-mo	923	27	73.0	165	1	FTN2_HAEIN	FTN2	haemophilus
851	28	75.7	2333	2	Q6PN34_9PICO	Q6pn34	foot-and-mo	924	27	73.0	165	2	Q4QK97_HAEI8	Q4qk97	haemophilus
852	28	75.7	2334	2	Q6PM22_9PICO	Q6pm22	foot-and-mo	925	27	73.0	165	2	Q9CMY3_PASMU	Q9cmv3	paasteurella
853	28	75.7	2334	2	Q6PM25_9PICO	Q6pm25	foot-and-mo	926	27	73.0	165	2	Q65TM4_MANSM	Q65tm4	mannheimia
854	28	75.7	2335	2	Q6PM27_9PICO	Q6pm27	foot-and-mo	927	27	73.0	167	2	Q61C84_CABER	Q61c84	caenorhabdi
855	28	75.7	2336	2	Q6PMY3_9PICO	Q6pmv3	foot-and-mo	928	27	73.0	167	2	Q84AP0_SERMA	Q84ap0	serratia ma
856	28	75.7	2350	2	Q6PN10_9PICO	Q6pn10	foot-and-mo	929	27	73.0	167	2	Q8ZDP6_YERPE	Q8zdp6	yersinia pe
857	28	75.7	2358	1	MOK13_SCHPO	Q9y719	schizosacch	930	27	73.0	167	2	Q669B1_YERPS	Q669e1	yersinia ps
858	28	75.7	2369	2	Q96VL6_CANAL	Q96vl6	candida alb	931	27	73.0	168	2	Q7VKV8_HABDU	Q7vkv8	haemophilus
859	28	75.7	2435	2	Q4VTY1_PLABE	Q4vtv1	plasmodium	932	27	73.0	169	2	Q19541_CABEL	Q19541	caenorhabdi
860	28	75.7	2508	2	Q96175_PLAF7	Q96175	plasmodium	933	27	73.0	170	2	Q6Z3R1_CABER	Q6z3r1	caenorhabdi
861	28	75.7	2510	2	Q5AZW6_EMENI	Q5azw6	aspergillus	934	27	73.0	170	2	Q97G12_CIOAB	Q97g12	clostridium
862	28	75.7	2624	2	Q5ALR4_CANAL	Q5alr4	candida alb	935	27	73.0	175	2	Q8IX76_HUMAN	Q8ix76	homo sapien
863	28	75.7	2624	2	Q5AM63_CANAL	Q5am63	candida alb	936	27	73.0	177	2	Q9CNG3_PASMU	Q9cng3	paasteurella
864	28	75.7	2779	2	Q8ILH0_PLAF7	Q8ilh0	plasmodium	937	27	73.0	179	1	YOP1_YEAST	YOP1	saccharomyc
865	28	75.7	2900	2	Q81FI2_PLAF7	Q81fi2	plasmodium	938	27	73.0	182	2	Q74GW5_GEOSL	Q74gw5	geobacter s
866	28	75.7	3011	1	YOS1_SCHPO	P87319	schizosacch	939	27	73.0	183	2	Q86KE9_DICDI	Q86ke9	dictyosteli
867	28	75.7	3171	2	Q7RSE3_PLAYO	Q7rse3	plasmodium	940	27	73.0	185	2	Q8VR81_ECOLI	Q8vr81	escherichia
868	28	75.7	3612	2	Q7QU21_GIALA	Q7qu21	giardia lam	941	27	73.0	187	2	Q510T3_GROKA	Q510t3	geobacillus
869	28	75.7	3655	1	YAMB_SCHPO	Q10064	schizosacch	942	27	73.0	189	2	Q7ZZQ9_FUGRU	Q7zzq9	fugu rubrip
870	28	75.7	3896	2	Q81581_PLAF7	Q81581	plasmodium	943	27	73.0	192	2	Q8COR0_STAEP	Q8cor0	staphylococ
871	28	75.7	4071	2	Q7PH68_ANOGA	Q7ph68	anopheles g	944	27	73.0	192	2	Q5HRX4_STAEP	Q5hrx4	staphylococ
872	28	75.7	4098	2	Q7FQ9G_ANOGA	Q7fq9g	anopheles g	945	27	73.0	193	2	Q4L383_STAHO	Q4l383	staphylococ
873	28	75.7	4612	2	Q5CSN7_CRYPV	Q5csn7	cryptospori	946	27	73.0	194	1	Y1459_HAEIN	Y1459	haemophilus
874	28	75.7	5808	2	Q4UFB3_THEAN	Q4ufb3	theileria a	947	27	73.0	195	2	Q7P7N6_FUSNV	Q7p7n6	fusobacteri
875	28	73.0	23	2	Q9TRE7_RABIT	Q9tre7	oryctolagus	948	27	73.0	195	2	Q8CQ23_STAEP	Q8cq23	staphylococ
876	28	73.0	25	2	Q4UX48_PLACH	Q4ux48	plasmodium	949	27	73.0	195	2	Q8RHT7_FUSNN	Q8rht7	fuobacteri
877	28	73.0	29	2	Q4VPX7_PLABE	Q4vpv7	plasmodium	950	27	73.0	196	2	Q5HKY5_STAEP	Q5hky5	staphylococ
878	28	73.0	33	2	Q5C529_SCHJA	Q5c529	schistosoma	951	27	73.0	198	2	Q4QKI3_HAEI8	Q4qki3	haemophilus
879	28	73.0	42	2	Q91PE1_IRV6	Q91pe1	chilo iride	952	27	73.0	200	2	Q8DVX1_STRMU	Q8dvx1	streptococ
880	28	73.0	50	2	Q92GM8_RICCN	Q92gm8	rickettsia	953	27	73.0	200	2	Q4TAH4_TETNG	Q4tah4	tetradon n
881	28	73.0	51	2	Q64MM0_BACFR	Q64mm0	bacteroides	954	27	73.0	201	2	Q22508_CABEL	Q22508	caenorhabdi
882	28	73.0	56	2	Q647U4_9ARCH	Q647u4	uncultured	955	27	73.0	203	1	THGA_ECOLI	P07464	escherichia
883	28	73.0	60	2	Q7RNB2_PLAYO	Q7rnb2	plasmodium	956	27	73.0	203	2	Q8GXZ9_ARATH	Q8gxz9	arabidopsis
884	28	73.0	65	2	Q4TCS3_TETNG	Q4tcs3	tetradon n	957	27	73.0	203	2	Q8X686_ECO57	Q8x686	escherichia
885	28	73.0	66	2	Q9ZAH1_9LACT	Q9zah1	lactococcus	958	27	73.0	206	2	Q8DWL4_STRMU	Q8dwl4	streptococ
886	28	73.0	71	2	Q98533_CHVP1	Q98533	paramecium	959	27	73.0	207	2	Q5E468_VIBF1	Q5e468	vibrio fiac
887	28	73.0	74	2	Q8U2V9_PYRPU	Q8u2v9	pyrococcus	960	27	73.0	208	1	FGF9_HUMAN	P51371	homo sapien
888	28	73.0	77	2	Q9FLJ3_ARATH	Q9flj3	arabidopsis	961	27	73.0	208	1	FGF9_MOUSE	P54130	mus musculus
889	28	73.0	87	1	GLRX_BPT4	P00276	bacterioph	962	27	73.0	208	1	FGF9_RAT	P53364	rattus norv
890	28	73.0	87	2	Q5QC19_9AUD	Q5qc19	enterobacte	963	27	73.0	208	2	Q95LI2_PIG	Q95li2	sus scrofa
891	28	73.0	90	2	Q5TQ90_ANOGA	Q5tq90	anopheles g	964	27	73.0	208	2	Q50819_BORBU	Q50819	borrelia bu
892	28	73.0	90	2	Q5TQ95_ANOGA	Q5tq95	anopheles g	965	27	73.0	208	2	Q7ZZN4_CHICK	Q7zzn4	gallus gall
893	28	73.0	90	2	Q5TXR8_ANOGA	Q5txr8	anopheles g	966	27	73.0	208	2	Q9PVV1_XENLA	Q9pvy1	xenopus lae
894	28	73.0	90	2	Q8OL19_9VIRU	Q8ol19	sulfolobus	967	27	73.0	212	1	RL4_CANBF	RL4	canibacter
895	28	73.0	92	2	Q5TQ91_ANOGA	Q5tq91	anopheles g	968	27	73.0	212	2	Q7D5R1_MYCTU	Q7d5r1	mycobacteri
896	28	73.0	93	2	Q5TU82_9VIRU	Q5tj82	sulfolobus	969	27	73.0	213	2	Q9NS08_HUMAN	Q9ns08	homo sapien
897	28	73.0	101	2	Q4MJW6_BACCE	Q4mjw6	bacillus ce	970	27	73.0	213	2	Q5W6Y9_ORYSA	Q5w6y9	oryza sativ
898	28	73.0	101	2	Q9YUH3_9ROEV	Q9yuh3	rotavirus b	971	27	73.0	213	2	Q4T7T8_TETNG	Q4t7t8	tetradon n
899	28	73.0	105	2	Q4Z7S0_PLABE	Q4z7s0	plasmodium	972	27	73.0	217	2	Q6IDL4_ARATH	Q6idl4	arabidopsis
900	28	73.0	107	2	Q4YKP2_PLABE	Q4ykp2	plasmodium	973	27	73.0	218	2	Q8FST7_COREF	Q8fst7	corynebacte
901	28	73.0	107	2	Q546T3_ORYSA	Q5z6t3	oryza sativ	974	27	73.0	219	2	Q5SVB0_CRYNE	Q5svb0	cryptococcu
902	28	73.0	118	2	Q87J9E_VIBPA	Q87je9	vibrio para	975	27	73.0	219	2	Q5KKX5_CRYNE	Q5kkx5	cryptococcu
903	28	73.0	132	2	Q4MNY8_BACCE	Q4mny8	bacillus ce	976	27	73.0	219	2	Q54QY0_DICDI	Q54qy0	dictyosteli
904	28	73.0	132	2	Q730N5_BACC1	Q730n5	bacillus ce	977	27	73.0	219	2	Q9K1X3_CHLNP	Q9k1x3	chlamydia p
905	28	73.0	132	2	Q818G0_BACCR	Q818g0	bacillus ce	978	27	73.0	219	2	Q9D4A3_MOUSE	Q9d4a3	mus musculus
906	28	73.0	132	2	Q6HDM0_BACHK	Q6hdm0	bacillus th	979	27	73.0	220	2	Q8FKG8_ECOL6	Q8fk98	escherichia
907	28	73.0	132	2	Q634P0_BACCCZ	Q634p0	bacillus ce	980	27	73.0	222	2	Q83Z94_ENTFA	Q83z94	enterococcu

981 27 73.0 226 2 Q6P074 mouse  
982 27 73.0 227 2 Q8RW2 metacharsarc  
983 27 73.0 227 2 Q4XJX8 plasmodium  
984 27 73.0 227 2 Q6QPD1 simian aden  
985 27 73.0 228 2 Q97DM6 clostridium  
986 27 73.0 231 2 Q4YZY8 plasmidum  
987 27 73.0 231 2 Q8C6Y8 mus musculus  
988 27 73.0 233 2 Q4RV40 tetragon n  
989 27 73.0 235 2 Q50LK6 entamoeba h  
990 27 73.0 238 2 Q4I095 gibberella  
991 27 73.0 239 2 Q4N4A3 theileria p  
992 27 73.0 241 2 Q4SBJ9 tetragon n  
993 27 73.0 241 2 Q4THM1 tetragon n  
994 27 73.0 242 2 Q5TQJ4 anopheles g  
995 27 73.0 242 2 Q4NVE0 bacillus ce  
996 27 73.0 244 2 Q7VPR1 chlamydia p  
997 27 73.0 244 2 Q9Z6P1 chlamydia p  
998 27 73.0 244 2 Q7ZTV1 tetragon f  
999 27 73.0 244 2 Q9YH94 xenopus lae  
1000 27 73.0 246 2 Q4UYI9 xanthomonas

## ALIGNMENTS

RESULT 1  
Q8IE54 PLAF7 PRELIMINARY; PRT; 4780 AA.  
AC Q8IE54;  
DT 01-MAR-2003 (TRENBLrel. 23, Created)  
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)  
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)  
DE Hypothetical protein PF13\_0148.  
GN Name=PF13\_0148;  
OS Plasmodium falciparum (isolate 3D7).  
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
OX NCBI\_TaxID=36329;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=3D7;  
RA Harris B., Lennard N., Clark L., Line A., Barron A., Corton C.,  
RA Berriman M., Pain A., Hall N., Atkin R., Chillingworth C., Doggett J.,  
RA Ormond D., Sanders M., Hayes R., Hall S., Quail M., Barrell B.,  
RA Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AL844509; CAD52412.1; -; Genomic DNA.  
DR InterPro; IPR008266; Tyr\_kinase AS.  
DR PROSITE; PS00109; PROTEIN\_KINASE\_TYR; UNKNOWN 1.  
KW Hypothetical protein.  
SQ SEQUENCE 4780 AA; 575455 MW; 568F461F83657D44 CRC64;

Query Match 100.0%; Score 37; DB 2; Length 4780;  
Best Local Similarity 100.0%; Pred. No. 3.4e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLHS 7  
|||  
Db 1325 YSSNLHS 1331

RESULT 2  
Q4JBN8 SULAC PRELIMINARY; PRT; 423 AA.  
AC Q4JBN8;  
DT 13-SEP-2005 (TRENBLrel. 31, Created)  
DT 13-SEP-2005 (TRENBLrel. 31, Last sequence update)  
DT 13-SEP-2005 (TRENBLrel. 31, Last annotation update)  
DE Peptidase (EC 3.4.-.-). 0375;  
GN OrderedLocustNames=Sacii. 0375;  
OS Sulfolobus acidocaldarius.  
OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;  
OC Sulfolobus.  
OX NCBI\_TaxID=2285;  
RN [1]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
RC STRAIN=ATCC 33909 / NCIB 11770 / DSM 639;  
RX PubMed=1595515; DOI=10.1128/JB.187.14.4992-4999.2005;  
RA Chen L., Bruegger K., Skovgaard M., Redder P., She Q., Torarinsson E.,  
RA Greve B., Awayez M., Zibat A., Klenk H.-P., Garrett R.A.;  
RT "The genome of Sulfolobus acidocaldarius, a model organism of the  
RT Crenarchaeota.";  
RL J. Bacteriol. 187:4992-4999(2005).  
DR EMBL; CP000077; AAY79791.1; -; Genomic\_DNA.  
KW Complete proteome; Hydrolase.  
SQ SEQUENCE 423 AA; 48005 MW; 09D8A73C6CE7F1AD CRC64;

Query Match 94.6%; Score 35; DB 2; Length 423;  
Best Local Similarity 85.7%; Pred. No. 62;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLHS 7  
|||  
Db 391 YSSNLHS 397

RESULT 3  
Q5ND44 MOUSE PRELIMINARY; PRT; 112 AA.  
AC Q5ND44;  
DT 01-FEB-2005 (TRENBLrel. 29, Created)  
DT 01-FEB-2005 (TRENBLrel. 29, Last sequence update)  
DT 01-FEB-2005 (TRENBLrel. 29, Last annotation update)  
DE Putative phosphatase (Fragment).  
GN Name=Pps; ORFNames=RP23-136K12.4-002;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Hammond S.;  
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AL591440; CAI24090.1; -; Genomic\_DNA.  
FT NON TER 1  
SQ SEQUENCE 112 AA; 13014 MW; F7B93FCA4B2930FE CRC64;

Query Match 91.9%; Score 34; DB 2; Length 112;  
Best Local Similarity 85.7%; Pred. No. 23;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLHS 7  
|||  
Db 78 YSSNLHS 84

RESULT 4  
Q7RI06 PLAYO PRELIMINARY; PRT; 404 AA.  
AC Q7RI06;  
DT 01-MAR-2004 (TRENBLrel. 26, Created)  
DT 01-MAR-2004 (TRENBLrel. 26, Last sequence update)  
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)  
DE Asparagine-rich protein.  
GN Name=PY03561;  
OS Plasmodium yoelii yoelii.  
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
OX NCBI\_TaxID=73239;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=17XNL;  
RX MEDLINE=22355706; PubMed=12368865; DOI=10.1038/nature01099;  
RA Carlton J.M., Anguoli S.V., Suh B.B., Kooij T.W., Perteau M.,  
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,  
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,  
RA Shallow S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,  
RA Cho J.K., Quackenbush J., Sedegah M., Shoabai A., Cummings L.M.,

RA Florens L., Yates J.R. III, Raine J.D., Raine R.E., Harris M.A.,  
RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,  
RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,  
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,  
RA Carucci D.J.;  
RT "Genome sequence and comparative analysis of the model rodent malaria  
RT parasite Plasmodium yoelii yoelii";  
RL Nature 419:512-519(2002).  
CC -!- CAUTION: The sequence shown here is derived from an  
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
CC preliminary data.  
DR EMBL; AABL01001031; EAA15290.1; -; Genomic DNA.  
SQ SEQUENCE 404 AA; 47311 MW; 7D9DFBACAF487ADC CRC64;  
  
Query Match 91.9%; Score 34; DB 2; Length 404;  
Best Local Similarity 85.7%; Pred. No. 97;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 YSNNLHS 7  
DB 302 YSNNLHS 308  
  
RESULT 5  
QXIU8 RAT PRELIMINARY; PRT; 446 AA.  
AC QXIU8;  
DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
DE Skeletal muscle and kidney enriched inositol phosphatase.  
GN Name=LOC287533;  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Testis;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klauener R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skaleka U., Smalios D.E.,  
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Testis;  
RG NIH MGC Project;  
RL Submitted (Oct-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC083572; AAH8572.1; -; mRNA.  
DR GO; GO:0016787; F:hydrolase activity; IEA.  
DR GO; GO:0004437; F:inositol or phosphatidylinositol phosphatas. . .; IEA.  
DR InterPro; IPR005135; Exo\_endo\_phos.  
DR InterPro; IPR000300; IPFC.  
DR Pfam; PF03372; Exo\_endo\_phos; 1.  
DR SMART; SM00128; IPFC; 1.

SQ SEQUENCE 446 AA; 51851 MW; 1B65B6A5B7BCBA7D CRC64;  
  
Query Match 91.9%; Score 34; DB 2; Length 446;  
Best Local Similarity 85.7%; Pred. No. 1.1e+02;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 YSNNLHS 7  
DB 412 YSNNLHS 418  
  
RESULT 6  
SKIP MOUSE  
ID SKIP MOUSE STANDARD; PRT; 468 AA.  
AC Q8C5L6; O09040;  
DT 10-OCT-2003 (Rel. 42, Created)  
DT 29-MAR-2004 (Rel. 43, Last sequence update)  
DT 10-MAY-2005 (Rel. 47, Last annotation update)  
DE Skeletal muscle and kidney enriched inositol phosphatase  
DE (EC 3.1.3.56).  
GN Name=Skip; Synonyms=Pps;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Murinae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=97325785; PubMed=9182797; DOI=10.1016/S0896-6273(00)80312-8;  
RA Hamilton B.A., Smith D.J., Mueller K.L., Kerrebrock A.W.,  
RA Brenson R.T., van Berkel V., Daly M.J., Kruglyak L., Reeve M.P.,  
RA Numaier J.L., Hawkins T.B., Rubin E.M., Lander E.S.;  
RT "The vibrator mutation causes neurodegeneration via reduced expression  
RT of PTP alpha: positional complementation cloning and extragenic  
RT suppression";  
RL Neuron 18:711-722(1997).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=ILS, and ISS;  
RA Ehringer M.A., Thompson J., Conroy O., Xu Y., Yang F., Canniff J.,  
RA Beeson M., Gordon L., Bennett B., Johnson T.E., Sikela J.M.;  
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].  
RX STRAIN=C57BL/6J; TISSUE=Medulla oblongata, and Ovary;  
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;  
RA Okazaki Y., Furuto M., Kasukawa T., Adachi J., Bono H., Kondo S.,  
RA Nikaido I., Oeono M., Saito R., Suzuki H., Yamanaoka I., Kiyosawa H.,  
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,  
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,  
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisels K.W.,  
RA Blake J.A., Bradt D., Bruscia V., Chothia C., Corbani L.E., Cousins S.,  
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,  
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,  
RA Girardot S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,  
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,  
RA Kologay A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,  
RA Maglott D.R., Marchionni L., Marchionni L., McKenzie L., Miki H.,  
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,  
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramchandran S.,  
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,  
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,  
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,  
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,  
RA Wilming L.G., Wyshaw-Boris A., Yanagisawa M., Yang I., Yang L.,  
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,  
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,  
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,  
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,  
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,  
RA Yaeunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,  
RA Birney E., Hayashizaki Y.;  
RT "Analysis of the mouse transcriptome based on functional annotation of

```
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
RN [4]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Scheffen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hsieh F.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toehyuki S., Carninci P., Prance C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullhy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Sainood J., Hsieh F.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodargren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
CC -!- FUNCTION: Inositol 5-phosphatase which acts on inositol 1,4,5-
CC triphosphate, inositol 1,3,4,5-tetrakisphosphate,
CC phosphatidylinositol 4,5-bisphosphate and phosphatidylinositol
CC 3,4,5-trisphosphate. Has 6-fold higher affinity for
CC phosphatidylinositol 4,5-bisphosphate than for inositol 1,4,5-
CC triphosphate. May negatively regulate assembly of the actin
CC cytoskeleton (By similarity).
CC -!- CATALYTIC ACTIVITY: D-myo-Inositol 1,4,5-trisphosphate + H(2)O =
CC myo-Inositol 1,4-bisphosphate + phosphate.
CC -!- SUBCELLULAR LOCATION: Endoplasmic reticulum. Following stimulation
CC with EGF, translocates to membrane ruffles (By similarity).
CC -!- SIMILARITY: Belongs to the inositol-1,4,5-trisphosphate 5-
CC phosphatase type II family.
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CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
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DR EMBL; U96724; AAC53265.1; -; mRNA.
DR EMBL; U96726; AAC60757.1; -; Genomic_DNA.
DR EMBL; AF483522; AAL90796.1; -; mRNA.
DR EMBL; AF483523; AAL90797.1; -; mRNA.
DR EMBL; AK054436; BAC35778.1; -; mRNA.
DR EMBL; AK078104; BAC37126.1; -; mRNA.
DR EMBL; BC066112; AAH66112.1; -; mRNA.
DR HSP; O43001; 1192.
DR Ensembl; ENSMUSG0000006127; Mus musculus.
DR MGI; MGI:1194899; Pps.
DR GO; GO:0005829; C:cytosol; ISS.
DR GO; GO:0043005; C:neuron projection; ISS.
DR GO; GO:0016312; F:inositol bisphosphate phosphatase activity; ISS.
DR GO; GO:0046030; F:inositol triphosphate phosphatase activity; ISS.
DR GO; GO:0042577; F:lipid phosphatase activity; ISS.
DR GO; GO:0030036; P:actin cytoskeleton organization and biogenesis; ISS.
DR InterPro; IPR005135; Exo_endo_phos.
DR Pfam; PF03372; Exo_endo_phos; 1.
DR SMART; SM00128; IP3c; 1.
KW Endoplasmic reticulum; Hydrolase.
FT REGION 34 337 Catalytic (Potential).
FT REGION 340 468 Required for ruffle localization.
FT CONFLICT 329 329 D -> E (in Ref. 3; BAC37126).
SQ SEQUENCE 468 AA; 54159 MW; F2E1CA370B97A8A1 CRC64;
Query Match 91.9%; Score 34; DB 1; Length 468;
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Best Local Similarity 85.7%; Pred. No. 1.1e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLHS 7
Db 434 YSSNLHS 440
||:||||
||:||||

RESULT 7
Q5ND43 MOUSE PRELIMINARY; PRT; 468 AA.
ID Q5ND43
AC Q5ND43
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Putative phosphatase.
GN Name=Pps; ORFNames=RP23-136K12.4-001;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hammond S.;
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL591440; CA124091.1; -; Genomic DNA.
SQ SEQUENCE 468 AA; 54158 MW; F2E1CA370B97A8A1 CRC64;

Query Match 91.9%; Score 34; DB 2; Length 468;
Best Local Similarity 85.7%; Pred. No. 1.1e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLHS 7
Db 434 YSSNLHS 440
||:||||
||:||||

RESULT 8
Q9FC03 STRCO PRELIMINARY; PRT; 642 AA.
ID Q9FC03
AC Q9FC03
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Putative secreted amidase.
GN OrderedLocusNames=SCO7179; ORFNames=SC8A11.07c;
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=A3(2) / M145;
RX MEDLINE=21996410; PubMed=12000953; DOI=10.1038/417141a;
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kieser T., Larke L., Murphy L.D., Oliver K., O'Neill S.,
RA Rabinowitz E., Rajandream M.A., Rutherford K.M., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares S., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J.R., Barrall B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
RT coelicolor A3(2).";
RL Nature 417:141-147 (2002).
DR EMBL; AL939130; CAC01579.1; -; Genomic_DNA.
DR HSP; P82974; IJ3G.
DR GO; GO:0008745; F:N-acetylmuramoyl-L-alanine amidase activity; IEA.
DR GO; GO:0009253; P:peptidoglycan catabolism; IEA.
DR InterPro; IPR002502; Amidase 2.
DR InterPro; IPR008258; LT_catalytic.
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DR Pfam; PF01510; Amidase 2; 1.
DR Pfam; PF01464; SUT; 1.
DR SMART; SM00644; Ami_2; 1.
KW Complete proteome.
SQ SEQUENCE 642 AA; 67149 MW; 4659E4422C31A033 CRC64;

Query Match          91.9%; Score 34; DB 2; Length 642;
Best Local Similarity 85.7%; Pred. No. 1.9e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLHS 7
DB 323 YSTNLHS 329

RESULT 9
Q62788 RAT PRELIMINARY; PRT; 744 AA.
AC Q62788
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Cys2/His2 zinc finger protein.
GN Name=Zfp111; Synonyms=rkr2;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=96033674; PubMed=7595478;
RA Pott U., Thiesen H.J., Colello R.J., Schwab M.E.;
RT "A new Cys2/His2 zinc finger gene, rkr2, is expressed in
RT differentiated rat oligodendrocytes and encodes a protein with a
RT functional repressor domain.";
RL J. Neurochem. 65:1955-1966(1995).
DR EMBL; U27186; AAB60512.1; -; mRNA.
DR HSP; P25490; 1ZNN.
DR RGD; 620595; Zfp111.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0046872; P:metal ion binding; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0006350; P:transcription; IEA.
DR InterPro; IPR001909; KRAB.
DR InterPro; IPR007087; Znf_C2H2.
DR InterPro; IPR007086; Znf_C2H2_sub.
DR Pfam; PF01352; KRAB; 1.
DR Pfam; PF00096; zf_C2H2; 17.
DR PRINTS; PR00048; ZINC_FINGER.
DR ProDom; PD000003; Znf_C2H2; 17.
DR SMART; SM00349; KRAB_1.
DR SMART; SM00355; Znf_C2H2; 19.
DR PROSITE; PS00805; KRAB; 1.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 17.
DR PROSITE; PS0157; ZINC_FINGER_C2H2_2; 17.
SQ SEQUENCE 744 AA; 85422 MW; 02EDA246E4EAE0F5 CRC64;

Query Match          91.9%; Score 34; DB 2; Length 744;
Best Local Similarity 85.7%; Pred. No. 1.9e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLHS 7
DB 501 YSSNLHT 507

RESULT 10
Q4RJ14 TETNG PRELIMINARY; PRT; 177 AA.
ID Q4RJ14_TETNG PRELIMINARY;
AC Q4RJ14;

DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Chromosome 3 SCAP15037, whole genome shotgun sequence.
DE (Fragment).
GN ORFNames=GSTENG00033419001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA Blemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Wolff JN., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Winkler P., Lander E.S., Weissbach J., Roest Crolius H.;
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT the early vertebrate proto-karyotype.";
RL Nature 431:946-957(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RG Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAEE01015037; CAG11448.1; -; Genomic_DNA.
FT NON_TER 177 177
SQ SEQUENCE 177 AA; 19671 MW; 3922CF4341B3CE01 CRC64;

Query Match          89.2%; Score 33; DB 2; Length 177;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLH 6
DB 60 YSSNLH 65

RESULT 11
Q94192 CAEBL PRELIMINARY; PRT; 219 AA.
ID Q94192 CAEBL PRELIMINARY;
AC Q94192
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein F22H10.6.
GN ORFNames=F22H10.6;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peleoderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Bristol N2;
RX MEDLINE=93069613; PubMed=9851916;
RG The C. elegans sequencing consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology.";
RL Science 282:2012-2018(1998).
DR EMBL; U70845; AAB09103.1; -; Genomic_DNA.
DR PIR; T30122; T30122.
DR Ensembl; F22H10.6; Caenorhabditis elegans.

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DR WormBase; WBGene00017730; F22H10.6.
DR WormPep; F22H10.6; C909575.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 219 AA; 25258 MW; 2091CC121B3E5FDA CRC64;

Query Match      89.2%; Score 33; DB 2; Length 219;
Best Local Similarity 85.7%; Pred. No. 80;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSSNLHS 7
Db 22 FSSNLHS 28

RESULT 12
Q504E5 BRARE PRELIMINARY; PRT; 219 AA.
AC Q504E5
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein zgc:109929.
GN Name=zgc:109929;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udani T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skaleka U., Smaluk D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Liver;
RG NIH MGC Project;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC095057; AAH95057.1; -, mRNA.
DR InterPro; IPR002529; FAA hydrolase.
DR Pfam; PF01557; FAA hydrolase; 1.
KW Hypothetical protein.
SQ SEQUENCE 219 AA; 24162 MW; 6EBD2CC0FADDEB6 CRC64;

Query Match      89.2%; Score 33; DB 2; Length 219;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSSNLH 6
Db 60 YSSNLH 65

, RESULT 13
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Q5CDQ1 LACLA
ID Q5CDQ1_LACLA PRELIMINARY; PRT; 368 AA.
AC Q5CDQ1;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein yweB.
GN Name=yweB; OrderedLocNames=LL2167;
OS Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
OX NCBI_TaxID=11360;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=IL1403;
RX MEDLINE=21235186; PubMed=11337471; DOI=10.1101/gr-GR-1697R;
RA Bolotin A., Wincker P., Manger S., Jaillon O., Malarne K.,
RA Weissenbach J., Ehrlich S.D., Sorokin A.;
RT "The complete genome sequence of the lactic acid bacterium Lactococcus
RT lactis ssp. lactis IL1403";
RL Genome Res. 11:731-753 (2001).
DR EMBL; AE006445; AAK06265.1; -, Genomic_DNA.
DR PIR; G86895; G86895.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 368 AA; 41726 MW; C1243C3B9F140D0D CRC64;

Query Match      89.2%; Score 33; DB 2; Length 368;
Best Local Similarity 85.7%; Pred. No. 1.4e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSSNLHS 7
Db 121 FSSNLHS 127

RESULT 14
Q8RR04 9SPHI PRELIMINARY; PRT; 391 AA.
AC Q8RR04;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE DNA gyrase subunit B (EC 5.99.1.3) (Fragment).
GN Name=gyrB;
OS Cytophaga sp. T-588.
OC Bacteria; Bacteroidetes; Sphingobacteriales;
OC Flexibacteraceae; Cytophaga.
OX NCBI_TaxID=173740;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22431356; PubMed=12542710;
RX DOI=10.1046/j.1462-2920.2003.00382.x;
RA Matsuo Y., Suzuki M., Kasai H., Shizuri Y., Harayama S.;
RT "Isolation and phylogenetic characterization of bacteria capable of
RT inducing differentiation in the green alga Monostroma oxyspermum."
RL Environ. Microbiol. 5:25-35 (2003).
CC -1- SIMILARITY: Belongs to the type II topoisomerase family.
DR EMBL; AB073038; BAB88340.1; -, Genomic_DNA.
DR HSSP; P06982; 1KZN.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003918; F:DNA topoisomerase (ATP-hydrolyzing) activity; IEA.
DR GO; GO:0006265; P:DNA topological change; IEA.
DR InterPro; IPR003594; ATP_bd_ATPase.
DR InterPro; IPR001241; DNA_topoisoi.
DR InterPro; IPR000565; DNA_topoisoi.
DR Pfam; PF0204; DNA_gyraseB; 1.
DR Pfam; PF02518; HATPase; 1.
DR PRINTS; PR00418; TP12FAMILY.
DR SMART; SM00433; TOP2c; 1.
DR PROSITE; PS00177; TOPOISOMERASE II; 1.
KW ATP-binding; Isomerase; Nucleotide-binding; Topoisomerase.
FT NON_TER 1
FT NON_TER 391
SQ SEQUENCE 391 AA; 43486 MW; 0C5E029383468759 CRC64;
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Query Match      89.2%; Score 33; DB 2; Length 391;
Best Local Similarity 85.7%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 YSSNLHS 7
      || |||||
DB      158 YSENLHS 164

RESULT 15
Q4L146 9FLAO
ID Q4L146 9FLAO PRELIMINARY; PRT; 423 AA.
AC Q4L146;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Gyrase B (Fragment).
GN Name=gvrB;
OS Capnocytophaga canimorsus.
OC Bacteria; Bacteroidetes; Flavobacteria; Flavobacteriales;
OC Flavobacteriaceae; Capnocytophaga.
OX NCBI_TaxID=28188;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=24231, and CIP 103936;
RA Fenner L., Roux V., Raoult D.;
RT "Description of two distinctive types of 16S rRNA in a Capnocytophaga
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AV643074; AAT49057.1; -; Genomic_DNA.
DR EMBL; AY643072; AAT49055.1; -; Genomic_DNA.
FT NON_TER 1
FT NON_TER 423 423
SQ SEQUENCE 423 AA; 47202 MW; F28D3721216971A6 CRC64;

Query Match      89.2%; Score 33; DB 2; Length 423;
Best Local Similarity 85.7%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 YSSNLHS 7
      || |||||
DB      160 YSENLHS 166

RESULT 16
Q845X4 9FLAO
ID Q845X4 9FLAO PRELIMINARY; PRT; 470 AA.
AC Q845X4;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE DNA gyrase B subunit (Fragment).
GN Name=gvrB;
OS Cellulophaga fucicola.
OC Bacteria; Bacteroidetes; Flavobacteria; Flavobacteriales;
OC Flavobacteriaceae; Cellulophaga.
OX NCBI_TaxID=76595;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=LMG18536;
RX MEDLINE=22431356; PubMed=12542710;
RX DOI=10.1046/j.1462-2920.2003.00382.x;
RA Mateuo Y., Suzuki M., Kasai H., Shizuri Y., Harayama S.;
RT "Isolation and phylogenetic characterization of bacteria capable of
RT inducing differentiation in the green alga Monostroma oxyspermum.";
RT Environ. Microbiol. 5:25-35(2003).
CC -!- SIMILARITY: Belongs to the type II topoisomerase family.
DR EMBL; AB071140; BAC65173.1; -; Genomic_DNA.
DR HSSP; P06982; 1KZN.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003918; F:DNA topoisomerase (ATP-hydrolyzing) activity; IEA.
DR GO; GO:0006304; P:DNA modification; IEA.

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DR GO; GO:0006265; P:DNA topological change; IEA.
DR InterPro; IPR003594; ATP bd ATPase.
DR InterPro; IPR011558; DNA_gyrase_B.
DR InterPro; IPR001241; DNA_topoisoiI.
DR InterPro; IPR000565; DNA_topoisoiV_B.
DR InterPro; IPR006171; Toprim dom.
DR Pfam; PF00204; DNA_gyraseB_1.
DR Pfam; PF02518; HATPase_c; 1.
DR Pfam; PF01751; Toprim; 1.
DR PRINTS; PR00418; TP12FAMILY.
DR ProDom; PD149633; DNA_gyrase_B; 1.
DR SMART; SM00433; TOP2c; 1.
DR PROSITE; PS00177; TOPOISOMERASE II; 1.
KW ATP-binding; Isomerase; Nucleotide-binding; Topoisomerase.
FT NON_TER 1
FT NON_TER 470 470
SQ SEQUENCE 470 AA; 52527 MW; DF6BAE2EFD21A7D6 CRC64;

Query Match      89.2%; Score 33; DB 2; Length 470;
Best Local Similarity 85.7%; Pred. No. 1.9e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 YSSNLHS 7
      || |||||
DB      165 YSENLHS 171

RESULT 17
Q9FAV9 CYTLY PRELIMINARY; PRT; 474 AA.
AC Q9FAV9;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE DNA gyrase B subunit (Fragment).
GN Name=gvrB;
OS Cytophaga lytica.
OC Bacteria; Bacteroidetes; Flavobacteria; Flavobacteriales;
OC Flavobacteriaceae; Cellulophaga.
OX NCBI_TaxID=979;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=IFO15986;
RX MEDLINE=21477783; PubMed=11594591;
RA Suzuki M., Nakagawa Y., Harayama S., Yamamoto S.;
RT "Phylogenetic analysis and taxonomic study of marine Cytophaga-like
RT bacteria: proposal for Tenacibaculum gen. nov. with Tenacibaculum
RT maritimum comb. nov. and Tenacibaculum ovolyticum comb. nov., and
RT description of Tenacibaculum mesophilum sp. nov. and Tenacibaculum
RT amyolyticum sp. nov.";
RT Int. J. Syst. Evol. Microbiol. 51:1639-1652(2001).
CC -!- SIMILARITY: Belongs to the type II topoisomerase family.
DR EMBL; AB034217; BAB12475.1; -; Genomic_DNA.
DR HSSP; P06982; 1KZN.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003918; F:DNA topoisomerase (ATP-hydrolyzing) activity; IEA.
DR GO; GO:0006304; P:DNA modification; IEA.
DR GO; GO:0006265; P:DNA topological change; IEA.
DR InterPro; IPR003594; ATP bd ATPase.
DR InterPro; IPR011558; DNA_gyrase_B.
DR InterPro; IPR000565; DNA_topoisoiI.
DR InterPro; IPR001241; DNA_topoisoiV_B.
DR InterPro; IPR006171; Toprim dom.
DR Pfam; PF00204; DNA_gyraseB; 1.
DR Pfam; PF02518; HATPase_c; 1.
DR Pfam; PF01751; Toprim; 1.
DR PRINTS; PR00418; TP12FAMILY.
DR ProDom; PD149633; DNA_gyrase_B; 1.
DR SMART; SM00433; TOP2c; 1.
DR PROSITE; PS00177; TOPOISOMERASE II; 1.
KW ATP-binding; Isomerase; Nucleotide-binding; Topoisomerase.
FT NON_TER 1
FT NON_TER 474 474

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SQ SEQUENCE 474 AA; 53133 MW; E1B3FE15802A948B CRC64;
Query Match 89.2%; Score 33; DB 2; Length 474;
Best Local Similarity 85.7%; Pred. No. 1.9e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSNLHS 7
DB 164 YSENLHS 170

RESULT 18
Q9FLY9_9FLAO PRELIMINARY; PRT; 474 AA.
AC Q9FLY9;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DE DNA gyrase B subunit (Fragment).
GN Name=gyrB;
OS Tenacibaculum maritimum.
OC Bacteria; Bacteroidetes; Flavobacteriales;
OC Flavobacteriaceae; Tenacibaculum.
OX NCBI_TaxID=107401;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC43398;
RX MEDLINE=2147783; PubMed=11594591;
RA Suzuki M., Nakagawa Y., Harayama S., Yamamoto S.;
RT "Phylogenetic analysis and taxonomic study of marine Cytophaga-like
RT bacteria: proposal for Tenacibaculum gen. nov. with Tenacibaculum
RT maritimum comb. nov. and Tenacibaculum ovolyticum comb. nov., and
RT description of Tenacibaculum mesophilum sp. nov. and Tenacibaculum
RT amylolyticum sp. nov.";
RL Int. J. Syst. Evol. Microbiol. 51:1639-1652(2001).
CC -!- SIMILARITY: Belongs to the type II topoisomerase family.
DR EMBL; AB034229; BAB12487.1; -; Genomic_DNA.
DR HSSP; P06982; IEI1.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003918; F:DNA topoisomerase (ATP-hydrolyzing) activity; IEA.
DR GO; GO:0006304; P:DNA modification; IEA.
DR GO; GO:0006265; P:DNA topological change; IEA.
DR InterPro; IPR003594; ATP_bd_ATPase.
DR InterPro; IPR011558; DNA_gyrase_B.
DR InterPro; IPR001241; DNA_topoisoi.
DR InterPro; IPR005655; DNA_topoisoi_B.
DR InterPro; IPR006171; Toprim dom.
DR Pfam; PF00204; DNA_gyraseB_1.
DR Pfam; PF02518; HATPase_c; 1.
DR Pfam; PF01751; Toprim; 1.
DR PRINTS; PR00418; TPI2FAMILY.
DR ProDom; PD149633; DNA_gyrase_B; 1.
DR SMART; SM00433; TOP2c; 1.
DR PROSITE; PS00177; TOPOISOMERASE II; 1.
KW ATP-binding; Isomerase; Nucleotide-binding; Topoisomerase.
FT NON_TER 1
FT NON_TER 474
SQ SEQUENCE 474 AA; 52921 MW; 1E1E631B9CEDFCC2 CRC64;

Query Match 89.2%; Score 33; DB 2; Length 474;
Best Local Similarity 85.7%; Pred. No. 1.9e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSNLHS 7
DB 164 YSENLHS 170

RESULT 20
Q9FAW2_CYTLY PRELIMINARY; PRT; 474 AA.
AC Q9FAW2;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DE DNA gyrase B subunit (Fragment).
GN Name=gyrB;
OS Cytophaga lytica.
OC Bacteria; Bacteroidetes; Flavobacteria; Flavobacteriales;
OC Flavobacteriaceae; Cellulophaga.
OX NCBI_TaxID=979;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=IFO16020;
RX MEDLINE=2147783; PubMed=11594591;
RA Suzuki M., Nakagawa Y., Harayama S., Yamamoto S.;
RT "Phylogenetic analysis and taxonomic study of marine Cytophaga-like
RT bacteria: proposal for Tenacibaculum gen. nov. with Tenacibaculum
RT maritimum comb. nov. and Tenacibaculum ovolyticum comb. nov., and
RT description of Tenacibaculum mesophilum sp. nov. and Tenacibaculum
RT amylolyticum sp. nov.";
RL Int. J. Syst. Evol. Microbiol. 51:1639-1652(2001).
CC -!- SIMILARITY: Belongs to the type II topoisomerase family.
DR EMBL; AB034213; BAB12471.1; -; Genomic_DNA.
DR HSSP; P06982; 1KZN.
DR GO; GO:0005524; F:ATP binding; IEA.

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DR GO; GO:0003918; F:DNA topoisomerase (ATP-hydrolyzing) activity; IEA.  
 DR GO; GO:0006304; P:DNA modification; IEA.  
 DR GO; GO:0006265; P:DNA topological change; IEA.  
 DR InterPro; IPR003594; ATP\_bd\_ATPase.  
 DR InterPro; IPR011558; DNA\_gyrase\_B.  
 DR InterPro; IPR001241; DNA\_topoisomII.  
 DR InterPro; IPR000565; DNA\_topoisomIV\_B.  
 DR InterPro; IPR006171; Toprim\_dom.  
 DR Pfam; PF00204; DNA\_gyraseB; 1.  
 DR Pfam; PF02518; HATPase\_c; 1.  
 DR Pfam; PF01751; Toprim; 1.  
 DR PRINTS; PR00418; TP12FAMILY.  
 DR ProDom; PD149633; DNA\_gyrase\_B; 1.  
 DR SMART; SM00433; TOP2C; 1.  
 DR PROSITE; PS00177; TOPOISOMERASE\_II; 1.  
 KW ATP-binding; Isomerase; Nucleotide-binding; Topoisomerase.  
 FT NON\_TER 1  
 FT SEQUENCE 474 AA; 53119 MW; 38D059D7E0FE1F93 CRC64;  
 SQ  
 Query Match 89.2%; Score 33; DB 2; Length 474;  
 Best Local Similarity 85.7%; Pred. No. 1.9e+02;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 YSSNLHS 7  
 Db 164 YSENLHS 170

RESULT 21  
 Q9FAW1\_CVTLY PRELIMINARY; PRT; 474 AA.  
 ID Q9FAW1; AC Q9FAW1; DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE DNA gyrase B subunit (Fragment).  
 GN Name=gyrB; OS Cytophaga lytica.  
 OC Bacteria; Bacteroidetes; Flavobacteria; Flavobacteriales;  
 OC Flavobacteriaceae; Cellulophaga.  
 OX NCBI\_TaxID=979; RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=IFO16021;  
 RX MEDLINE=21477783; PubMed=11594591;  
 RA Suzuki M., Nakagawa Y., Harayama S., Yamamoto S.;  
 RT "Phylogenetic analysis and taxonomic study of marine Cytophaga-like  
 RT bacteria: proposal for Tenacibaculum gen. nov. with Tenacibaculum  
 RT maritimum comb. nov. and Tenacibaculum ovolyticum comb. nov., and  
 RT description of Tenacibaculum mesophilum sp. nov. and Tenacibaculum  
 RT amylolyticum sp. nov.";  
 RL Int. J. Syst. Evol. Microbiol. 51:1639-1652(2001).  
 CC -1- SIMILARITY: Belongs to the type II topoisomerase family.  
 DR EMBL; AB034214; BAB12472.1; -; Genomic\_DNA.  
 DR HSSP; P06982; IE11.  
 DR GO; GO:0005524; F:ATP binding; IEA.  
 DR GO; GO:0003918; F:DNA topoisomerase (ATP-hydrolyzing) activity; IEA.  
 DR GO; GO:0006304; P:DNA modification; IEA.  
 DR GO; GO:0006265; P:DNA topological change; IEA.  
 DR InterPro; IPR003594; ATP\_bd\_ATPase.  
 DR InterPro; IPR011558; DNA\_gyrase\_B.  
 DR InterPro; IPR001241; DNA\_topoisomII.  
 DR InterPro; IPR000565; DNA\_topoisomIV\_B.  
 DR InterPro; IPR006171; Toprim\_dom.  
 DR Pfam; PF00204; DNA\_gyraseB; 1.  
 DR Pfam; PF02518; HATPase\_c; 1.  
 DR PRINTS; PR00418; TP12FAMILY.  
 DR ProDom; PD149633; DNA\_gyrase\_B; 1.  
 DR SMART; SM00433; TOP2C; 1.  
 DR PROSITE; PS00177; TOPOISOMERASE\_II; 1.  
 KW ATP-binding; Isomerase; Nucleotide-binding; Topoisomerase.  
 FT NON\_TER 1  
 FT SEQUENCE 474 AA; 52960 MW; 4D738B7455D49FA8 CRC64;  
 SQ  
 Query Match 89.2%; Score 33; DB 2; Length 474;  
 Best Local Similarity 85.7%; Pred. No. 1.9e+02;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 YSSNLHS 7  
 Db 164 YSENLHS 170

RESULT 23  
 Q9FLY8\_9FLAO PRELIMINARY; PRT; 474 AA.  
 ID Q9FLY8\_9FLAO

FT NON\_TER 1  
 FT SEQUENCE 474 AA; 53001 MW; 1F874F9A8626182D CRC64;  
 SQ  
 Query Match 89.2%; Score 33; DB 2; Length 474;  
 Best Local Similarity 85.7%; Pred. No. 1.9e+02;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 YSSNLHS 7  
 Db 164 YSENLHS 170

RESULT 22  
 Q9FIZ0\_9FLAO PRELIMINARY; PRT; 474 AA.  
 ID Q9FIZ0; AC Q9FIZ0; DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE DNA gyrase B subunit (Fragment).  
 GN Name=gyrB; OS Tenacibaculum maritimum.  
 OC Bacteria; Bacteroidetes; Flavobacteria; Flavobacteriales;  
 OC Flavobacteriaceae; Tenacibaculum.  
 OX NCBI\_TaxID=107401; RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=IFO16015;  
 RX MEDLINE=21477783; PubMed=11594591;  
 RA Suzuki M., Nakagawa Y., Harayama S., Yamamoto S.;  
 RT "Phylogenetic analysis and taxonomic study of marine Cytophaga-like  
 RT bacteria: proposal for Tenacibaculum gen. nov. with Tenacibaculum  
 RT maritimum comb. nov. and Tenacibaculum ovolyticum comb. nov., and  
 RT description of Tenacibaculum mesophilum sp. nov. and Tenacibaculum  
 RT amylolyticum sp. nov.";  
 RL Int. J. Syst. Evol. Microbiol. 51:1639-1652(2001).  
 CC -1- SIMILARITY: Belongs to the type II topoisomerase family.  
 DR EMBL; AB034228; BAB12486.1; -; Genomic\_DNA.  
 DR HSSP; P06982; IE11.  
 DR GO; GO:0005524; F:ATP binding; IEA.  
 DR GO; GO:0003918; F:DNA topoisomerase (ATP-hydrolyzing) activity; IEA.  
 DR GO; GO:0006304; P:DNA modification; IEA.  
 DR GO; GO:0006265; P:DNA topological change; IEA.  
 DR InterPro; IPR003594; ATP\_bd\_ATPase.  
 DR InterPro; IPR011558; DNA\_gyrase\_B.  
 DR InterPro; IPR001241; DNA\_topoisomII.  
 DR InterPro; IPR000565; DNA\_topoisomIV\_B.  
 DR InterPro; IPR006171; Toprim\_dom.  
 DR Pfam; PF00204; DNA\_gyraseB; 1.  
 DR Pfam; PF02518; HATPase\_c; 1.  
 DR PRINTS; PR00418; TP12FAMILY.  
 DR ProDom; PD149633; DNA\_gyrase\_B; 1.  
 DR SMART; SM00433; TOP2C; 1.  
 DR PROSITE; PS00177; TOPOISOMERASE\_II; 1.  
 KW ATP-binding; Isomerase; Nucleotide-binding; Topoisomerase.  
 FT NON\_TER 1  
 FT SEQUENCE 474 AA; 52960 MW; 4D738B7455D49FA8 CRC64;  
 SQ  
 Query Match 89.2%; Score 33; DB 2; Length 474;  
 Best Local Similarity 85.7%; Pred. No. 1.9e+02;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 YSSNLHS 7  
 Db 164 YSENLHS 170

RESULT 23  
 Q9FLY8\_9FLAO PRELIMINARY; PRT; 474 AA.  
 ID Q9FLY8\_9FLAO

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AC Q9F1Y8:
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE DNA gyrase B subunit (Fragment).
GN Name=gyrB;
OS Tenacibaculum ovolyticum.
OC Bacteria; Bacteroidetes; Flavobacteriia; Flavobacteriales;
OC Flavobacteriaceae; Tenacibaculum.
OX NCBI_TaxID=104270;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=IFO15993;
RX MEDLINE=21477783; PubMed=11594591;
RA Suzuki M., Nakagawa Y., Harayama S., Yamamoto S.;
RT "Phylogenetic analysis and taxonomic study of marine Cytophaga-like
RT bacteria: proposal for Tenacibaculum gen. nov., with Tenacibaculum
RT maritimum comb. nov., and Tenacibaculum ovolyticum comb. nov., and
RT description of Tenacibaculum mesophilum sp. nov. and Tenacibaculum
RT amyolyticum sp. nov.";
RL Int. J. Syst. Evol. Microbiol. 51:1639-1652(2001).
CC -!- SIMILARITY: Belongs to the type II topoisomerase family.
DR EMBL; AB034232; BAB12490.1; -; Genomic_DNA.
DR HSSP; P06982; 1E11.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003918; F:DNA topoisomerase (ATP-hydrolyzing) activity; IEA.
DR GO; GO:0006304; P:DNA topological change; IEA.
DR GO; GO:0006265; P:DNA topological change; IEA.
DR InterPro; IPR003594; ATP bd ATPase.
DR InterPro; IPR011558; DNA_gyrase_B.
DR InterPro; IPR001241; DNA_topoisomII.
DR InterPro; IPR000565; DNA_topoisomIV_B.
DR InterPro; IPR006171; Toprim_dom.
DR Pfam; PF02024; DNA_gyraseB; 1.
DR Pfam; PF01751; HATPase_c; 1.
DR PRINTS; PR00418; TP12FAMILY.
DR ProDom; PD149633; TOP2c; 1.
DR SMART; SM00433; TOP2c; 1.
DR PROSITE; PS00177; TOPOISOMERASE II; 1.
KW ATP-binding; Isomerase; Nucleotide-binding; Topoisomerase.
FT NON_TER 1 474
FT NON_TER 474 474
SQ SEQUENCE 474 AA; 53068 MW; 7FEFA02ABE986F9 CRC64;

Query Match 89.2%; Score 33; DB 2; Length 474;
Best Local Similarity 85.7%; Pred. No. 1.9e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSNLHS 7
DB 164 YSENLHS 170

RESULT 24
Q9FAV1_9FLAO PRELIMINARY; PRT; 474 AA.
AC Q9FAV1;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE DNA gyrase B subunit (Fragment).
GN Name=gyrB;
OS Psychrofloxus gondwanensis.
OC Bacteria; Bacteroidetes; Flavobacteria; Flavobacteriales;
OC Flavobacteriaceae; Psychrofloxus.
OX NCBI_TaxID=251;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=DSM5423;
RX MEDLINE=21477783; PubMed=11594591;
RA Suzuki M., Nakagawa Y., Harayama S., Yamamoto S.;
RT "Phylogenetic analysis and taxonomic study of marine Cytophaga-like

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RT bacteria: proposal for Tenacibaculum gen. nov., with Tenacibaculum
RT maritimum comb. nov., and Tenacibaculum ovolyticum comb. nov., and
RT description of Tenacibaculum mesophilum sp. nov., and Tenacibaculum
RT amyolyticum sp. nov.";
RL Int. J. Syst. Evol. Microbiol. 51:1639-1652(2001).
CC -!- SIMILARITY: Belongs to the type II topoisomerase family.
DR EMBL; AB034226; BAB12484.1; -; Genomic_DNA.
DR HSSP; P06982; 1KZN.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003918; F:DNA topoisomerase (ATP-hydrolyzing) activity; IEA.
DR GO; GO:0006304; P:DNA modification; IEA.
DR GO; GO:0006265; P:DNA topological change; IEA.
DR InterPro; IPR003594; ATP bd ATPase.
DR InterPro; IPR011558; DNA_gyrase_B.
DR InterPro; IPR001241; DNA_topoisomIV_B.
DR InterPro; IPR000565; DNA_topoisomIV_B.
DR InterPro; IPR006171; Toprim_dom.
DR Pfam; PF00204; DNA_gyraseB; 1.
DR Pfam; PF02518; HATPase_c; 1.
DR Pfam; PF01751; Toprim_1.
DR PRINTS; PR00418; TP12FAMILY.
DR ProDom; PD149633; DNA_gyrase_B; 1.
DR SMART; SM00433; TOP2c; 1.
DR PROSITE; PS00177; TOPOISOMERASE II; 1.
KW ATP-binding; Isomerase; Nucleotide-binding; Topoisomerase.
FT NON_TER 1 474
FT NON_TER 474 474
SQ SEQUENCE 474 AA; 53686 MW; 417E2D2C2C8BDFB CRC64;

Query Match 89.2%; Score 33; DB 2; Length 474;
Best Local Similarity 85.7%; Pred. No. 1.9e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSNLHS 7
DB 164 YSENLHS 170

RESULT 25
Q9FAW0_CYTLY PRELIMINARY; PRT; 474 AA.
AC Q9FAW0;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE DNA gyrase B subunit (Fragment).
GN Name=gyrB;
OS Cytophaga lytica.
OC Bacteria; Bacteroidetes; Flavobacteria; Flavobacteriales;
OC Flavobacteriaceae; Cellulophaga.
OX NCBI_TaxID=979;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=IAM14306;
RX MEDLINE=21477783; PubMed=11594591;
RA Suzuki M., Nakagawa Y., Harayama S., Yamamoto S.;
RT "Phylogenetic analysis and taxonomic study of marine Cytophaga-like
RT bacteria: proposal for Tenacibaculum gen. nov., with Tenacibaculum
RT maritimum comb. nov., and Tenacibaculum ovolyticum comb. nov., and
RT description of Tenacibaculum mesophilum sp. nov., and Tenacibaculum
RT amyolyticum sp. nov.";
RL Int. J. Syst. Evol. Microbiol. 51:1639-1652(2001).
CC -!- SIMILARITY: Belongs to the type II topoisomerase family.
DR EMBL; AB034216; BAB12474.1; -; Genomic_DNA.
DR HSSP; P06982; 1KZN.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003918; F:DNA topoisomerase (ATP-hydrolyzing) activity; IEA.
DR GO; GO:0006304; P:DNA modification; IEA.
DR GO; GO:0006265; P:DNA topological change; IEA.
DR InterPro; IPR003594; ATP bd ATPase.
DR InterPro; IPR011558; DNA_gyrase_B.
DR InterPro; IPR001241; DNA_topoisomIV_B.
DR InterPro; IPR000565; DNA_topoisomIV_B.

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DR InterPro; IPR006171; Toprim dom.
DR Pfam; PF00204; DNA gyraseB; 1.
DR Pfam; PF02518; HATPase_c; 1.
DR Pfam; PF01751; Toprim; 1.
DR PRINTS; PR00418; TP12FAMILY.
DR ProDom; PD149633; DNA gyrase_B; 1.
DR SMART; SM00433; TOP2c; 1.
DR PROSITE; PS00177; TOPOISOMERASE II; 1.
KW ATP-binding; Isomerase; Nucleotide-binding; Topoisomerase.
FT NON_TER 1
FT NON_TER 474 474
SQ SEQUENCE 474 AA; 53147 MW; 2601AA18DC0DC7E CRC64;

Query Match 89.2%; Score 33; DB 2; Length 474;
Best Local Similarity 85.7%; Pred. No. 1.9e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSNLHS 7
DB 164 YSENLHS 170

RESULT 28
Q9FTV9_CYTLY PRELIMINARY; PRT; 474 AA.
ID Q9FTV9_CYTLY PRELIMINARY; PRT; 474 AA.
AC Q9FTV9;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE DNA gyrase B subunit (Fragment).
GN Name=gyrB;
OS Cytophaga lytica.
OC Bacteria; Bacteroidetes; Flavobacteriia; Flavobacteriales;
OC Flavobacteriaceae; Cellulophaga.
OX NCBI_TaxID=979;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=WBIC1544, and IFO16022;
RX MEDLINE=21477783; PubMed=11594591;
RA Suzuki M., Nakagawa Y., Harayama S., Yamamoto S.;
RT "Phylogenetic analysis and taxonomic study of marine Cytophaga-like
bacteria: proposal for Tenacibaculum gen. nov. with Tenacibaculum
maritimum comb. nov. and Tenacibaculum ovolyticum comb. nov., and
RT description of Tenacibaculum mesophilum sp. nov. and Tenacibaculum
RT amolyticum sp. nov.";
RL Int. J. Syst. Evol. Microbiol. 51:1639-1652(2001).
CC -!- SIMILARITY: Belongs to the type II topoisomerase family.
DR EMBL; AB034215; BAB12473.1; -; Genomic DNA.
DR EMBL; AB034218; BAB12476.1; -; Genomic DNA.
DR HSSP; P06982; 1KZN.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003918; F:DNA topoisomerase (ATP-hydrolyzing) activity; IEA.
DR GO; GO:0006304; P:DNA topological change; IEA.
DR GO; GO:0006265; P:DNA topological change; IEA.
DR InterPro; IPR003594; ATP bd ATPase.
DR InterPro; IPR011558; DNA gyrase B.
DR InterPro; IPR001241; DNA topoisom.
DR InterPro; IPR000565; DNA_topoisom.
DR InterPro; IPR006171; Toprim dom.
DR Pfam; PF00204; DNA gyraseB; 1.
DR Pfam; PF02518; HATPase_c; 1.
DR Pfam; PF01751; Toprim; 1.
DR PRINTS; PR00418; TP12FAMILY.
DR ProDom; PD149633; DNA gyrase_B; 1.
DR SMART; SM00433; TOP2c; 1.
DR PROSITE; PS00177; TOPOISOMERASE II; 1.
KW ATP-binding; Isomerase; Nucleotide-binding; Topoisomerase.
FT NON_TER 1
FT NON_TER 474 474
SQ SEQUENCE 474 AA; 53160 MW; 792A989704B43027 CRC64;

Query Match 89.2%; Score 33; DB 2; Length 474;
Best Local Similarity 85.7%; Pred. No. 1.9e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSNLHS 7
DB 164 YSENLHS 170

RESULT 28
Q9FAW4_9FLAO PRELIMINARY; PRT; 480 AA.
ID Q9FAW4_9FLAO PRELIMINARY; PRT; 480 AA.
AC Q9FAW4;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 26, Last annotation update)
DE DNA gyrase B subunit (Fragment).

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GN Name=gvrB;  
OS Capnocytophaga canimorsus.  
OC Bacteria; Bacteroidetes; Flavobacteriia; Flavobacteriales;  
OC Flavobacteriaceae; Capnocytophaga.  
OX NCBI\_TaxID=28188;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=ATCC35979;  
RX MEDLINE=21477783; PubMed=11594591;  
RA Suzuki M., Nakagawa Y., Harayama S., Yamamoto S.;  
RT "Phylogenetic analysis and taxonomic study of marine Cytophaga-like  
bacteria: proposal for Tenacibaculum gen. nov. with Tenacibaculum  
maritimum comb. nov. and Tenacibaculum ovolyticum comb. nov. and  
RT description of Tenacibaculum mesophilum sp. nov. and Tenacibaculum  
RT amyolyticum sp. nov.";  
RL Int. J. Syst. Evol. Microbiol. 51:1639-1652(2001).  
CC -!- SIMILARITY: Belongs to the type II topoisomerase family.  
DR EMBL; AB034211; BAB12469.1; -; Genomic\_DNA.  
DR HSSP; P06982; 1E11.  
DR CO; GO:0005524; F:ATP binding; IEA.  
DR GO; GO:0003918; F:DNA topoisomerase (ATP-hydrolyzing) activity; IEA.  
DR GO; GO:0006304; P:DNA modification; IEA.  
DR GO; GO:0006265; P:DNA topological change; IEA.  
DR InterPro; IPR003594; ATP bd ATPase.  
DR InterPro; IPR011558; DNA\_gyrase\_B.  
DR InterPro; IPR001241; DNA\_topoisomII.  
DR InterPro; IPR000565; DNA\_topoisomIV\_B.  
DR InterPro; IPR006171; Toprim dom.  
DR Pfam; PF02024; DNA\_gyraseB; 1.  
DR Pfam; PF02518; HATPase c; 1.  
DR Pfam; PF01751; Toprim; 1.  
DR PRINTS; PRO04418; TP12FAMILY.  
DR ProDom; PD149633; DNA\_gyrase\_B; 1.  
DR SMART; SM00433; TOP2C; 1.  
DR PROSITE; PS00177; TOPOISOMERASE II; 1.  
KW ATP-binding; Isomerase; Nucleotide-binding; Topoisomerase.  
FT NON\_TER 1  
FT NON\_TER 480  
FT NON\_TER 1  
FT NON\_TER 480  
SQ SEQUENCE 480 AA; 53889 MW; 5F1F48BD18CEE052 CRC64;  
  
Query Match 89.2%; Score 33; DB 2; Length 480;  
Best Local Similarity 85.7%; Pred. No. 1.9e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 YSSNLHS 7  
Db 164 YSNLHS 170  
  
RESULT 29  
Q7PX57 ANOGA  
ID Q7PX57 ANOGA PRELIMINARY; PRT; 817 AA.  
AC Q7PX57;  
DT 01-MAR-2004 (TrEMBLrel. 26, Created)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE ENSANGP0000013991 (Fragment).  
GN ORFNames=ENSANG0000011502;  
OS Anopheles gambiae str. PEST.  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae;  
OC Anophelinae; Anopheles.  
OX NCBI\_TaxID=180454;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=PEST;  
RA Anopheles Genome Sequencing Consortium;  
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.  
CC -!- CAUTION: The sequence shown here is derived from an  
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
CC preliminary data.  
DR EMBL; AA01006987; EAA01793.1; -; Genomic\_DNA.  
DR NON\_TER 1  
DR NON\_TER 1

SQ SEQUENCE 817 AA; 87412 MW; F898PB905B8B2995 CRC64;  
  
Query Match 89.2%; Score 33; DB 2; Length 817;  
Best Local Similarity 100.0%; Pred. No. 3.5e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 YSSNLH 6  
Db 589 YSSNLH 594  
  
RESULT 30  
Q9S950 LYCES  
ID Q9S950 LYCES PRELIMINARY; PRT; 169 AA.  
AC Q9S950;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE CEL2=CELLULOSE 2 (Fragment).  
OS Lycopersicon esculentum (Tomato).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;  
OC lamiales; Solanales; Solanaceae; Solanum; Lycopersicon.  
OX NCBI\_TaxID=4081;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=96291721; PubMed=8754682; DOI=10.1104/pp.111.3.813;  
RA del Campillo E., Bennett A.B.;  
RT "Pedicel breakstrength and cellulase gene expression during tomato  
RT flower abscission.";  
RL Plant Physiol. 111:813-820(1996).  
DR HSSP; O77044; 1KS8.  
DR GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . . ; IEA.  
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.  
DR InterPro; IPR001701; Glyco\_hydro\_9.  
DR Pfam; PF00759; Glyco\_hydro\_9; 1.  
FT NON\_TER 1  
FT NON\_TER 169  
FT NON\_TER 169  
SQ SEQUENCE 169 AA; 18674 MW; CE8AB3AC5637C481 CRC64;  
  
Query Match 86.5%; Score 32; DB 2; Length 169;  
Best Local Similarity 85.7%; Pred. No. 99;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 YSSNLHS 7  
Db 143 YSSSLHS 149  
  
RESULT 31  
Q70Y33 LYCES  
ID Q70Y33 LYCES PRELIMINARY; PRT; 172 AA.  
AC Q70Y33;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Putative endo-1,4,-beta-glucanase (Fragment).  
GN Name=cel;  
OS Lycopersicon esculentum (Tomato).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;  
OC lamiales; Solanales; Solanaceae; Solanum; Lycopersicon.  
OX NCBI\_TaxID=4081;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Fruit;  
RA Saiprasad G.V.S., Lalitha A.;  
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ505749; CAD44274.1; -; mRNA.  
DR HSSP; P37700; 1K72.  
DR GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . . ; IEA.  
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.  
DR InterPro; IPR001701; Glyco\_hydro\_9.  
DR NON\_TER 1

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DR Pfam: PF00759; Glyco_hydro_9; 1.
FT NON_TER 1
RT NON_TER 172
SQ SEQUENCE 172 AA; 19004 MW; F8584877ABEB83F9 CRC64;

Query Match      86.5%; Score 32; DB 2; Length 172;
Best Local Similarity 85.7%; Pred. No. 1e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLHS 7
Db 144 YSSSLHS 150

RESULT 32
QSTQ70 ANOQA
ID Q5TQ70 ANOQA PRELIMINARY; PRT; 236 AA.
AC Q5TQ70;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DE ENSANGP0000026753 (Fragment).
GN ORFNames=ENSANGG0000023859;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Culicidae;
OC Anophelinae; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PEST;
RG The Anopheles gambiae Sequence Committee;
RT "Anopheles gambiae re-annotation.";
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PEST;
RG The Anopheles gambiae Sequence Committee;
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAAB01008964; BAU39533.1; -; Genomic_DNA.
DR GO; GO:0042765; C:GPI-anchor transamidase complex; IEA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR007245; Gp116.
DR Pfam; PF04113; Gp116; 1.
DR NON_TER 236
FT SEQUENCE 236 AA; 27046 MW; 2674788B839E7A4D CRC64;

Query Match      86.5%; Score 32; DB 2; Length 236;
Best Local Similarity 85.7%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSNLHS 7
Db 212 YSSNYHS 218

RESULT 33
Q43751 CAPAN
ID Q43751 CAPAN PRELIMINARY; PRT; 325 AA.
AC Q43751;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Cellulase (EC 3.2.1.4) (fragment).
GN Name=ccx3;
OS Capsicum annuum (Bell pepper).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC asterids; lamids; Solanales; Solanaceae; Capsicum.
OX NCBI_TaxID=4072;
```

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RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Leaf abscission zones;
RA Ferrarese L., Trainotti L., Moretto P., De Laureto P.P., Rascio N.,
RA Casadoro G.;
RT "Differential ethylene-inducible expression of cellulase in pepper
plants.";
RL Mol. Biol. 29:735-747(1995).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=8541500;
RA Ferrarese L., Trainotti L., Moretto P., Polverino de Laureto P.,
RA Rascio N., Casadoro G.;
RT "Differential ethylene-inducible expression of cellulase in pepper
plants.";
RL Plant Mol. Biol. 29:735-747(1995).
DR EMBL; X83711; CAA58686.1; -; mRNA.
DR PIR; S61447; S61447.
DR HSSP; O77044; 1KS8.
DR GO; GO:0008810; P:cellulase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR001701; Glyco_hydro_9.
DR InterPro; IPR012343; Glyco_trans_sub.
DR Pfam; PF00759; Glyco_hydro_9; 1.
KW Glycosidase; Hydrolase.
FT NON_TER 325
FT NON_TER 325
SQ SEQUENCE 325 AA; 36087 MW; CE2040A6C7B17937 CRC64;

Query Match      86.5%; Score 32; DB 2; Length 325;
Best Local Similarity 85.7%; Pred. No. 2.1e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLHS 7
Db 144 YSSSLHS 150

RESULT 34
Q22124 CAEBL
ID Q22124 CAEBL PRELIMINARY; PRT; 331 AA.
AC Q22124;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Serpentine receptor, class u protein 48.
GN Name=sru-48; ORFNames=T03G11.2;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Bristol N2;
RX MEDLINE=95069613; PubMed=9851916;
RG The C. elegans sequencing consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
investigating biology.";
RL Science 282:2012-2018(1998).
DR EMBL; U41272; AAA82450.2; -; Genomic_DNA.
DR PIR; T29924; T29924.
DR Ensembl; T03G11.2; Caenorhabditis elegans.
DR WormBase; WBGene0005711; T03G11.2.
DR WormPep; T03G11.2; CE33303.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR003839; DUF215.
DR Pfam; PF02688; DUF215; 1.
KW Complete proteome; Receptor.
SQ SEQUENCE 331 AA; 37830 MW; 7FC40A485BB9F837 CRC64;

Query Match      86.5%; Score 32; DB 2; Length 331;
Best Local Similarity 85.7%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 1 YSSNLHS 7
DB 325 YRSNLHS 331

RESULT 35
Q8ESQ5 OCEIH PRELIMINARY; PRT; 478 AA.
AC Q8ESQ5;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Poly1-trNA synthetase.
GN OrderedLocusNames=OB0566;
OS Oceanobacillus iheyensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Oceanobacillus.
OX NCBI_TaxID=182710;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=HTE831 / DSM 14371 / JCM 11309;
RX MEDLINE=2220767; PubMed=12235376; DOI=10.1093/nar/gkf526;
RA Takami H., Takaki Y., Uchiyama I.;
RT "Genome sequence of Oceanobacillus iheyensis isolated from the Iheya
RT Ridge and its unexpected adaptive capabilities to extreme
RT environments.";
RL Nucleic Acids Res. 30:3927-3935(2002).
DR EMBL; BA000028; BAC12522.1; -; Genomic_DNA.
DR HSSP; Q93N97; 1HC7.
DR GO; GO:0005737; C:cytoplasm; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0016874; F:ligase activity; IEA.
DR GO; GO:0004827; F:proline-trNA ligase activity; IEA.
DR GO; GO:0006433; P:prolyl-trNA aminoacylation; IEA.
DR GO; GO:0006412; P:protein biosynthesis; IEA.
DR InterPro; IPR004154; anticodon_bd.
DR InterPro; IPR004499; ProS_fam_I.
DR InterPro; IPR002314; trNA-synt_2b.
DR InterPro; IPR002316; trNA-synt_pro.
DR InterPro; IPR006195; trNA ligase II.
DR Pfam; PF03129; HGTP anticodon; 1.
DR Pfam; PF00587; trNA-synt_2b; 1.
DR PRINTS; PRO1046; TRNASYNTHPRO.
DR TIGRFAMs; TIGR00408; ProS_fam_I; 1.
DR PROSITE; PS50862; AA_TRNA_LIGASE_II; 1.
KW Aminoacyl-trNA synthetase; Complete proteome.
SQ SEQUENCE 478 AA; 54750 MW; 5E37D3553928D880 CRC64;

Query Match 86.5%; Score 32; DB 2; Length 478;
Best Local Similarity 71.4%; Pred. No. 3.2e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLHS 7
DB 125 YSNLHS 131

RESULT 36
Q6DBD4 ARATH PRELIMINARY; PRT; 480 AA.
AC Q6DBD4;
DT 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DT 01-FEB-2005 (TREMBlrel. 29, Last annotation update)
DE At5g16410.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC Cheuk R., Chen H., Kim C.J., Shinn P., Ecker J.R.;
```

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RL Submitted (JUL-2004) to the EMBL/GenBank/DBAJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Cheuk R., Chen H., Kim C.J., Shinn P., Ecker J.R.;
RT "Arabidopsis ORF clones.";
RL Submitted (OCT-2004) to the EMBL/GenBank/DBAJ databases.
DR EMBL; BT015088; AAT71960.1; -; mRNA.
DR EMBL; BT015909; AAU95445.1; -; mRNA.
DR InterPro; IPR003480; Transferase.
DR Pfam; PF02458; Transferase; 1.
SQ SEQUENCE 480 AA; 53687 MW; 4984BFD029021C5A CRC64;

Query Match 86.5%; Score 32; DB 2; Length 480;
Best Local Similarity 85.7%; Pred. No. 3.2e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLHS 7
DB 5 YSSSLHS 11

RESULT 37
Q9FFE4 ARATH PRELIMINARY; PRT; 481 AA.
AC Q9FFE4;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Similarity to N-hydroxycinnamoyl/benzoyltransferase.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=97471969; PubMed=9330910;
RA Sato S., Kotani H., Nakamura Y., Kaneko T., Asamizu E., Fukami M.,
RA Miyajima N., Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. I. Sequence
RT features of the 1.6 Mb regions covered by twenty physically assigned
RT pl clones.";
RL DNA Res. 4:215-230(1997).
DR EMBL; AB05242; BAB09608.1; -; Genomic DNA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR InterPro; IPR003480; Transferase.
DR Pfam; PF02458; Transferase; 1.
KW Transferase.
SQ SEQUENCE 481 AA; 53819 MW; B7991EF5C4A339B7 CRC64;

Query Match 86.5%; Score 32; DB 2; Length 481;
Best Local Similarity 85.7%; Pred. No. 3.2e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLHS 7
DB 6 YSSSLHS 12

RESULT 38
Q96547 CAPAN PRELIMINARY; PRT; 485 AA.
AC Q96547;
DT 01-FEB-1997 (TREMBlrel. 02, Created)
DT 01-FEB-1997 (TREMBlrel. 02, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Cellulase (Endo-beta-1,4-glucanase) (EC 3.2.1.4).
GN Name=ccl3;
OS Capsicum annuum (Bell pepper).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC lamiales; Solanales; Solanaceae; Capsicum.
OX NCBI_TaxID=4072;
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RN NUCLEOTIDE SEQUENCE.
RC TISSUE=Abscission zone;
RA Trainotti L., Ferrarese L., Casadoro G.;
RT "Different endo-beta-1,4-glucanases are expressed during abscission
and fruit ripening in pepper and peach plants.";
RL (In) Kanellis A.K., Chang C., Kende and Grierson D. (eds.);
RL BIOLOGY AND BIOTECHNOLOGY OF THE PLANT HORMONE ETHYLENE, pp.191-196,
KL Kluwer Academic Publishers, Dordrecht (1998).
RN [2]

RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Abscission zone;
RA Casadoro G.;
RL Submitted (Apr-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; X97189; CAA65827.1; -; mRNA.
DR HSSP; O77044; 1KS8.
DR GO; GO:0008810; F:cellulase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR001701; Glyco_hydro_9.
DR Pfam; PF00759; Glyco_hydro_9; 1.
DR PROSITE; PS00698; GLYCOSYL_HYDROL_F9_2; UNKNOWN_1.
KW Glycosidase; Hydrolase.
SQ SEQUENCE 485 AA; 53631 MW; A8BCCB32E3FFA18A CRC64;

Query Match 86.5%; Score 32; DB 2; Length 485;
Best Local Similarity 85.7%; Pred. No. 3.2e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLHS 7
DB 213 YSSSLHS 219
|||||

RESULT 39
Q42872_LYCES PRELIMINARY; PRT; 489 AA.
AC Q42872;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Endo-1,4-beta-glucanase precursor (EC 3.2.1.4).
GN Name=Cel2;
OS Lycopersicon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.
OX NCBI_TaxID=4081;
RN [1]_TaxID=4081;
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Castlemart; TISSUE=Pericarp;
RX MEDLINE=95086382; PubMed=7994180; DOI=10.1105/tpc.6.10.1485;
RA Lashbrook C.C., Gonzales-Bosch C., Bennett A.B.;
RT "Two divergent endo-beta-1,4-glucanase genes exhibit overlapping
expression in ripening fruit and abscising flowers.";
RL Plant Cell 6:1485-1493 (1994).
RN [2]

RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Castlemart; TISSUE=Pericarp;
RA Brummell D.A., Lashbrook C.C., Bennett A.B.;
RT "Plant endo-1,4-beta-D-glucanases: structure, properties, and
physiological function.";
RL ACS Symp. Ser. 566:100-129 (1994).
DR EMBL; U13055; AAA69909.1; -; mRNA.
DR PIR; T06350; T06350.
DR HSSP; O77044; 1KS8.
DR GO; GO:0008810; F:cellulase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR001701; Glyco_hydro_9.
DR Pfam; PF00759; Glyco_hydro_9; 1.
DR PROSITE; PS00698; GLYCOSYL_HYDROL_F9_2; UNKNOWN_1.
KW Glycosidase; Hydrolase; Signal.
FT SIGNAL 1 23 Potential.
FT CHAIN 24 489 endo-1,4-beta-glucanase.
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SQ SEQUENCE 489 AA; 54118 MW; FFA8A8C4675F685F CRC64;

Query Match 86.5%; Score 32; DB 2; Length 489;
Best Local Similarity 85.7%; Pred. No. 3.2e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLHS 7
DB 216 YSSSLHS 222
|||||

RESULT 40
Q93WZ0_TOBAC PRELIMINARY; PRT; 500 AA.
AC Q93WZ0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Endo-beta-1,4-glucanase precursor (EC 3.2.1.4).
GN Name=Cel2;
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC asterids; lamids; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]_TaxID=4097;
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Nematode-infected roots;
RX MEDLINE=21480065; PubMed=11595799; DOI=10.1105/tpc.13.10.2241;
RA Goellner M., Wang X., Davis E.L.;
RT "Endo-beta-1,4-glucanase expression in compatible plant-nematode
interactions.";
RL Plant Cell 13:2241-2255 (2001).
DR EMBL; AF362948; AAL30453.1; -; mRNA.
DR HSSP; O77044; 1KS8.
DR GO; GO:0008810; F:cellulase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR001701; Glyco_hydro_9.
DR Pfam; PF00759; Glyco_hydro_9; 1.
DR PROSITE; PS00592; GLYCOSYL_HYDROL_F9_1; 1.
DR PROSITE; PS00698; GLYCOSYL_HYDROL_F9_2; UNKNOWN_1.
KW Glycosidase; Hydrolase; Signal.
FT SIGNAL 1 35 Potential.
FT CHAIN 36 500 endo-beta-1,4-glucanase.
SQ SEQUENCE 500 AA; 55075 MW; 28BB48D421165798 CRC64;

Query Match 86.5%; Score 32; DB 2; Length 500;
Best Local Similarity 85.7%; Pred. No. 3.3e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLHS 7
DB 228 YSSSLHS 234
|||||

RESULT 41
Q83Z58_9MOLU PRELIMINARY; PRT; 536 AA.
AC Q83Z58;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE DNA gyrase subunit B (fragment).
GN Name=gvrB;
OS Acholeplasma pleciae.
OC Bacteria; Firmicutes; Mollicutes; Acholeplasmatales;
OC Acholeplasmataceae; Acholeplasma.
OX NCBI_TaxID=228419;
RN [1]_TaxID=228419;
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC 49582;
RA Knight T.P. Jr.;
RT "Reclassification of Mesoplasma pleciae as Acholeplasma pleciae comb.
```

RT nov. on the basis of 16S rRNA and gyrB gene sequence data. ";  
RL Int. J. Syst. Evol. Microbiol. 54:1951-1952(2004).  
RN (2)  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=ATCC 49582;  
RA Knight T.F. Jr, Lawhorn I., Gasparich G.E.;  
RT "Entomoplasmata / Mesoplasmata phylogeny";  
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.  
CC -!- SIMILARITY: Belongs to the EMBL/GenBank/DBJ topoisomerase family.  
DR EMBL; AY257486; AAP13529.1; -; Genomic\_DNA.  
DR HSSP; P06982; 1AJ6.  
DR GO; GO:0005524; P:ATP binding; IEA.  
DR GO; GO:0003918; P:DNA topoisomerase (ATP-hydrolyzing) activity; IEA.  
DR GO; GO:0006304; P:DNA modification; IEA.  
DR GO; GO:0006265; P:DNA topological change; IEA.  
DR InterPro; IPR003594; ATP bd ATPase.  
DR InterPro; IPR011558; DNA gyrase B.  
DR InterPro; IPR000565; DNA\_topoisomIV\_B.  
DR InterPro; IPR006171; Toprim\_dom.  
DR Pfam; PF00204; DNA\_gyraseB; 1.  
DR Pfam; PF02518; HATPase\_c; 1.  
DR Pfam; PF01751; Toprim; 1.  
DR PRINTS; PR00418; TPI2FAMILY.  
DR ProDom; PD149633; DNA\_gyrase\_B; 1.  
DR SMART; SM00387; HATPase\_c; 1.  
DR SMART; SM00433; TOP2c; 1.  
DR PROSITE; PS00177; TOPOISOMERASE II; 1.  
KW ATP-binding; Isomerase; Nucleotide-binding; Topoisomerase.  
FT NON\_TER 1  
FT NON\_TER 536 536  
SQ SEQUENCE 536 AA; 60040 MW; E302FC23AB9CSD09 CRC64;  
  
Query Match 86.5%; Score 32; DB 2; Length 536;  
Best Local Similarity 85.7%; Pred. No. 3.6e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 YSSNLHS 7  
DB 235 YSPNLHS 241  
  
RESULT 42  
Q7Q8MG ANOGA PRELIMINARY; PRT; 551 AA.  
AC Q7Q8MG;  
DT 01-MAR-2004 (TrEMBLrel. 26, Created)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE ENSANGP00000020793 (Fragment).  
OS ORFNames=ENSANGG00000018304;  
GN Anopheles gambiae str. PEST.  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicidae;  
OC Anophelinae; Anopheles.  
OX NCBI\_TaxID=180454;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=PEST;  
RG The Anopheles gambiae Sequence Committee;  
RT "Anopheles gambiae re-annotation.";  
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=PEST;  
RG The Anopheles gambiae Sequence Committee;  
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.  
CC -!- CAUTION: The sequence shown here is derived from an  
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
CC preliminary data.  
DR EMBL; AAAB01008944; EAA10074.2; -; Genomic DNA.  
DR GO; GO:0042765; C:GPI-anchor transamidase complex; IEA.  
DR GO; GO:0016021; C:integral to membrane; IEA.

DR InterPro; IPR007245; Gpi16.  
DR Pfam; PF04113; Gpi16; 1.  
FT NON\_TER 551 551  
SQ SEQUENCE 551 AA; 62245 MW; 5DE6B1AD50183076 CRC64;  
  
Query Match 86.5%; Score 32; DB 2; Length 551;  
Best Local Similarity 85.7%; Pred. No. 3.7e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 YSSNLHS 7  
DB 212 YSSNVHS 218  
  
RESULT 43  
Q9RP84 ACHLA PRELIMINARY; PRT; 615 AA.  
AC Q9RP84;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE DNA gyrase beta subunit.  
GN Name=gyrB;  
OS Acholeplasma laidlawii.  
OC Bacteria; Firmicutes; Mollicutes; Acholeplasmatales;  
OC Acholeplasmataceae; Acholeplasma.  
OX NCBI\_TaxID=2148;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=PG-8B;  
RX MEDLINE=20242229; PubMed=1077957;  
RA Taganov K.D., Gushchin A.E., Akopian T.A., Oparina N.Y.,  
RT "Analysis of genes, coding for DNA gyrase from the mycoplasma  
RT Acholeplasma laidlawii PG-8B.";  
RL Mol. Biol. (Mosk.) 34:292-299(2000).  
CC -!- SURUNIT: Made up of two chains. The A chain is responsible for DNA  
CC breakage and rejoining; the B chain catalyzes ATP hydrolysis. The  
CC enzyme forms an A2B2 tetramer (By similarity).  
CC -!- SIMILARITY: Belongs to the type II topoisomerase family.  
DR EMBL; AF167102; AAD52967.1; -; Genomic\_DNA.  
DR HSSP; P06982; 1AJ6.  
DR GO; GO:0005524; P:ATP binding; IEA.  
DR GO; GO:0003918; P:DNA topoisomerase (ATP-hydrolyzing) activity; IEA.  
DR GO; GO:0006304; P:DNA modification; IEA.  
DR GO; GO:0006265; P:DNA topological change; IEA.  
DR InterPro; IPR003594; ATP bd ATPase.  
DR InterPro; IPR011558; DNA\_gyrase\_B.  
DR InterPro; IPR002288; DNA\_gyraseB\_C.  
DR InterPro; IPR001241; DNA\_topoisomII.  
DR InterPro; IPR011557; GyrB.  
DR InterPro; IPR006171; Toprim\_dom.  
DR Pfam; PF00204; DNA\_gyraseB; 1.  
DR Pfam; PF00986; DNA\_gyraseB\_C; 1.  
DR Pfam; PF02518; HATPase\_c; 1.  
DR Pfam; PF01751; Toprim; 1.  
DR PRINTS; PR00418; TPI2FAMILY.  
DR ProDom; PD149633; DNA\_gyrase\_B; 1.  
DR SMART; SM00387; HATPase\_c; 1.  
DR SMART; SM00433; TOP2c; 1.  
DR TIGRFAMs; TIGR01059; GyrB; 1.  
DR PROSITE; PS00177; TOPOISOMERASE II; 1.  
KW ATP-binding; Isomerase; Nucleotide-binding; Topoisomerase.  
SQ SEQUENCE 615 AA; 68900 MW; 4D9962C35BAB73FE CRC64;  
  
Query Match 86.5%; Score 32; DB 2; Length 615;  
Best Local Similarity 85.7%; Pred. No. 4.2e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 YSSNLHS 7  
DB 267 YSPNLHS 273

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RESULT 44
Q50YV5 ENTHI
AC Q50YV5 ENTHI PRELIMINARY; PRT; 907 AA.
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Protein kinase, putative.
GN ORFNames=128.t00022;
OS Entamoeba histolytica HM-1:IMSS.
OC Eukaryota; Entamoebidae; Entamoeba.
OX NCBI_TaxID=294381;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=HM-1:IMSS;
RX PubMed=15729342; DOI=10.1038/nature03291;
RA Loftus B., Anderson I., Davies R., Alemark U.C., Samuelson J.,
RA Amedeo P., Roncaglia P., Berriman M., Hirt R.P., Mann B.J., Nozaki T.,
RA Suh B., Pop M., Duchene M., Ackers J., Tannich E., Leippe M.,
RA Hofer M., Bruchhaus I., Willhoft U., Bhattacharya A.,
RA Chillingworth T., Churcher C., Hance Z., Harris B., Harris D.,
RA Jagels K., Moule S., Mungall K., Ormond D., Squares R., Whitehead S.,
RA Quail M.A., Rabinowitsch E., Norbertczak H., Price C., Wang Z.,
RA Guillen N., Gilchrist C., Stroup S.E., Bhattacharya S., Lohia A.,
RA Foster P.G., Sichezitz-Ponten T., Weber C., Singh U., Mukherjee C.,
RA El-Sayed N.M., Petri W.A., Clark C.G., Embley T.M., Barrell B.,
RA Fraser C.M., Hall N.;
RT "The genome of the protist parasite Entamoeba histolytica.";
RL Nature 433:865-868(2005).
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAFB01000444; BAI46803.1; -; Genomic_DNA.
DR GO; GO:0016301; F:kinase activity; IEA.
DR InterPro; IPR006158; B12-binding.
DR InterPro; IPR012351; Cytokine_hlx.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 2.
DR SMART; SM00220; S_TKc_1.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW Kinase.
SQ SEQUENCE 907 AA; 105177 MW; 3F4DA690EFAA241B CRC64;

Query Match 86.5%; Score 32; DB 2; Length 907;
Best Local Similarity 71.4%; Pred. No. 6.4e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLHS 7
Db 710 YSSNLHT 716
|||||:

RESULT 45
Q64G72 9HIV1
ID Q64G72 9HIV1 PRELIMINARY; PRT; 132 AA.
AC Q64G72;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=MYD4002;

Query Match 83.8%; Score 31; DB 2; Length 158;
Best Local Similarity 85.7%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSNLHS 7
Db 147 YFSNLHS 153
|||||

RESULT 47
Q5TR20 ANOGA
ID Q5TR20 ANOGA PRELIMINARY; PRT; 187 AA.
AC Q5TR20;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE ENSANGP00000026473.
GN ORFNames=ENSANGG00000023329;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicidae; Culicidae;
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OC Anophelinae; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PEST;
RG The Anopheles gambiae Sequence Committee;
RT "Anopheles gambiae re-annotation.";
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PEST;
RG The Anopheles gambiae Sequence Committee;
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAB01008960; EAL0043.1; -; Genomic DNA.
DR GO; GO:0042302; P:structural constituent of cuticle; IEA.
DR InterPro; IPR000618; Insect_bind_4; 1.
DR Pfam; PF00379; Chitin_bind_4; 1.
DR PRINTS; PR00947; CUTICLE.
SQ SEQUENCE 187 AA; 21084 MW; 9ADA812AAF1B9557 CRC64;

Query Match 83.8%; Score 31; DB 2; Length 187;
Best Local Similarity 85.7%; Pred. NO. 1.8e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSNLHS 7
DB 102 YSSNHS 108

RESULT 48
Q50FZ3 CAMJE
ID Q50FZ3 CAMJE PRELIMINARY; PRT; 200 AA.
AC Q50FZ3_
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Cj81-008 (Fragment).
OS Campylobacter jejuni.
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
OC Campylobacteraceae; Campylobacter.
OX NCBI_TaxID=197;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=81-176;
RA Poly P., Threadgill D., Stintzi A.;
RT "Genomic Diversity in Campylobacter jejuni: Identification of C.
RT jejuni 81-176-Specific Genes.";
RL J. Clin. Microbiol. 43:2330-2338(2005).
DR EMBL; AY681241; AAW56101.1; -; Genomic DNA.
FT NON_TER 1
SQ SEQUENCE 200 AA; 24476 MW; 50B04F55BA26F213 CRC64;

Query Match 83.8%; Score 31; DB 2; Length 200;
Best Local Similarity 71.4%; Pred. NO. 2e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLHS 7
DB 121 FSSNIHS 127

RESULT 49
Q5YT42 NOCEA
ID Q5YT42_NOCEA PRELIMINARY; PRT; 218 AA.
AC Q5YT42;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=nfa38010;

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OS Nocardia farcinica.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Nocardiaceae; Nocardia.
OX NCBI_TaxID=37329;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=IFM 10152;
RX PubMed=15466710; DOI=10.1073/pnas.0406410101;
RA Ishikawa J., Yamashita A., Mikami Y., Hoshino Y., Kurita H., Hotta K.,
RA Shiba T., Hattori M.;
RT "The complete genomic sequence of Nocardia farcinica IFM 10152.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:14925-14930(2004).
DR EMBL; AP006618; BAD58649.1; -; Genomic DNA.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 218 AA; 23129 MW; B340A07CD64B8FFD CRC64;

Query Match 83.8%; Score 31; DB 2; Length 218;
Best Local Similarity 71.4%; Pred. NO. 2.2e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSNLHS 7
DB 10 YGSNMHS 16

RESULT 50
Q5T189 HUMAN
ID Q5T189 HUMAN PRELIMINARY; PRT; 296 AA.
AC Q5T189;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE SHC (Src homology 2 domain containing) transforming protein 1
DE (Fragment).
GN Name=SHC1; ORFNames=RP11-307C12.1-010;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Brown A.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL451085; CAI13245.1; -; Genomic DNA.
DR SMR; Q5T189; 143-204.
DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR InterPro; IPR000980; SH2.
DR Pfam; PF00017; SH2; 1.
DR PRINTS; PR00401; SH2DOMAIN.
DR ProDom; PD000093; SH2; 1.
DR SMART; SM00252; SH2; 1.
DR PROSITE; PS50001; SH2; 1.
FT NON_TER 1
SQ SEQUENCE 296 AA; 32507 MW; 7B08BF9F06AF9A47 CRC64;

Query Match 83.8%; Score 31; DB 2; Length 296;
Best Local Similarity 85.7%; Pred. NO. 3e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSNLHS 7
DB 267 YSSQLHS 273

Search completed: April 6, 2006, 09:09:53
Job time : 90.6751 secs

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GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: April 6, 2006, 08:58:56 ; Search time 9.37288 Seconds  
(without alignments)  
61.745 Million cell updates/sec

Title: US-10-089-500-7

Perfect score: 37

Sequence: 1 YSSNLHS 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

- 1: /cgn2\_6/ptodata/1/iaa/5 COMB.pep.\*
- 2: /cgn2\_6/ptodata/1/iaa/6 COMB.pep.\*
- 3: /cgn2\_6/ptodata/1/iaa/H COMB.pep.\*
- 4: /cgn2\_6/ptodata/1/iaa/PCTUS COMB.pep.\*
- 5: /cgn2\_6/ptodata/1/iaa/RE COMB.pep.\*
- 6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	37	100.0	128	2	US-09-225-322B-10
2	37	100.0	128	2	US-09-225-322B-19
3	37	100.0	128	2	US-09-764-304-10
4	37	100.0	128	2	US-09-764-304-19
5	34	91.9	273	1	US-08-403-853-18
6	32	86.5	36	2	US-09-570-921-100
7	32	86.5	489	1	US-08-434-702-4
8	32	86.5	500	2	US-09-970-367-2
9	31	83.8	347	2	US-09-495-406-13
10	31	83.8	347	2	US-09-816-028A-17
11	31	83.8	347	2	US-10-303-162-17
12	31	83.8	347	2	US-10-303-134-17
13	31	83.8	347	2	US-10-303-118-17
14	31	83.8	347	2	US-10-303-128-17
15	30	81.1	67	2	US-09-248-796A-22868
16	30	81.1	172	2	US-09-270-767-41649
17	30	81.1	238	2	US-09-270-767-45029
18	30	81.1	410	2	US-09-252-991A-28155
19	30	81.1	458	2	US-09-538-092-1356
20	30	81.1	609	2	US-09-198-452A-579
21	30	81.1	741	2	US-09-328-352-5898
22	30	81.1	788	2	US-08-630-915A-30
23	30	81.1	788	2	US-09-879-957-30
24	30	81.1	1744	2	US-09-438-185A-542
25	29	78.4	107	1	US-08-652-558-2
26	29	78.4	107	1	US-08-652-558-35
27	29	78.4	107	2	US-09-254-189-1

28	29	78.4	219	2	US-09-270-767-45934	Sequence 45934, A
29	29	78.4	329	2	US-09-252-991A-21191	Sequence 21191, A
30	29	78.4	334	2	US-09-165-522-14	Sequence 14, Appl
31	29	78.4	496	2	US-09-710-279-1386	Sequence 1386, Ap
32	29	78.4	497	2	US-09-134-001C-4411	Sequence 4411, Ap
33	29	78.4	677	1	US-08-522-269B-3	Sequence 3, Appl
34	29	78.4	677	2	US-09-294-923-3	Sequence 3, Appl
35	29	78.4	747	2	US-09-291-922-2	Sequence 2, Appl
36	28	75.7	7	1	US-08-137-117D-118	Sequence 118, Appl
37	28	75.7	7	1	US-08-480-434-78	Sequence 78, Appl
38	28	75.7	7	1	US-08-436-717-118	Sequence 118, Appl
39	28	75.7	7	1	US-08-053-451B-78	Sequence 78, Appl
40	28	75.7	7	2	US-08-649-100-13	Sequence 13, Appl
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42	28	75.7	7	2	US-09-563-222C-39	Sequence 39, Appl
43	28	75.7	32	2	US-08-525-539A-14	Sequence 14, Appl
44	28	75.7	98	2	US-09-134-000C-5271	Sequence 5271, Ap
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49	28	75.7	107	1	US-08-458-516-8	Sequence 8, Appl
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52	28	75.7	107	1	US-07-934-373C-16	Sequence 16, Appl
53	28	75.7	107	1	US-08-053-451B-74	Sequence 74, Appl
54	28	75.7	107	1	US-08-053-451B-176	Sequence 176, Appl
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58	28	75.7	107	2	US-09-705-392A-16	Sequence 16, Appl
59	28	75.7	107	2	US-09-705-398-16	Sequence 16, Appl
60	28	75.7	107	2	US-10-268-883-6	Sequence 6, Appl
61	28	75.7	107	4	PCT-US93-07832-16	Sequence 16, Appl
62	28	75.7	108	1	US-08-202-047-24	Sequence 24, Appl
63	28	75.7	108	2	US-08-964-690-24	Sequence 24, Appl
64	28	75.7	108	2	US-09-065-059-3	Sequence 3, Appl
65	28	75.7	108	2	US-09-199-149-7	Sequence 7, Appl
66	28	75.7	108	2	US-09-199-149-14	Sequence 14, Appl
67	28	75.7	108	2	US-09-232-290-16	Sequence 16, Appl
68	28	75.7	108	2	US-09-232-290-21	Sequence 21, Appl
69	28	75.7	108	2	US-09-905-243-73	Sequence 73, Appl
70	28	75.7	108	2	US-08-913-555-3	Sequence 3, Appl
71	28	75.7	108	2	US-08-913-555-21	Sequence 21, Appl
72	28	75.7	109	1	US-07-942-245-10	Sequence 10, Appl
73	28	75.7	109	1	US-07-934-373C-47	Sequence 47, Appl
74	28	75.7	109	1	US-08-561-521-42	Sequence 42, Appl
75	28	75.7	109	2	US-08-437-642B-47	Sequence 47, Appl
76	28	75.7	109	2	US-09-357-710A-21	Sequence 21, Appl
77	28	75.7	109	2	US-09-357-707-21	Sequence 21, Appl
78	28	75.7	109	2	US-09-357-708-21	Sequence 21, Appl
79	28	75.7	109	4	PCT-US95-01219-42	Sequence 42, Appl
80	28	75.7	111	1	US-08-137-117D-67	Sequence 67, Appl
81	28	75.7	111	1	US-08-436-717-67	Sequence 67, Appl
82	28	75.7	112	2	US-08-487-761-13	Sequence 13, Appl
83	28	75.7	113	2	US-09-270-767-60373	Sequence 60373, A
84	28	75.7	126	1	US-08-137-117D-71	Sequence 71, Appl
85	28	75.7	126	1	US-08-436-717-71	Sequence 71, Appl
86	28	75.7	126	2	US-09-107-532A-4794	Sequence 4794, Ap
87	28	75.7	127	1	US-08-458-516-5	Sequence 5, Appl
88	28	75.7	127	1	US-08-137-117D-29	Sequence 29, Appl
89	28	75.7	127	1	US-08-137-117D-37	Sequence 37, Appl
90	28	75.7	127	1	US-08-436-717-29	Sequence 29, Appl
91	28	75.7	127	1	US-08-436-717-37	Sequence 37, Appl
92	28	75.7	127	1	US-08-574-699A-2	Sequence 2, Appl
93	28	75.7	127	2	US-08-649-100-17	Sequence 17, Appl
94	28	75.7	127	2	US-08-649-100-33	Sequence 33, Appl
95	28	75.7	127	2	US-10-268-883-5	Sequence 5, Appl
96	28	75.7	131	1	US-08-236-520-2	Sequence 2, Appl
97	28	75.7	131	4	PCT-US95-05262-2	Sequence 2, Appl
98	28	75.7	173	2	US-09-270-767-44904	Sequence 44904, A
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100	28	75.7	214	1	US-08-425-763-1	Sequence 1, Appl

101	28	75.7	214	1	US-08-458-516-12	Sequence 12, Appl	174	27	73.0	27	1	US-08-290-373B-10	Sequence 10, Appl
102	28	75.7	214	1	US-07-934-373C-24	Sequence 24, Appl	175	27	73.0	27	2	US-09-270-767-35765	Sequence 35765, A
103	28	75.7	214	1	US-07-934-373C-40	Sequence 40, Appl	176	27	73.0	27	40	US-09-270-767-50982	Sequence 50982, A
104	28	75.7	214	1	US-08-788-800-11	Sequence 11, Appl	177	27	73.0	27	62	US-09-248-796A-23684	Sequence 23684, A
105	28	75.7	214	2	US-08-437-642B-24	Sequence 24, Appl	178	27	73.0	27	76	US-09-621-976-7706	Sequence 7706, Ap
106	28	75.7	214	2	US-08-437-642B-40	Sequence 40, Appl	179	27	73.0	27	123	US-09-640-211A-728	Sequence 728, App
107	28	75.7	214	2	US-08-811-757-1	Sequence 1, Appl	180	27	73.0	27	130	US-09-621-976-5866	Sequence 5866, Ap
108	28	75.7	214	2	US-09-097-309-2	Sequence 2, Appl	181	27	73.0	27	132	US-09-454-034-6	Sequence 6, Appl
109	28	75.7	214	2	US-09-097-171A-2	Sequence 2, Appl	182	27	73.0	27	142	US-08-340-820-1	Sequence 1, Appl
110	28	75.7	214	2	US-09-249-230-1	Sequence 1, Appl	183	27	73.0	27	142	US-08-172-328-1	Sequence 1, Appl
111	28	75.7	214	2	US-09-460-587-2	Sequence 2, Appl	184	27	73.0	27	142	US-08-593-535-1	Sequence 1, Appl
112	28	75.7	214	2	US-08-146-206C-24	Sequence 24, Appl	185	27	73.0	27	144	US-09-082-920-6	Sequence 6, Appl
113	28	75.7	214	2	US-09-705-686-24	Sequence 24, Appl	186	27	73.0	27	159	US-08-172-328-8	Sequence 8, Appl
114	28	75.7	214	2	US-09-940-168A-2	Sequence 2, Appl	187	27	73.0	27	160	US-08-172-328-9	Sequence 9, Appl
115	28	75.7	214	2	US-09-705-392A-24	Sequence 24, Appl	188	27	73.0	27	173	US-03-270-767-46341	Sequence 46341, A
116	28	75.7	214	2	US-09-705-398-24	Sequence 24, Appl	189	27	73.0	27	175	US-08-172-328-6	Sequence 6, Appl
117	28	75.7	214	4	PCT-US93-07832-24	Sequence 24, Appl	190	27	73.0	27	176	US-08-172-328-7	Sequence 7, Appl
118	28	75.7	214	4	PCT-US93-07832-40	Sequence 40, Appl	191	27	73.0	27	177	US-08-340-820-4	Sequence 4, Appl
119	28	75.7	233	1	US-07-934-373C-25	Sequence 25, Appl	192	27	73.0	27	177	US-08-593-535-4	Sequence 4, Appl
120	28	75.7	233	2	US-08-437-642B-25	Sequence 25, Appl	193	27	73.0	27	178	US-08-340-820-6	Sequence 6, Appl
121	28	75.7	233	2	US-08-146-206C-25	Sequence 25, Appl	194	27	73.0	27	178	US-08-593-535-6	Sequence 6, Appl
122	28	75.7	233	2	US-09-705-686-25	Sequence 25, Appl	195	27	73.0	27	190	US-08-441-629-16	Sequence 16, Appl
123	28	75.7	233	2	US-09-705-392A-25	Sequence 25, Appl	196	27	73.0	27	190	US-08-776-207-16	Sequence 16, Appl
124	28	75.7	233	2	US-09-705-398-25	Sequence 25, Appl	197	27	73.0	27	190	US-09-507-773-16	Sequence 16, Appl
125	28	75.7	233	4	PCT-US93-07832-25	Sequence 25, Appl	198	27	73.0	27	190	US-10-016-447-16	Sequence 16, Appl
126	28	75.7	237	2	US-09-097-309-6	Sequence 6, Appl	199	27	73.0	27	190	PCT-US95-09172-16	Sequence 16, Appl
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129	28	75.7	237	2	US-09-607-756-2	Sequence 2, Appl	202	27	73.0	27	192	US-09-710-279-2304	Sequence 2304, Ap
130	28	75.7	237	2	US-09-460-587-6	Sequence 6, Appl	203	27	73.0	27	193	US-08-438-439C-21	Sequence 21, Appl
131	28	75.7	237	2	US-09-940-166A-6	Sequence 6, Appl	204	27	73.0	27	195	US-09-710-279-2014	Sequence 2014, Ap
132	28	75.7	267	2	US-09-510-322A-8	Sequence 8, Appl	205	27	73.0	27	197	US-09-270-767-60613	Sequence 60613, A
133	28	75.7	270	2	US-09-514-768B-8	Sequence 8, Appl	206	27	73.0	27	201	US-03-134-001C-4319	Sequence 4319, Ap
134	28	75.7	274	2	US-09-813-659-30	Sequence 30, Appl	207	27	73.0	27	205	US-08-340-820-5	Sequence 5, Appl
135	28	75.7	274	2	US-09-549-067A-30	Sequence 30, Appl	208	27	73.0	27	205	US-08-172-328-4	Sequence 4, Appl
136	28	75.7	302	1	US-08-121-054C-18	Sequence 18, Appl	209	27	73.0	27	205	US-08-593-535-5	Sequence 5, Appl
137	28	75.7	302	1	US-08-121-054C-30	Sequence 30, Appl	210	27	73.0	27	206	US-08-340-820-7	Sequence 7, Appl
138	28	75.7	302	2	US-08-539-436-18	Sequence 18, Appl	211	27	73.0	27	206	US-08-340-820-8	Sequence 8, Appl
139	28	75.7	302	2	US-08-539-436-30	Sequence 30, Appl	212	27	73.0	27	206	US-08-172-328-5	Sequence 5, Appl
140	28	75.7	302	2	US-09-813-659-18	Sequence 18, Appl	213	27	73.0	27	206	US-08-593-535-7	Sequence 7, Appl
141	28	75.7	302	2	US-09-813-659-32	Sequence 32, Appl	214	27	73.0	27	206	US-08-593-535-8	Sequence 8, Appl
142	28	75.7	302	2	US-09-549-067A-18	Sequence 18, Appl	215	27	73.0	27	207	US-08-340-820-2	Sequence 2, Appl
143	28	75.7	302	2	US-09-549-067A-32	Sequence 32, Appl	216	27	73.0	27	207	US-08-172-328-2	Sequence 2, Appl
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145	28	75.7	380	2	US-09-248-796A-15708	Sequence 15708, A	218	27	73.0	27	208	US-08-340-820-3	Sequence 3, Appl
146	28	75.7	421	2	US-09-198-452A-232	Sequence 932, App	219	27	73.0	27	208	US-08-439-725A-7	Sequence 7, Appl
147	28	75.7	421	2	US-09-438-185A-869	Sequence 869, App	220	27	73.0	27	208	US-08-464-590A-10	Sequence 10, Appl
148	28	75.7	440	2	US-09-615-192A-290	Sequence 290, App	221	27	73.0	27	208	US-08-462-169B-17	Sequence 17, Appl
149	28	75.7	444	2	US-09-328-352-5392	Sequence 5392, App	222	27	73.0	27	208	US-08-207-412B-13	Sequence 13, Appl
150	28	75.7	466	2	US-09-248-796A-20516	Sequence 20516, A	223	27	73.0	27	208	US-08-867-471-7	Sequence 7, Appl
151	28	75.7	467	2	US-09-328-352-5378	Sequence 5378, Ap	224	27	73.0	27	208	US-08-438-439C-12	Sequence 12, Appl
152	28	75.7	524	2	US-09-625-188-2	Sequence 2, Appl	225	27	73.0	27	208	US-08-951-822-34	Sequence 34, Appl
153	28	75.7	630	2	US-10-222-100-3	Sequence 3, Appl	226	27	73.0	27	208	US-08-943-915-3	Sequence 3, Appl
154	28	75.7	637	2	US-09-328-352-7722	Sequence 7722, Ap	227	27	73.0	27	208	US-09-103-079-17	Sequence 17, Appl
155	28	75.7	630	2	US-09-248-796A-19619	Sequence 19619, A	228	27	73.0	27	208	US-08-705-245-7	Sequence 7, Appl
156	28	75.7	666	2	US-09-198-452A-409	Sequence 409, App	229	27	73.0	27	208	US-08-718-904-18	Sequence 18, Appl
157	28	75.7	666	2	US-09-438-185A-390	Sequence 390, App	230	27	73.0	27	208	US-08-023-082A-18	Sequence 18, Appl
158	28	75.7	786	2	US-10-002-344A-221	Sequence 221, App	231	27	73.0	27	208	US-09-093-585-10	Sequence 10, Appl
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160	28	75.7	1088	1	US-08-742-026-23	Sequence 2, Appl	233	27	73.0	27	208	US-08-981-030-3	Sequence 3, Appl
161	28	75.7	1088	1	US-08-742-026-23	Sequence 23, Appl	234	27	73.0	27	208	US-08-981-030-10	Sequence 10, Appl
162	28	75.7	1422	2	US-08-469-260A-86	Sequence 86, Appl	235	27	73.0	27	208	US-08-981-030-11	Sequence 11, Appl
163	28	75.7	1422	2	US-08-468-446-86	Sequence 86, Appl	236	27	73.0	27	208	US-08-437-721-13	Sequence 13, Appl
164	28	75.7	1422	2	US-08-467-344A-86	Sequence 86, Appl	237	27	73.0	27	208	US-09-425-021-17	Sequence 17, Appl
165	28	75.7	1422	2	US-08-424-550B-86	Sequence 86, Appl	238	27	73.0	27	208	US-09-449-249-18	Sequence 18, Appl
166	28	75.7	2318	2	US-09-091-219-24	Sequence 24, Appl	239	27	73.0	27	208	US-09-390-207-23	Sequence 23, Appl
167	28	75.7	2218	2	US-09-660-541-24	Sequence 24, Appl	240	27	73.0	27	208	US-09-390-207-33	Sequence 33, Appl
168	28	75.7	2584	2	US-08-936-135-4	Sequence 4, Appl	241	27	73.0	27	208		
169	28	75.7	2588	2	US-08-936-135-2	Sequence 2, Appl	242	27	73.0	27	208		
170	28	75.7	2887	2	US-08-462-467B-8	Sequence 8, Appl	243	27	73.0	27	208		
171	28	73.0	16	2	US-08-810-009-49	Sequence 49, Appl	244	27	73.0	27	208		
172	27	73.0	16	2	US-09-776-490-49	Sequence 49, Appl	245	27	73.0	27	208		
173	27	73.0	19	2	US-09-155-260C-17	Sequence 17, Appl	246	27	73.0	27	208		

247	27	73.0	208	2	US-09-229-947-34	Sequence 34, Appl	320	26	70.3	21	2	US-09-962-756-512	Sequence 512, App
248	27	73.0	208	2	US-09-564-829-11	Sequence 11, Appl	321	26	70.3	27	2	US-09-270-767-53397	Sequence 53397, A
249	27	73.0	208	2	US-09-248-998-11	Sequence 18, Appl	322	26	70.3	46	2	US-09-270-767-37739	Sequence 37739, A
250	27	73.0	208	2	US-09-572-406B-4	Sequence 4, Appl	323	26	70.3	46	2	US-09-270-767-52956	Sequence 52956, A
251	27	73.0	208	2	US-09-490-714-7	Sequence 7, Appl	324	26	70.3	66	2	US-09-248-796A-27606	Sequence 27606, A
252	27	73.0	208	2	US-09-610-651-18	Sequence 18, Appl	325	26	70.3	67	2	US-09-248-796A-25846	Sequence 25846, A
253	27	73.0	208	2	US-09-692-945-16	Sequence 16, Appl	326	26	70.3	71	2	US-09-621-976-5251	Sequence 5251, Ap
254	27	73.0	208	2	US-09-949-016-6160	Sequence 6160, Ap	327	26	70.3	81	2	US-09-540-236-3111	Sequence 3111, Ap
255	27	73.0	208	2	US-09-345-373-18	Sequence 18, Appl	328	26	70.3	84	2	US-09-270-767-34384	Sequence 34384, A
256	27	73.0	208	2	US-10-075-446-18	Sequence 18, Appl	329	26	70.3	84	2	US-09-270-767-49601	Sequence 49601, A
257	27	73.0	220	2	US-09-981-030-5	Sequence 5, Appl	330	26	70.3	99	2	US-09-424-311-3	Sequence 3, Appl
258	27	73.0	243	2	US-09-270-767-60835	Sequence 60835, A	331	26	70.3	103	2	US-09-484-577A-74	Sequence 74, Appl
259	27	73.0	245	2	US-09-198-452A-1091	Sequence 1091, Ap	332	26	70.3	109	2	US-09-726-219A-268	Sequence 268, App
260	27	73.0	245	2	US-09-438-185A-1019	Sequence 1019, Ap	333	26	70.3	109	2	US-09-196-522-268	Sequence 268, App
261	27	73.0	248	2	US-09-248-796A-17668	Sequence 17668, A	334	26	70.3	111	1	US-07-634-278-46	Sequence 46, Appl
262	27	73.0	253	2	US-09-949-016-9815	Sequence 9815, Ap	335	26	70.3	111	1	US-07-634-278-47	Sequence 47, Appl
263	27	73.0	257	2	US-09-248-796A-24138	Sequence 24138, A	336	26	70.3	111	1	US-08-477-728-46	Sequence 46, Appl
264	27	73.0	264	2	US-09-270-767-41787	Sequence 41787, A	337	26	70.3	111	1	US-08-477-728-47	Sequence 47, Appl
265	27	73.0	279	2	US-09-134-000C-5430	Sequence 5430, Ap	338	26	70.3	111	1	US-08-474-040-45	Sequence 46, Appl
266	27	73.0	283	2	US-09-248-796A-19345	Sequence 19345, A	339	26	70.3	111	1	US-08-474-040-47	Sequence 47, Appl
267	27	73.0	286	2	US-09-583-110-5126	Sequence 5126, Ap	340	26	70.3	111	1	US-08-487-200-46	Sequence 46, Appl
268	27	73.0	286	2	US-09-107-433-4083	Sequence 4083, Ap	341	26	70.3	111	1	US-08-487-200-47	Sequence 47, Appl
269	27	73.0	310	2	US-09-248-796A-24034	Sequence 24034, A	342	26	70.3	111	2	US-08-484-537-46	Sequence 46, Appl
270	27	73.0	312	2	US-09-270-767-47024	Sequence 47024, A	343	26	70.3	111	2	US-08-484-537-47	Sequence 47, Appl
271	27	73.0	328	2	US-09-198-452A-637	Sequence 637, App	344	26	70.3	111	2	US-09-249-542-17	Sequence 17, Appl
272	27	73.0	340	2	US-09-438-185A-597	Sequence 597, App	345	26	70.3	111	2	US-09-249-542-18	Sequence 18, Appl
273	27	73.0	340	2	US-09-740-027-2	Sequence 2, Appl	346	26	70.3	112	1	US-08-888-366-18	Sequence 18, Appl
274	27	73.0	340	2	US-10-274-968-2	Sequence 4, Appl	347	26	70.3	112	1	US-09-249-542-24	Sequence 24, Appl
275	27	73.0	358	2	US-09-740-027-4	Sequence 4, Appl	348	26	70.3	117	2	US-09-270-767-36131	Sequence 36131, A
276	27	73.0	358	2	US-09-248-796A-19916	Sequence 19916, A	349	26	70.3	117	2	US-09-270-767-51348	Sequence 51348, A
277	27	73.0	358	2	US-09-949-016-6470	Sequence 6470, Ap	350	26	70.3	121	2	US-09-270-767-47240	Sequence 47240, A
278	27	73.0	358	2	US-10-274-968-4	Sequence 4, Appl	351	26	70.3	129	2	US-09-556-605-2	Sequence 2, Appl
279	27	73.0	362	2	US-09-949-016-11064	Sequence 11064, A	352	26	70.3	130	2	US-09-339-596A-28	Sequence 28, Appl
280	27	73.0	368	2	US-09-270-767-45335	Sequence 45335, A	353	26	70.3	130	2	US-09-339-596A-24	Sequence 24, Appl
281	27	73.0	422	2	US-09-347-878-26	Sequence 26, Appl	354	26	70.3	131	2	US-09-248-796A-21583	Sequence 21583, A
282	27	73.0	428	2	US-09-134-001C-4879	Sequence 4879, Ap	355	26	70.3	132	1	US-08-379-057-16	Sequence 16, Appl
283	27	73.0	428	2	US-09-949-016-9739	Sequence 9739, Ap	356	26	70.3	173	2	US-09-605-703B-2386	Sequence 2386, Ap
284	27	73.0	447	2	US-08-836-687B-39	Sequence 39, Appl	357	26	70.3	174	2	US-09-149-476-526	Sequence 526, App
285	27	73.0	450	1	US-08-665-037-2	Sequence 2, Appl	358	26	70.3	178	2	US-09-107-532A-6465	Sequence 6465, Ap
286	27	73.0	450	1	US-08-666-067-2	Sequence 2, Appl	359	26	70.3	191	2	US-09-248-796A-15004	Sequence 15004, A
287	27	73.0	450	1	US-08-732-870-2	Sequence 2, Appl	360	26	70.3	194	2	US-09-248-796A-27860	Sequence 27860, A
288	27	73.0	471	2	US-09-248-796A-14351	Sequence 14351, A	361	26	70.3	199	2	US-09-198-452A-595	Sequence 595, App
289	27	73.0	527	2	US-09-712-363-156	Sequence 156, App	362	26	70.3	199	2	US-09-438-185A-558	Sequence 558, App
290	27	73.0	567	2	US-09-270-767-45121	Sequence 45121, A	363	26	70.3	206	2	US-09-270-767-43990	Sequence 43990, A
291	27	73.0	646	2	US-09-583-110-4692	Sequence 4692, Ap	364	26	70.3	210	2	US-09-538-092-343	Sequence 243, App
292	27	73.0	654	2	US-09-107-433-4540	Sequence 4540, Ap	365	26	70.3	218	4	PCT-US94-14106-57	Sequence 57, Appl
293	27	73.0	769	2	US-09-949-016-8149	Sequence 8149, Ap	366	26	70.3	223	2	US-09-270-767-38301	Sequence 38301, A
294	27	73.0	880	2	US-09-538-092-441	Sequence 441, App	367	26	70.3	223	2	US-09-270-767-53518	Sequence 53518, A
295	27	73.0	880	2	US-09-487-558B-440	Sequence 440, App	368	26	70.3	250	2	US-10-100-252-2	Sequence 2, Appl
296	27	73.0	902	2	US-10-104-047-2387	Sequence 2387, Ap	369	26	70.3	252	2	US-09-248-796A-20003	Sequence 20003, A
297	27	73.0	969	2	US-09-118-276-2	Sequence 2, Appl	370	26	70.3	281	2	US-09-270-767-60699	Sequence 60699, A
298	27	73.0	980	2	US-09-118-276-11	Sequence 11, Appl	371	26	70.3	292	2	US-09-710-279-3636	Sequence 3636, Ap
299	27	73.0	982	2	US-09-236-995D-2	Sequence 2, Appl	372	26	70.3	292	2	US-09-543-681A-6846	Sequence 6846, Ap
300	27	73.0	1010	2	US-09-248-796A-16379	Sequence 16379, A	373	26	70.3	302	2	US-08-809-665A-36	Sequence 36, Appl
301	27	73.0	1021	2	US-09-543-681A-7383	Sequence 7383, Ap	374	26	70.3	302	2	US-09-809-665A-107	Sequence 107, App
302	27	73.0	1066	1	US-08-633-770A-1	Sequence 1, Appl	375	26	70.3	315	2	US-09-248-796A-17439	Sequence 17439, A
303	27	73.0	1066	2	US-09-280-197-5	Sequence 5, Appl	376	26	70.3	324	2	US-09-270-767-42915	Sequence 42915, A
304	27	73.0	1066	2	US-09-423-126-3	Sequence 3, Appl	377	26	70.3	333	2	US-09-252-991A-17113	Sequence 17113, A
305	27	73.0	1070	1	US-08-633-770A-2	Sequence 2, Appl	378	26	70.3	359	1	US-08-307-382-2	Sequence 2, Appl
306	27	73.0	1070	2	US-09-280-197-6	Sequence 6, Appl	379	26	70.3	359	1	US-08-366-779-2	Sequence 2, Appl
307	27	73.0	1070	2	US-09-423-126-4	Sequence 4, Appl	380	26	70.3	359	1	US-08-478-727-2	Sequence 2, Appl
308	27	73.0	1112	2	US-09-176-664-1	Sequence 1, Appl	381	26	70.3	359	1	US-08-473-508-2	Sequence 2, Appl
309	27	73.0	1112	2	US-09-519-076-1	Sequence 1, Appl	382	26	70.3	359	1	US-08-789-936-2	Sequence 2, Appl
310	27	73.0	1134	2	US-09-176-664-20	Sequence 20, Appl	383	26	70.3	359	1	US-08-833-610-6	Sequence 6, Appl
311	27	73.0	1134	2	US-09-519-076-20	Sequence 20, Appl	384	26	70.3	359	2	US-08-834-033A-16	Sequence 16, Appl
312	27	73.0	1155	1	US-08-094-948A-29	Sequence 29, Appl	385	26	70.3	359	2	US-08-934-254-2	Sequence 2, Appl
313	27	73.0	1155	4	PCT-US96-09319-29	Sequence 29, Appl	386	26	70.3	359	2	US-09-377-452-6	Sequence 6, Appl
314	26	70.3	7	2	US-09-192-854-141	Sequence 141, App	387	26	70.3	359	2	US-09-685-775-2	Sequence 2, Appl
315	26	70.3	7	2	US-09-511-939-251	Sequence 251, App	388	26	70.3	368	2	US-09-270-767-45204	Sequence 45204, A
316	26	70.3	12	2	US-09-339-596A-36	Sequence 36, Appl	389	26	70.3	369	2	US-09-248-796A-23009	Sequence 23009, A
317	26	70.3	20	2	US-09-556-605-19	Sequence 19, Appl	390	26	70.3	377	2	US-09-248-796A-25454	Sequence 25454, A
318	26	70.3	20	2	US-09-556-605-20	Sequence 20, Appl	391	26	70.3	378	2	US-09-234-245-3	Sequence 3, Appl
319	26	70.3	21	2	US-09-881-572A-13	Sequence 13, Appl	392	26	70.3	379	2	US-09-583-110-3811	Sequence 3811, Ap



393	26	70.3	382	2	US-09-107-433-3703	Sequence 3703, Ap	466	26	70.3	1451	1	US-08-308-872B-4	Sequence 4, Appl
394	26	70.3	400	2	US-09-134-000C-3791	Sequence 3791, Ap	467	26	70.3	1453	1	US-08-308-872B-6	Sequence 6, Appl
395	26	70.3	414	2	US-09-949-016-11741	Sequence 11741, A	468	25	67.6	7	2	US-08-908-469-5	Sequence 5, Appl
396	26	70.3	429	2	US-09-949-016-9689	Sequence 9689, Ap	469	25	67.6	7	2	US-08-908-469-124	Sequence 124, App
397	26	70.3	443	2	US-09-710-279-1200	Sequence 1200, Ap	470	25	67.6	9	2	US-08-142-590B-1	Sequence 1, Appl
398	26	70.3	445	2	US-09-710-279-2644	Sequence 2644, Ap	471	25	67.6	10	1	US-08-552-907-13	Sequence 13, Appl
399	26	70.3	448	2	US-09-134-001C-4146	Sequence 4146, Ap	472	25	67.6	10	1	US-08-747-915-8	Sequence 8, Appl
400	26	70.3	450	2	US-09-134-001C-4858	Sequence 4858, Ap	473	25	67.6	10	2	US-08-691-045-13	Sequence 13, Appl
401	26	70.3	451	2	US-09-134-001C-3092	Sequence 3092, Ap	474	25	67.6	10	2	US-08-285-783-8	Sequence 8, Appl
402	26	70.3	470	2	US-09-543-681A-7894	Sequence 7894, Ap	475	25	67.6	11	1	US-08-747-915-3	Sequence 3, Appl
403	26	70.3	488	1	US-08-933-750C-17	Sequence 17, Appl	476	25	67.6	11	2	US-09-181-816-2	Sequence 2, Appl
404	26	70.3	488	2	US-09-234-613-17	Sequence 17, Appl	477	25	67.6	11	2	US-09-285-783-3	Sequence 3, Appl
405	26	70.3	489	2	US-09-533-023-60	Sequence 60, Appl	478	25	67.6	11	2	US-09-402-641-7	Sequence 7, Appl
406	26	70.3	493	2	US-09-543-681A-5068	Sequence 5068, Ap	479	25	67.6	12	2	US-08-142-590B-6	Sequence 6, Appl
407	26	70.3	504	2	US-09-234-245-2	Sequence 2, Appl	480	25	67.6	12	2	US-09-402-641-8	Sequence 8, Appl
408	26	70.3	504	2	US-09-234-245-4	Sequence 4, Appl	481	25	67.6	13	1	US-07-932-200-12	Sequence 12, Appl
409	26	70.3	522	2	US-09-549-519-33	Sequence 33, Appl	482	25	67.6	13	1	US-08-387-749-12	Sequence 12, Appl
410	26	70.3	522	2	US-09-549-519-34	Sequence 34, Appl	483	25	67.6	13	2	US-09-402-641-1	Sequence 1, Appl
411	26	70.3	533	2	US-09-248-796A-14367	Sequence 14367, A	484	25	67.6	13	2	US-09-402-641-3	Sequence 3, Appl
412	26	70.3	550	2	US-10-100-252-17	Sequence 17, Appl	485	25	67.6	13	4	PCT-US93-08231-12	Sequence 12, Appl
413	26	70.3	561	2	US-09-233-989-5	Sequence 5, Appl	486	25	67.6	15	2	US-08-142-590B-5	Sequence 5, Appl
414	26	70.3	580	2	US-10-104-047-2103	Sequence 2103, Ap	487	25	67.6	15	2	US-09-402-642-2	Sequence 2, Appl
415	26	70.3	598	2	US-09-583-110-3070	Sequence 3070, Ap	488	25	67.6	18	1	US-08-747-915-4	Sequence 4, Appl
416	26	70.3	604	2	US-09-107-433-4348	Sequence 4348, Ap	489	25	67.6	18	2	US-08-142-590B-4	Sequence 4, Appl
417	26	70.3	631	2	US-09-345-468-12	Sequence 12, Appl	490	25	67.6	18	2	US-08-142-590B-24	Sequence 24, Appl
418	26	70.3	631	2	US-09-414-453A-12	Sequence 12, Appl	491	25	67.6	18	2	US-09-252-586-27	Sequence 27, Appl
419	26	70.3	635	2	US-10-100-252-16	Sequence 16, Appl	492	25	67.6	19	2	US-09-285-783-4	Sequence 4, Appl
420	26	70.3	646	2	US-09-949-016-7344	Sequence 7344, Ap	493	25	67.6	19	2	US-09-791-524A-1	Sequence 1, Appl
421	26	70.3	648	2	US-09-134-001C-5161	Sequence 5161, Ap	494	25	67.6	20	2	US-09-791-524A-2	Sequence 2, Appl
422	26	70.3	661	2	US-09-248-796A-17080	Sequence 17080, A	495	25	67.6	20	2	US-08-142-590B-23	Sequence 23, Appl
423	26	70.3	685	2	US-09-248-796A-20197	Sequence 20197, A	496	25	67.6	21	1	US-08-747-915-2	Sequence 2, Appl
424	26	70.3	710	2	US-09-487-558B-276	Sequence 276, App	497	25	67.6	21	2	US-09-046-106-2	Sequence 2, Appl
425	26	70.3	749	2	US-08-997-685A-10	Sequence 10, Appl	498	25	67.6	21	2	US-08-142-590B-3	Sequence 3, Appl
426	26	70.3	749	2	US-09-086-436-39	Sequence 39, Appl	499	25	67.6	21	2	US-08-442-108B-32	Sequence 32, Appl
427	26	70.3	817	1	US-08-820-170A-28	Sequence 28, Appl	500	25	67.6	21	2	US-09-285-783-2	Sequence 2, Appl
428	26	70.3	817	2	US-09-055-699-28	Sequence 28, Appl	501	25	67.6	22	1	US-08-370-567-37	Sequence 37, Appl
429	26	70.3	817	2	US-09-273-565-28	Sequence 28, Appl	502	25	67.6	22	1	US-08-438-759-37	Sequence 37, Appl
430	26	70.3	817	2	US-09-563-538-28	Sequence 28, Appl	503	25	67.6	22	1	US-08-538-911-12	Sequence 12, Appl
431	26	70.3	817	2	US-09-661-468-28	Sequence 28, Appl	504	25	67.6	22	4	PCT-US94-05591-12	Sequence 12, Appl
432	26	70.3	817	2	US-09-976-165-28	Sequence 28, Appl	505	25	67.6	22	4	PCT-US94-05684-37	Sequence 37, Appl
433	26	70.3	824	2	US-09-399-081A-8	Sequence 8, Appl	506	25	67.6	23	2	US-09-791-524A-7	Sequence 7, Appl
434	26	70.3	829	1	US-08-820-170A-31	Sequence 31, Appl	507	25	67.6	23	2	US-09-791-524A-8	Sequence 8, Appl
435	26	70.3	829	2	US-09-055-699-31	Sequence 31, Appl	508	25	67.6	25	2	US-09-791-524A-16	Sequence 16, Appl
436	26	70.3	829	2	US-09-273-565-31	Sequence 31, Appl	509	25	67.6	25	2	US-09-791-524A-17	Sequence 17, Appl
437	26	70.3	829	2	US-09-565-538-31	Sequence 31, Appl	510	25	67.6	27	2	US-09-046-106-1	Sequence 1, Appl
438	26	70.3	829	2	US-09-661-468-31	Sequence 31, Appl	511	25	67.6	32	2	US-08-101-272G-18	Sequence 18, Appl
439	26	70.3	829	2	US-09-976-165-31	Sequence 31, Appl	512	25	67.6	44	1	US-08-747-915-1	Sequence 1, Appl
440	26	70.3	886	2	US-09-248-796A-18004	Sequence 18004, A	513	25	67.6	44	2	US-09-285-783-1	Sequence 1, Appl
441	26	70.3	892	2	US-09-513-151A-4	Sequence 4, Appl	514	25	67.6	44	2	US-09-670-537A-1	Sequence 1, Appl
442	26	70.3	910	2	US-08-997-685A-2	Sequence 2, Appl	515	25	67.6	47	2	US-09-880-503-2	Sequence 2, Appl
443	26	70.3	910	2	US-09-086-436-31	Sequence 31, Appl	516	25	67.6	48	2	US-08-438-745-22	Sequence 22, Appl
444	26	70.3	916	2	US-09-543-681A-5205	Sequence 5205, Ap	517	25	67.6	48	2	US-09-219-019-52	Sequence 22, Appl
445	26	70.3	916	2	US-09-489-039A-14125	Sequence 14125, A	518	25	67.6	48	4	PCT-US94-05669A-22	Sequence 22, Appl
446	26	70.3	931	2	US-09-949-016-8988	Sequence 8988, Ap	519	25	67.6	49	1	US-08-747-915-5	Sequence 5, Appl
447	26	70.3	940	2	US-09-512-250C-2	Sequence 2, Appl	520	25	67.6	49	2	US-09-285-783-5	Sequence 5, Appl
448	26	70.3	944	2	US-09-134-001C-4352	Sequence 4352, Ap	521	25	67.6	51	2	US-09-533-993C-6060	Sequence 6060, Ap
449	26	70.3	958	2	US-09-706-594-5	Sequence 5, Appl	522	25	67.6	59	2	US-09-270-767-40021	Sequence 40021, A
450	26	70.3	966	2	US-09-964-956-32	Sequence 32, Appl	523	25	67.6	59	2	US-09-270-767-55237	Sequence 55237, A
451	26	70.3	990	2	US-09-627-376-7	Sequence 7, Appl	524	25	67.6	62	2	US-09-328-352-5663	Sequence 5663, Ap
452	26	70.3	990	2	US-10-047-676B-7	Sequence 7, Appl	525	25	67.6	63	2	US-09-345-236B-30	Sequence 30, Appl
453	26	70.3	1024	2	US-09-562-737-45	Sequence 45, Appl	526	25	67.6	65	1	US-08-358-160-96	Sequence 96, Appl
454	26	70.3	1034	2	US-09-543-681A-8172	Sequence 8172, Ap	527	25	67.6	65	2	US-09-621-976-7033	Sequence 7033, Ap
455	26	70.3	1257	1	US-08-049-783-2	Sequence 2, Appl	528	25	67.6	66	2	US-09-248-796A-28075	Sequence 28075, A
456	26	70.3	1257	1	US-08-158-232-6	Sequence 6, Appl	529	25	67.6	77	2	US-09-448-806C-2	Sequence 2, Appl
457	26	70.3	1257	1	US-08-304-626-6	Sequence 6, Appl	530	25	67.6	79	2	US-09-621-976-6352	Sequence 6352, Ap
458	26	70.3	1257	1	US-08-316-301A-6	Sequence 6, Appl	531	25	67.6	79	2	US-09-248-796A-24331	Sequence 24331, A
459	26	70.3	1257	1	US-08-611-928-6	Sequence 6, Appl	532	25	67.6	83	2	US-09-583-110-4978	Sequence 4978, Ap
460	26	70.3	1257	2	US-09-173-891-6	Sequence 6, Appl	533	25	67.6	84	2	US-09-270-767-57811	Sequence 57811, A
461	26	70.3	1257	2	US-09-076-137-6	Sequence 6, Appl	534	25	67.6	84	2	US-09-248-796A-22433	Sequence 22433, A
462	26	70.3	1257	2	US-09-738-363-6	Sequence 6, Appl	535	25	67.6	100	2	US-09-621-976-4364	Sequence 4364, Ap
463	26	70.3	1257	4	PCT-US92-03624-6	Sequence 6, Appl	536	25	67.6	105	1	US-08-467-420A-16	Sequence 16, Appl
464	26	70.3	1271	2	US-09-270-767-45803	Sequence 45803, A	537	25	67.6	105	1	US-08-470-110A-16	Sequence 16, Appl
465	26	70.3	1356	2	US-09-487-558B-306	Sequence 306, App	538	25	67.6	105	1	US-08-940-371-16	Sequence 16, Appl



539	25	67.6	105	2	US-08-637-647-16	Sequence 16, Appl	612	25	67.6	224	2	US-09-710-279-1002	Sequence 1002, Ap
540	25	67.6	106	2	US-09-513-999C-4918	Sequence 4918, Ap	613	25	67.6	230	2	US-09-270-767-62021	Sequence 62021, A
541	25	67.6	107	2	US-08-908-469-13	Sequence 13, Appl	614	25	67.6	231	2	US-09-248-796A-19730	Sequence 19730, A
542	25	67.6	108	2	US-08-908-469-15	Sequence 15, Appl	615	25	67.6	233	2	US-08-438-745-15	Sequence 15, Appl
543	25	67.6	108	2	US-08-908-469-8	Sequence 8, Appl	616	25	67.6	233	2	US-08-438-745-17	Sequence 17, Appl
544	25	67.6	108	2	US-08-908-469-10	Sequence 10, Appl	617	25	67.6	233	2	US-09-219-019-15	Sequence 15, Appl
545	25	67.6	108	2	US-08-908-469-126	Sequence 126, Appl	618	25	67.6	233	2	US-09-219-019-17	Sequence 17, Appl
546	25	67.6	110	2	US-09-440-781-94	Sequence 94, Appl	619	25	67.6	233	2	US-09-543-681A-8339	Sequence 8339, Ap
547	25	67.6	110	2	US-09-440-781-95	Sequence 95, Appl	620	25	67.6	233	4	PCT-US94-05669A-15	Sequence 15, Appl
548	25	67.6	110	2	US-08-908-469-103	Sequence 103, Appl	621	25	67.6	233	4	PCT-US94-05669A-17	Sequence 17, Appl
549	25	67.6	110	2	US-08-908-469-105	Sequence 105, Appl	622	25	67.6	234	2	US-09-710-279-1380	Sequence 1380, Ap
550	25	67.6	110	2	US-08-908-469-107	Sequence 107, Appl	623	25	67.6	235	2	US-08-438-745-13	Sequence 13, Appl
551	25	67.6	110	2	US-08-908-469-109	Sequence 109, Appl	624	25	67.6	235	2	US-09-219-019-13	Sequence 13, Appl
552	25	67.6	110	2	US-08-908-469-111	Sequence 111, Appl	625	25	67.6	235	4	PCT-US94-05669A-13	Sequence 13, Appl
553	25	67.6	110	2	US-08-908-469-113	Sequence 113, Appl	626	25	67.6	237	2	US-09-270-767-46789	Sequence 46789, A
554	25	67.6	110	2	US-08-908-469-115	Sequence 115, Appl	627	25	67.6	237	2	US-08-908-469-100	Sequence 100, App
555	25	67.6	110	2	US-08-908-469-117	Sequence 117, Appl	628	25	67.6	238	2	US-09-140-749-51	Sequence 51, Appl
556	25	67.6	111	2	US-09-513-999C-7501	Sequence 7501, Ap	629	25	67.6	245	2	US-09-071-035-310	Sequence 310, App
557	25	67.6	113	1	US-08-467-420A-21	Sequence 21, Appl	630	25	67.6	245	2	US-10-206-576-310	Sequence 310, App
558	25	67.6	113	1	US-08-467-420A-70	Sequence 70, Appl	631	25	67.6	246	2	US-09-134-000C-5137	Sequence 5137, Ap
559	25	67.6	113	1	US-08-470-110A-21	Sequence 21, Appl	632	25	67.6	249	2	US-09-949-016-8805	Sequence 8805, Ap
560	25	67.6	113	1	US-08-470-110A-70	Sequence 70, Appl	633	25	67.6	252	2	US-09-134-001C-4662	Sequence 4662, Ap
561	25	67.6	113	1	US-08-667-769A-16	Sequence 16, Appl	634	25	67.6	253	2	US-09-134-001C-3569	Sequence 3569, Ap
562	25	67.6	113	1	US-08-667-769A-21	Sequence 21, Appl	635	25	67.6	256	2	US-09-134-001C-5211	Sequence 5211, Ap
563	25	67.6	113	1	US-08-667-769A-70	Sequence 70, Appl	636	25	67.6	264	2	US-09-252-991A-24859	Sequence 24859, A
564	25	67.6	113	1	US-08-940-371-21	Sequence 21, Appl	637	25	67.6	267	2	US-09-270-767-45998	Sequence 45998, A
565	25	67.6	113	1	US-08-940-371-70	Sequence 70, Appl	638	25	67.6	275	2	US-09-634-238-390	Sequence 390, App
566	25	67.6	113	2	US-08-637-647-21	Sequence 21, Appl	639	25	67.6	277	1	US-08-375-709-5	Sequence 5, Appl1
567	25	67.6	113	2	US-10-700-740-16	Sequence 16, Appl	640	25	67.6	277	1	US-08-752-929-5	Sequence 5, Appl1
568	25	67.6	113	2	US-10-700-740-21	Sequence 21, Appl	641	25	67.6	280	2	US-09-489-039A-8803	Sequence 8803, Ap
569	25	67.6	113	2	US-10-700-740-70	Sequence 70, Appl	642	25	67.6	282	2	US-10-101-464A-614	Sequence 614, App
570	25	67.6	113	4	PCT-US95-17082A-16	Sequence 16, Appl	643	25	67.6	292	2	US-09-270-767-46494	Sequence 46494, A
571	25	67.6	113	4	PCT-US95-17082A-21	Sequence 21, Appl	644	25	67.6	296	2	US-09-134-001C-4473	Sequence 4473, Ap
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574	25	67.6	124	2	US-09-248-796A-14661	Sequence 14661, A	647	25	67.6	311	2	US-09-247-155-169	Sequence 169, App
575	25	67.6	125	2	US-09-270-767-61010	Sequence 61010, A	648	25	67.6	311	2	US-09-903-130-169	Sequence 169, App
576	25	67.6	132	2	US-09-248-796A-17523	Sequence 17523, A	649	25	67.6	313	2	US-09-943-016-8602	Sequence 8602, Ap
577	25	67.6	135	2	US-09-880-503-4	Sequence 4, Appl	650	25	67.6	323	2	US-09-880-503-7	Sequence 7, Appl1
578	25	67.6	138	1	US-08-797-689-12	Sequence 12, Appl	651	25	67.6	324	2	US-09-270-767-45502	Sequence 45502, A
579	25	67.6	138	1	US-09-984-186-12	Sequence 12, Appl	652	25	67.6	326	2	US-09-252-991A-28516	Sequence 28516, A
580	25	67.6	141	2	US-09-248-796A-20051	Sequence 20051, A	653	25	67.6	331	1	US-08-094-533B-10	Sequence 10, Appl
581	25	67.6	142	2	US-09-880-503-8	Sequence 8, Appl	654	25	67.6	331	1	US-08-276-860A-10	Sequence 10, Appl
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583	25	67.6	151	1	US-08-332-576-3	Sequence 3, Appl	656	25	67.6	331	1	US-08-799-913-10	Sequence 10, Appl
584	25	67.6	151	4	PCT-US95-13672-3	Sequence 3, Appl	657	25	67.6	331	1	US-08-711-893-10	Sequence 10, Appl
585	25	67.6	157	2	US-08-142-590B-25	Sequence 25, Appl	658	25	67.6	331	1	US-09-150-200-10	Sequence 10, Appl
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587	25	67.6	168	2	US-09-107-532A-4398	Sequence 4398, Ap	660	25	67.6	331	2	US-09-452-370-10	Sequence 10, Appl
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590	25	67.6	181	2	US-09-248-796A-21596	Sequence 21596, A	663	25	67.6	331	2	US-10-051-989A-10	Sequence 10, Appl
591	25	67.6	194	2	US-09-101-272G-80	Sequence 80, Appl	664	25	67.6	331	2	US-09-861-012A-10	Sequence 10, Appl
592	25	67.6	194	2	US-09-608-703B-2518	Sequence 2518, Ap	665	25	67.6	331	2	US-09-919-039-187	Sequence 187, App
593	25	67.6	198	2	US-09-710-279-2188	Sequence 2188, Ap	666	25	67.6	331	2	US-09-538-032-856	Sequence 856, App
594	25	67.6	200	2	US-09-101-272G-73	Sequence 73, Appl	667	25	67.6	331	2	US-09-861-098A-10	Sequence 10, Appl
595	25	67.6	201	2	US-09-101-272G-96	Sequence 96, Appl	668	25	67.6	331	2	US-09-861-037-10	Sequence 10, Appl
596	25	67.6	205	2	US-09-234-245-7	Sequence 7, Appl	669	25	67.6	331	4	PCT-US94-08119-10	Sequence 10, Appl
597	25	67.6	205	2	US-09-234-245-9	Sequence 9, Appl	670	25	67.6	331	4	PCT-US94-08120-10	Sequence 10, Appl
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600	25	67.6	211	2	US-09-692-945-4	Sequence 4, Appl	673	25	67.6	331	4	PCT-US95-15353-41	Sequence 41, Appl
601	25	67.6	211	2	US-09-665-493B-5	Sequence 5, Appl	674	25	67.6	333	2	US-09-949-016-9680	Sequence 9680, Ap
602	25	67.6	212	2	US-09-234-245-6	Sequence 6, Appl	675	25	67.6	337	2	US-09-710-279-148	Sequence 148, App
603	25	67.6	212	2	US-09-234-245-8	Sequence 8, Appl	676	25	67.6	337	2	US-09-710-279-156	Sequence 156, App
604	25	67.6	212	2	US-09-692-945-2	Sequence 2, Appl	677	25	67.6	337	2	US-09-710-279-458	Sequence 458, App
605	25	67.6	214	2	US-09-710-279-1898	Sequence 1898, Ap	678	25	67.6	337	2	US-09-710-279-1152	Sequence 1152, Ap
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607	25	67.6	217	2	US-10-206-576-312	Sequence 312, App	680	25	67.6	337	2	US-09-710-279-1220	Sequence 1220, Ap
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609	25	67.6	219	2	US-09-248-796A-23661	Sequence 23661, A	682	25	67.6	337	2	US-09-710-279-2044	Sequence 2044, Ap
610	25	67.6	222	2	US-09-710-279-1510	Sequence 1510, Ap	683	25	67.6	337	2	US-09-710-279-2154	Sequence 2154, Ap
611	25	67.6	223	2	US-09-710-279-1234	Sequence 1234, Ap	684	25	67.6	337	2	US-09-710-279-2196	Sequence 2196, Ap

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688	25	67.6	341	2	US-10-006-768A-77	Sequence 77, Appl	761	25	67.6	542	2	US-09-396-154-47	Sequence 47, Appl
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690	25	67.6	341	2	US-10-015-393A-77	Sequence 77, Appl	763	25	67.6	543	2	US-09-071-739B-2	Sequence 2, Appl
691	25	67.6	341	2	US-10-011-833A-77	Sequence 77, Appl	764	25	67.6	543	2	US-09-181-336-13	Sequence 13, Appl
692	25	67.6	341	2	US-10-006-041A-77	Sequence 77, Appl	765	25	67.6	543	2	US-09-260-038B-2	Sequence 2, Appl
693	25	67.6	341	2	US-10-013-064A-77	Sequence 77, Appl	766	25	67.6	543	2	US-08-487-183A-2	Sequence 2, Appl
694	25	67.6	345	2	US-09-222-817-2	Sequence 2, Appl	767	25	67.6	543	2	US-08-487-183A-4	Sequence 4, Appl
695	25	67.6	345	2	US-09-222-786-2	Sequence 2, Appl	768	25	67.6	543	2	US-08-487-183A-6	Sequence 6, Appl
696	25	67.6	345	2	US-09-543-681A-7459	Sequence 7459, Ap	769	25	67.6	543	2	US-08-487-183A-8	Sequence 8, Appl
697	25	67.6	368	2	US-09-724-519-10	Sequence 10, Appl	770	25	67.6	543	2	US-09-635-923-2	Sequence 2, Appl
698	25	67.6	368	2	US-09-592-037-10	Sequence 10, Appl	771	25	67.6	543	2	US-08-487-716A-2	Sequence 2, Appl
699	25	67.6	368	2	US-09-428-156B-10	Sequence 10, Appl	772	25	67.6	543	2	US-09-322-977-2	Sequence 2, Appl
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701	25	67.6	375	2	US-09-253-991A-26357	Sequence 26357, A	774	25	67.6	543	2	US-09-396-154-35	Sequence 35, Appl
702	25	67.6	382	2	US-09-724-519-4	Sequence 4, Appl	775	25	67.6	543	2	US-09-396-154-36	Sequence 36, Appl
703	25	67.6	382	2	US-09-592-037-4	Sequence 4, Appl	776	25	67.6	543	2	US-09-435-739-10	Sequence 10, Appl
704	25	67.6	382	2	US-09-428-156B-4	Sequence 4, Appl	777	25	67.6	543	2	US-09-930-218-3	Sequence 3, Appl
705	25	67.6	384	2	US-09-552-322-2	Sequence 2, Appl	778	25	67.6	543	2	US-09-704-772A-2	Sequence 2, Appl
706	25	67.6	387	2	US-09-457-302-1	Sequence 1, Appl	779	25	67.6	543	2	US-09-988-113-10	Sequence 10, Appl
707	25	67.6	393	2	US-09-270-767-43352	Sequence 43352, A	780	25	67.6	543	2	US-09-944-602-2	Sequence 2, Appl
708	25	67.6	395	1	US-07-931-943-2	Sequence 2, Appl	781	25	67.6	543	2	US-10-368-044A-1	Sequence 1, Appl
709	25	67.6	395	1	US-07-931-943-5	Sequence 5, Appl	782	25	67.6	543	2	US-10-384-450A-10	Sequence 10, Appl
710	25	67.6	395	1	US-08-624-601-15	Sequence 15, Appl	783	25	67.6	545	2	US-09-899-440-18	Sequence 18, Appl
711	25	67.6	397	2	US-09-949-016-9018	Sequence 9018, Ap	784	25	67.6	556	2	US-10-104-047-3914	Sequence 3914, Ap
712	25	67.6	400	2	US-09-270-767-42514	Sequence 42514, A	785	25	67.6	563	2	US-10-104-047-3392	Sequence 3392, Ap
713	25	67.6	403	2	US-09-880-503-6	Sequence 6, Appl	786	25	67.6	565	1	US-08-892-770-6	Sequence 6, Appl
714	25	67.6	411	1	US-08-087-163-1	Sequence 1, Appl	787	25	67.6	565	2	US-08-906-156A-12	Sequence 12, Appl
715	25	67.6	411	1	US-08-286-748B-18	Sequence 18, Appl	788	25	67.6	571	1	US-08-892-770-5	Sequence 5, Appl
716	25	67.6	411	1	US-08-153-799-18	Sequence 18, Appl	789	25	67.6	574	2	US-09-270-767-46174	Sequence 46174, A
717	25	67.6	411	1	US-08-560-098A-48	Sequence 48, Appl	790	25	67.6	575	2	US-09-724-519-8	Sequence 8, Appl
718	25	67.6	411	2	US-09-181-816-1	Sequence 1, Appl	791	25	67.6	575	2	US-09-592-037-8	Sequence 8, Appl
719	25	67.6	411	2	US-09-403-736-2	Sequence 2, Appl	792	25	67.6	575	2	US-09-428-156B-8	Sequence 8, Appl
720	25	67.6	411	2	US-09-880-503-3	Sequence 3, Appl	793	25	67.6	585	2	US-09-270-767-45446	Sequence 45446, A
721	25	67.6	413	2	US-09-134-001C-2891	Sequence 2891, Ap	794	25	67.6	585	2	US-09-601-777-2	Sequence 2, Appl
722	25	67.6	413	2	US-09-134-001C-3381	Sequence 3381, Ap	795	25	67.6	588	2	US-09-435-739-14	Sequence 14, Appl
723	25	67.6	413	2	US-09-134-001C-4058	Sequence 4058, Ap	796	25	67.6	592	2	US-09-988-113-14	Sequence 14, Appl
724	25	67.6	413	2	US-09-134-001C-4975	Sequence 4975, Ap	797	25	67.6	592	2	US-09-384-450A-14	Sequence 14, Appl
725	25	67.6	418	2	US-09-203-893B-4	Sequence 4, Appl	798	25	67.6	592	1	US-08-900-927-1	Sequence 1, Appl
726	25	67.6	425	2	US-09-270-767-45473	Sequence 45473, A	799	25	67.6	593	1	US-08-900-927-3	Sequence 3, Appl
727	25	67.6	430	1	US-07-942-157A-3	Sequence 3, Appl	800	25	67.6	593	1	US-08-900-927-4	Sequence 4, Appl
728	25	67.6	430	2	US-09-310-363C-6	Sequence 6, Appl	801	25	67.6	593	1	US-08-900-927-1	Sequence 1, Appl
729	25	67.6	430	2	US-10-117-015-6	Sequence 6, Appl	802	25	67.6	593	1	US-09-191-279-3	Sequence 3, Appl
730	25	67.6	430	6	5219569-2	Patent No. 5219569	803	25	67.6	593	1	US-09-191-279-4	Sequence 4, Appl
731	25	67.6	431	2	US-09-101-272G-1	Sequence 1, Appl	804	25	67.6	593	1	US-09-334-476-3	Sequence 3, Appl
732	25	67.6	431	2	US-09-949-002-345	Sequence 345, App	805	25	67.6	593	2	US-09-334-476-4	Sequence 4, Appl
733	25	67.6	431	6	5188829-1	Patent No. 5188829	806	25	67.6	593	2	US-09-334-476-4	Sequence 4, Appl
734	25	67.6	433	2	US-09-487-558B-226	Sequence 226, App	807	25	67.6	593	2	US-09-140-749-8	Sequence 8, Appl
735	25	67.6	434	2	US-09-252-991A-25931	Sequence 25931, A	808	25	67.6	597	2	US-09-248-796A-17030	Sequence 17030, A
736	25	67.6	437	2	US-09-949-002-415	Sequence 415, App	809	25	67.6	610	2	US-09-248-796A-17642	Sequence 17642, A
737	25	67.6	439	2	US-08-311-731A-178	Sequence 178, App	810	25	67.6	614	2	US-09-248-796A-19273	Sequence 19273, A
738	25	67.6	443	2	US-09-602-787A-532	Sequence 532, App	811	25	67.6	618	2	US-09-949-016-11531	Sequence 11531, A
739	25	67.6	450	2	US-09-248-796A-19998	Sequence 19998, A	812	25	67.6	625	2	US-09-328-352-4919	Sequence 4919, Ap
740	25	67.6	452	2	US-09-107-532A-4690	Sequence 4690, Ap	813	25	67.6	630	2	US-08-083-590A-16	Sequence 16, Appl
741	25	67.6	456	2	US-09-583-110-4185	Sequence 1185, Ap	814	25	67.6	654	1	US-08-346-128-35	Sequence 35, Appl
742	25	67.6	457	2	US-09-142-759-1	Sequence 1, Appl	815	25	67.6	654	1	US-08-532-384-16	Sequence 16, Appl
743	25	67.6	470	2	US-09-902-540-16052	Sequence 16052, A	816	25	67.6	654	2	US-08-514-014-4	Sequence 4, Appl
744	25	67.6	484	2	US-09-270-767-42785	Sequence 42785, A	817	25	67.6	661	1	US-08-833-823-4	Sequence 4, Appl
745	25	67.6	485	2	US-09-270-767-57976	Sequence 57976, A	818	25	67.6	661	1	US-09-902-540-11693	Sequence 11693, A
746	25	67.6	491	2	US-09-489-039A-7963	Sequence 7963, Ap	819	25	67.6	671	2	US-09-487-558B-302	Sequence 302, App
747	25	67.6	491	2	US-10-011-125A-2	Sequence 2, Appl	820	25	67.6	676	2	US-09-248-796A-15231	Sequence 15231, A
748	25	67.6	501	2	US-09-134-000C-4693	Sequence 4693, Ap	821	25	67.6	688	2	US-09-371-338-19	Sequence 19, Appl
749	25	67.6	513	2	US-09-724-519-6	Sequence 6, Appl	822	25	67.6	690	2	US-09-252-991A-17865	Sequence 17865, A
750	25	67.6	513	2	US-09-592-037-6	Sequence 6, Appl	823	25	67.6	703	2	US-08-311-731A-152	Sequence 152, App
751	25	67.6	513	2	US-09-428-156B-6	Sequence 6, Appl	824	25	67.6	706	2	US-09-270-767-45434	Sequence 45434, A
752	25	67.6	527	2	US-09-930-218-16	Sequence 16, Appl	825	25	67.6	706	2	US-09-538-052-582	Sequence 582, App
753	25	67.6	530	2	US-09-222-817-12	Sequence 12, Appl	826	25	67.6	708	2	US-09-487-558B-388	Sequence 388, App
754	25	67.6	530	2	US-09-222-817-14	Sequence 14, Appl	827	25	67.6	718	2	US-08-791-115B-5	Sequence 5, Appl
755	25	67.6	530	2	US-09-222-786-12	Sequence 12, Appl	828	25	67.6	742	2	US-09-248-796A-18005	Sequence 18005, A
756	25	67.6	530	2	US-09-222-786-14	Sequence 14, Appl	829	25	67.6	750	2	US-09-949-016-8793	Sequence 8793, Ap
757	25	67.6	530	2	US-09-252-586-2	Sequence 2, Appl	830	25	67.6	784	2		

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833	25	67.6	791	2	US-09-540-236-2153	Sequence 2153, Ap	906	24	64.9	80	2	US-09-270-767-60512	Sequence 60512, A
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835	25	67.6	805	2	US-09-949-016-9280	Sequence 9280, Ap	908	24	64.9	84	2	US-09-248-796A-25109	Sequence 25109, A
836	25	67.6	824	2	US-09-248-796A-14797	Sequence 14797, A	909	24	64.9	89	2	US-09-270-767-60514	Sequence 60514, A
837	25	67.6	839	2	US-09-538-092-274	Sequence 274, Ap	910	24	64.9	90	2	US-09-270-767-35482	Sequence 35482, A
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## ALIGNMENTS

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US-09-225-322B-10  
; Sequence 10, Application US/09225322B  
; Patent No. 6437098  
; GENERAL INFORMATION:  
; APPLICANT: SHITARA, KENYA  
; APPLICANT: HANAI, NOBUO  
; APPLICANT: HASEGAWA, MAMORU  
; APPLICANT: MIYAJI, HIROMASA  
; APPLICANT: KIWANA, YOSHIHISA  
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY  
; FILE REFERENCE: 249-101  
; CURRENT APPLICATION NUMBER: US/09/225,322B  
; PRIOR FILING DATE: 1999-01-05  
; PRIOR FILING DATE: 1995-05-31  
; PRIOR APPLICATION NUMBER: US 08/408,133  
; PRIOR FILING DATE: 1995-03-21  
; PRIOR APPLICATION NUMBER: US 08/292,178  
; PRIOR FILING DATE: 1994-08-17  
; PRIOR APPLICATION NUMBER: US07/947,674  
; PRIOR FILING DATE: 1992-09-17  
; PRIOR APPLICATION NUMBER: JP 3-238375  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 10  
; LENGTH: 128  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: cDNA KM-641  
US-09-225-322B-10

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Best Local Similarity 100.0%; Pred. No. 7.4;  
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DB 70 YSSNLHS 76

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US-09-225-322B-19  
; Sequence 19, Application US/09225322B  
; Patent No. 6437098  
; GENERAL INFORMATION:  
; APPLICANT: SHITARA, KENYA  
; APPLICANT: HANAI, NOBUO  
; APPLICANT: HASEGAWA, MAMORU  
; APPLICANT: MIYAJI, HIROMASA  
; APPLICANT: KIWANA, YOSHIHISA  
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY  
; FILE REFERENCE: 249-101  
; CURRENT APPLICATION NUMBER: US/09/225,322B  
; PRIOR FILING DATE: 1999-01-05  
; PRIOR APPLICATION NUMBER: US 08/454,680  
; PRIOR FILING DATE: 1995-05-31  
; PRIOR APPLICATION NUMBER: US 08/408,133  
; PRIOR FILING DATE: 1995-03-21  
; PRIOR APPLICATION NUMBER: US 08/292,178  
; PRIOR FILING DATE: 1994-08-17  
; PRIOR APPLICATION NUMBER: US07/947,674  
; PRIOR FILING DATE: 1992-09-17  
; PRIOR APPLICATION NUMBER: JP 3-238375  
; PRIOR FILING DATE: 1991-09-18  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 19  
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; TYPE: PRT  
; ORGANISM: Artificial Sequence  
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US-09-225-322B-19

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Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; Patent No. 6495666  
; GENERAL INFORMATION:  
; APPLICANT: SHITARA, KENYA  
; APPLICANT: HANAI, NOBUO  
; APPLICANT: HASEGAWA, MAMORU  
; APPLICANT: MIYAJI, HIROMASA  
; APPLICANT: KIWANA, YOSHIHISA  
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY  
; FILE REFERENCE: 249-101  
; CURRENT APPLICATION NUMBER: US/09/764,304  
; CURRENT FILING DATE: 2001-01-19  
; PRIOR FILING DATE: 1999-01-05  
; PRIOR APPLICATION NUMBER: US 08/454,680  
; PRIOR FILING DATE: 1995-05-31  
; PRIOR APPLICATION NUMBER: US 08/408,133  
; PRIOR FILING DATE: 1995-03-21  
; PRIOR APPLICATION NUMBER: US 08/292,178  
; PRIOR FILING DATE: 1994-08-17  
; PRIOR APPLICATION NUMBER: US07/947,674  
; PRIOR FILING DATE: 1992-09-17  
; PRIOR APPLICATION NUMBER: JP 3-238375  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: PatentIn Ver. 2.0  
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; ORGANISM: Artificial Sequence
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; OTHER INFORMATION: cDNA KM-641
US-09-764-304-10

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QY      1 YSNNLHS 7
Db      70 YSNNLHS 76

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US-09-764-304-19
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; Patent No. 6495666
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUMANA, YOSHIOHISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/09/764,304
; CURRENT FILING DATE: 2001-01-19
; EARLIER APPLICATION NUMBER: 09/225,322
; EARLIER FILING DATE: 1999-01-05
; EARLIER APPLICATION NUMBER: US 08/454,680
; EARLIER FILING DATE: 1995-05-31
; EARLIER APPLICATION NUMBER: US 08/408,133
; EARLIER FILING DATE: 1995-03-21
; EARLIER APPLICATION NUMBER: US 08/292,178
; EARLIER FILING DATE: 1994-08-17
; EARLIER APPLICATION NUMBER: US07/947,674
; EARLIER FILING DATE: 1992-09-17
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; SOFTWARE: PatentIn Ver. 2.0
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; OTHER INFORMATION: light chain
; OTHER INFORMATION: variable region
US-09-764-304-19

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Db      70 YSNNLHS 76

RESULT 5
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; Sequence 18, Application US/08403853
; Patent No. 5844094
; GENERAL INFORMATION:
; APPLICANT: HUDSON, Peter J.
; APPLICANT: LAH, Maria
; APPLICANT: KORRT, Alex A.
; APPLICANT: IRVING, Robert A.
; APPLICANT: ATWELL, John L.
; APPLICANT: MALBY, Robyn L.
; APPLICANT: POWER, Barbara B.
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; APPLICANT: COLMAN, Peter M.
; TITLE OF INVENTION: TARGET BINDING POLYPEPTIDE
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/403,853
; FILING DATE: 30-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/AU93/00491
; FILING DATE: 24-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU PL 4973
; FILING DATE: 25-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 16786/189/CHAC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 273 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-403-853-18

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RESULT 6
US-09-570-921-100
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; Patent No. 6455265
; GENERAL INFORMATION:
; APPLICANT: SERRES, PIERRE-FRANCOIS
; TITLE OF INVENTION: METHOD FOR OBTAINING VACCINES FOR PREVENTING THE
; FILE REFERENCE: 106213
; CURRENT APPLICATION NUMBER: US/09/570,921
; CURRENT FILING DATE: 2000-05-15
; PRIOR APPLICATION NUMBER: PCT/FR98/02447
; PRIOR FILING DATE: 1998-11-17
; PRIOR APPLICATION NUMBER: FR/97/14387
; PRIOR FILING DATE: 1997-11-17
; NUMBER OF SEQ ID NOS: 144
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US-09-570-921-100
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Db

RESULT 7  
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; Patent No. 5554743  
; GENERAL INFORMATION:  
; APPLICANT: Bennett, Alan B.  
; APPLICANT: Fischer, Robert L.  
; APPLICANT: Lashbrook, Coralie  
; APPLICANT: Giovanni, James  
; TITLE OF INVENTION: Endo-1,4-beta-Glucanase Genes and Their  
; TITLE OF INVENTION: Use in Plants  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew  
; STREET: One Market Plaza, Steuart Street Tower  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94105-1492  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
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; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/434,702  
; FILING DATE: 04-MAY-1995  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/271,883  
; FILING DATE: 07-JUL-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/687,466  
; FILING DATE: 18-APR-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/511,417  
; FILING DATE: 20-APR-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Bastian, Kevin L.  
; REGISTRATION NUMBER: 34,774  
; REFERENCE/DOCKET NUMBER: 02307E-30430US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 543-9600  
; TELEFAX: (415) 543-5043  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 489 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-434-702-4

Query Match 86.5%; Score 32; DB 1; Length 489;  
Best Local Similarity 85.7%; Pred. No. 2.5e+02;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLHS 7  
216 YSSSLHS 222

Db

RESULT 8  
US-09-970-367-2  
; Sequence 2, Application US/09970367

; Patent No. 6906241  
; GENERAL INFORMATION:  
; APPLICANT: Davis, Eric L.  
; APPLICANT: Goellner, Melissa  
; TITLE OF INVENTION: ENDOGLUCANASE GENE PROMOTER UPREGULATED BY NEMATODES  
; FILE REFERENCE: 5051.587  
; CURRENT APPLICATION NUMBER: US/09/970,367  
; CURRENT FILING DATE: 2001-10-02  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 2  
; LENGTH: 500  
; TYPE: PRT  
; ORGANISM: Nicotiana tabacum  
US-09-970-367-2

Query Match 86.5%; Score 32; DB 2; Length 500;  
Best Local Similarity 85.7%; Pred. No. 2.6e+02;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLHS 7  
228 YSSSLHS 234

Db

RESULT 9  
US-09-495-406-13  
; Sequence 13, Application US/09495406  
; Patent No. 6503744  
; GENERAL INFORMATION:  
; APPLICANT: Gilbert, Michel  
; APPLICANT: Wakarchuk, Warren W.  
; APPLICANT: National Research Council of Canada  
; TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of  
; TITLE OF INVENTION: Gangliosides and Ganglioside Mimics  
; FILE REFERENCE: 019633-000110US  
; CURRENT APPLICATION NUMBER: US/09/495,406  
; CURRENT FILING DATE: 2000-01-31  
; PRIOR APPLICATION NUMBER: US 60/118,213  
; PRIOR FILING DATE: 1999-02-01  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 13  
; LENGTH: 347  
; TYPE: PRT  
; ORGANISM: Campylobacter jejuni  
US-09-495-406-13

Query Match 83.8%; Score 31; DB 2; Length 347;  
Best Local Similarity 71.4%; Pred. No. 2.8e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLHS 7  
268 FSSNIHS 274

Db

RESULT 10  
US-09-816-028A-17  
; Sequence 17, Application US/09816028A  
; Patent No. 6699705  
; GENERAL INFORMATION:  
; APPLICANT: Gilbert, Michel  
; APPLICANT: Wakarchuk, Warren W.  
; APPLICANT: National Research Council of Canada  
; TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of  
; TITLE OF INVENTION: Gangliosides and Ganglioside Mimics  
; FILE REFERENCE: 019633-000110US  
; CURRENT APPLICATION NUMBER: US/09/816,028A  
; CURRENT FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: US 60/118,213  
; PRIOR FILING DATE: 1999-02-01  
; PRIOR APPLICATION NUMBER: US 09/495,406

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; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 347
; TYPE: PRT
; ORGANISM: Campylobacter jejuni
; FEATURE:
; OTHER INFORMATION: beta-1,4 N-acetyl-galactosaminyl (GalNAc)
; OTHER INFORMATION: transferase from C. jejuni strain OH4384 (ORF 5a
; OTHER INFORMATION: of lipooligosaccharide (LOS) biosynthesis locus)
US-09-816-028A-17

Query Match      83.8%; Score 31; DB 2; Length 347;
Best Local Similarity 71.4%; Pred. NO. 2.8e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 YSSNLHS 7
       :||||:|
Db      268 FSSNIHS 274

RESULT 11
US-10-303-162-17
; Sequence 17, Application US/10303162
; Patent No. 6723545
; GENERAL INFORMATION:
; APPLICANT: Wakarchuk, Michel
; APPLICANT: National Research Council of Canada
; TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of
; TITLE OF INVENTION: Gangliosides and Ganglioside Mimics
; FILE REFERENCE: 019633-000111US
; CURRENT APPLICATION NUMBER: US/10/303,162
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US/09/816,028
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/118,213
; PRIOR FILING DATE: 1999-02-01
; PRIOR APPLICATION NUMBER: US 09/495,406
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 347
; TYPE: PRT
; ORGANISM: Campylobacter jejuni
; FEATURE:
; OTHER INFORMATION: beta-1,4 N-acetyl-galactosaminyl (GalNAc)
; OTHER INFORMATION: transferase from C. jejuni strain OH4384 (ORF 5a
; OTHER INFORMATION: of lipooligosaccharide (LOS) biosynthesis locus)
US-10-303-162-17

Query Match      83.8%; Score 31; DB 2; Length 347;
Best Local Similarity 71.4%; Pred. NO. 2.8e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 YSSNLHS 7
       :||||:|
Db      268 FSSNIHS 274

RESULT 12
US-10-303-134-17
; Sequence 17, Application US/10303134
; Patent No. 6825019
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Michel
; APPLICANT: National Research Council of Canada
; TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of
; TITLE OF INVENTION: Gangliosides and Ganglioside Mimics
; FILE REFERENCE: 019633-000111US

; CURRENT APPLICATION NUMBER: US/10/303,118
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US/09/816,028
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/118,213
; PRIOR FILING DATE: 1999-02-01
; PRIOR APPLICATION NUMBER: US 09/495,406
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 347
; TYPE: PRT
; ORGANISM: Campylobacter jejuni
; FEATURE:
; OTHER INFORMATION: beta-1,4 N-acetyl-galactosaminyl (GalNAc)
; OTHER INFORMATION: transferase from C. jejuni strain OH4384 (ORF 5a
; OTHER INFORMATION: of lipooligosaccharide (LOS) biosynthesis locus)
US-10-303-118-17

Query Match      83.8%; Score 31; DB 2; Length 347;
Best Local Similarity 71.4%; Pred. NO. 2.8e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 YSSNLHS 7
       :||||:|
Db      268 FSSNIHS 274

RESULT 13
US-10-303-118-17
; Sequence 17, Application US/10303118
; Patent No. 6905867
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Michel
; APPLICANT: Wakarchuk, Warren W.
; APPLICANT: National Research Council of Canada
; TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of
; TITLE OF INVENTION: Gangliosides and Ganglioside Mimics
; FILE REFERENCE: 019633-000111US
; CURRENT APPLICATION NUMBER: US/10/303,118
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US/09/816,028
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/118,213
; PRIOR FILING DATE: 1999-02-01
; PRIOR APPLICATION NUMBER: US 09/495,406
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 347
; TYPE: PRT
; ORGANISM: Campylobacter jejuni
; FEATURE:
; OTHER INFORMATION: beta-1,4 N-acetyl-galactosaminyl (GalNAc)
; OTHER INFORMATION: transferase from C. jejuni strain OH4384 (ORF 5a
; OTHER INFORMATION: of lipooligosaccharide (LOS) biosynthesis locus)
US-10-303-118-17

Query Match      83.8%; Score 31; DB 2; Length 347;
Best Local Similarity 71.4%; Pred. NO. 2.8e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 YSSNLHS 7
       :||||:|
Db      268 FSSNIHS 274

RESULT 14
US-10-303-128-17
; Sequence 17, Application US/10303128
; Patent No. 6911337
```

```
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Michel
; APPLICANT: Wakarchuk, Warren W.
; APPLICANT: National Research Council of Canada
; TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of
; TITLE OF INVENTION: Gangliosides and Ganglioside Mimics
; FILE REFERENCE: 019633-000111US
; CURRENT APPLICATION NUMBER: US/10/303,128
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US/09/816,028
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/118,213
; PRIOR FILING DATE: 1999-02-01
; PRIOR APPLICATION NUMBER: US 09/495,406
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 347
; TYPE: PRT
; ORGANISM: Campylobacter jejuni
; FEATURE:
; OTHER INFORMATION: beta-1,4 N-acetylgalactosaminyl (GalNAc)
; OTHER INFORMATION: transferase from C. jejuni strain OH4384 (ORF 5a
; OTHER INFORMATION: of lipooligosaccharide (LOS) biosynthesis locus)
US-10-303-128-17

Query Match      83.8%; Score 31; DB 2; Length 347;
Best Local Similarity 71.4%; Pred. No. 2.8e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 YSSNLHS 7
       :|||:|
Db      268 FSSNIHS 274

RESULT 15
US-09-248-796A-22868
; Sequence 22868, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 22868
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-22868

Query Match      81.1%; Score 30; DB 2; Length 67;
Best Local Similarity 83.3%; Pred. No. 81;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 YSSNLH 6
       :|||:|
Db      44 YSNLH 49

RESULT 16
US-09-270-767-41649
; Sequence 41649, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
```

```
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 41649
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-41649

Query Match      81.1%; Score 30; DB 2; Length 172;
Best Local Similarity 83.3%; Pred. No. 2.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 YSSNLH 6
       :|||:|
Db      157 YSNLH 162

RESULT 17
US-09-270-767-45029
; Sequence 45029, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 45029
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-45029

Query Match      81.1%; Score 30; DB 2; Length 238;
Best Local Similarity 85.7%; Pred. No. 2.9e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 YSSNLHS 7
       :|||:|
Db      232 YSSNNHS 238

RESULT 18
US-09-252-991A-28155
; Sequence 28155, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 28155
; LENGTH: 410
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-28155

Query Match      81.1%; Score 30; DB 2; Length 410;
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```
Best Local Similarity 83.3%; Pred. No. 5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSNLH 6
Db 260 YSNLH 265

RESULT 19
US-09-538-092-1356
; Sequence 1356, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Giot, Loic
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CuraPatSeqFormatter Version 0.9
; SEQ ID NO 1356
; LENGTH: 458
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Polypeptide Accession Number Q16600
US-09-538-092-1356

Query Match 81.1%; Score 30; DB 2; Length 458;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SSNLH 7
Db 443 SSNLH 448

RESULT 20
US-09-198-452A-579
; Sequence 579, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griffais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments thereof and uses thereof, in particular for the diagnosis, prevention and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 579
; LENGTH: 609
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
; FEATURE:
; NAME/KEY: SITE
; LOCATION: 1...609
; OTHER INFORMATION: Xaa=unknown or other
US-09-198-452A-579

Query Match 81.1%; Score 30; DB 2; Length 609;
Best Local Similarity 100.0%; Pred. No. 7.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SSNLH 7
Db 443 SSNLH 448

Best Local Similarity 83.3%; Pred. No. 5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSNLH 6
Db 260 YSNLH 265

RESULT 21
US-09-328-352-5898
; Sequence 5898, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 5898
; LENGTH: 741
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-5898

Query Match 81.1%; Score 30; DB 2; Length 741;
Best Local Similarity 83.3%; Pred. No. 9.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSNLH 6
Db 512 YSNLH 517

RESULT 22
US-08-630-915A-30
; Sequence 30, Application US/08630915A
; Patent No. 6309820
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: HOFFMAN, No. 6309820h
; APPLICANT: KAY, Brian K.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: MCCONNELL, Stephen J.
; TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND USING SAME
; TITLE OF INVENTION: USING SAME
; NUMBER OF SEQUENCES: 227
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/08/630,915A
; FILING DATE: 03-APR-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-174
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 788 amino acids
; TYPE: amino acid
; STRANDEDNESS:
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Db 388 YSSNFHA 394

```
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-652-558-2

Query Match          78.4%; Score 29; DB 1; Length 107;
Best Local Similarity 71.4%; Pred. No. 2e+02; 0; Indels 0; Gaps 0;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 YSSNLHS 7
       |:|:|
Db      50 YTSSLHS 56

RESULT 26
US-08-652-558-35
; Sequence 35, Application US/08652558
; Patent No. 5861155
; GENERAL INFORMATION:
; APPLICANT: LIN, AUGUSTINE YEE-THARN
; TITLE OF INVENTION: HUMANIZED ANTIBODIES AND USES
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BANNER & WITCOFF
; STREET: 75 STATE STREET, 23RD FLOOR
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/652,558
; FILING DATE: JUNE 6, 1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/IB94/00387
; FILING DATE: NOVEMBER 21, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: YANKWICH, LEON R.
; REGISTRATION NUMBER: 30,237
; REFERENCE/DOCKET NUMBER: 95,497-L
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-345-9100
; TELEFAX: 617-345-9111
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-652-558-35

Query Match          78.4%; Score 29; DB 1; Length 107;
Best Local Similarity 71.4%; Pred. No. 2e+02; 0; Indels 0; Gaps 0;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 YSSNLHS 7
       |:|:|
Db      50 YTSSLHS 56

RESULT 27
US-09-254-189-1
; Sequence 1, Application US/09254189
; Patent No. 6150792
; GENERAL INFORMATION:
```

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; APPLICANT: Lundquist, Tomas
; TITLE OF INVENTION: Sequence Listing
; Patent No. 6150792
; FILE REFERENCE: 3526/00000
; CURRENT APPLICATION NUMBER: US/09/254,189
; CURRENT FILING DATE: 1999-03-02
; EARLIER APPLICATION NUMBER: 00/000,000
; EARLIER FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:humanized
US-09-254-189-1

Query Match          78.4%; Score 29; DB 2; Length 107;
Best Local Similarity 71.4%; Pred. No. 2e+02; 0; Indels 0; Gaps 0;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 YSSNLHS 7
       |:|:|
Db      50 YTSSLHS 56

RESULT 28
US-09-270-767-45934
; Sequence 45934, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 45934
; LENGTH: 219
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-45934

Query Match          78.4%; Score 29; DB 2; Length 219;
Best Local Similarity 57.1%; Pred. No. 4.1e+02; 0; Indels 0; Gaps 0;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 YSSNLHS 7
       |:|:|
Db      146 YATNIHS 152

RESULT 29
US-09-252-991A-21191
; Sequence 21191, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
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; SEQ ID NO 21191
; LENGTH: 329
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-21191

Query Match      78.4%; Score 29; DB 2; Length 329;
Best Local Similarity 71.4%; Pred. No. 6.2e+02;
Matches 5; Conservative 1; Mismatches 0; Gaps 0;

QY 1 YSSNLHS 7
   |||||
Db 188 YSRNLHT 194

RESULT 30
US-09-165-522-14
; Sequence 14, Application US/09165522
; Patent No. 6943000
; GENERAL INFORMATION:
; APPLICANT: Davis, Roger J.
; Flavell, Richard A.
; Rakic, Pasco
; Whitmarsh, Alan
; Kuan, Chia-Yi
; Yang, Di
; TITLE OF INVENTION: JNK3 MODULATORS AND METHODS OF USE
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/165,522
; FILING DATE: 02-Oct-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/060,995
; FILING DATE: 03-Oct-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Faese, J. Peter
; REGISTRATION NUMBER: 32,983
; REFERENCE/DOCKET NUMBER: 10363/005001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 334 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-165-522-14

Query Match      78.4%; Score 29; DB 2; Length 334;
Best Local Similarity 71.4%; Pred. No. 6.3e+02;
Matches 5; Conservative 2; Mismatches 0; Gaps 0;

QY 1 YSSNLHS 7
   |||||
Db 159 YSASLHS 165
```

```
RESULT 31
US-09-710-279-1386
; Sequence 1386, Application US/09710279
; Patent No. 6703492
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PUS480US
; CURRENT APPLICATION NUMBER: US/09/710,279
; CURRENT FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1386
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-09-710-279-1386

Query Match      78.4%; Score 29; DB 2; Length 496;
Best Local Similarity 83.3%; Pred. No. 9.4e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSNLH 6
   |||||
Db 274 YDSNLH 279

RESULT 32
US-09-134-001C-4411
; Sequence 4411, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 4411
; LENGTH: 497
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-4411

Query Match      78.4%; Score 29; DB 2; Length 497;
Best Local Similarity 83.3%; Pred. No. 9.5e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSNLH 6
   |||||
Db 275 YDSNLH 280

RESULT 33
US-08-522-269B-3
; Sequence 3, Application US/08522269B
; Patent No. 5919690
; GENERAL INFORMATION:
; APPLICANT: Knap, Inge Helmer
; APPLICANT: Hjort, Carsten M.
; APPLICANT: Halkier, Torben
; APPLICANT: Kofod, Lene Venke
; TITLE OF INVENTION: An Alpha-Galactosidase Enzyme
```

```
;
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5919690o No. 5919690disk of No. 5919690th America, Inc.
; STREET: 405 Lexington Avenue, Suite 6400
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/522,269B
; FILING DATE: 12-SEP-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Gregg, Valeta A.
; REGISTRATION NUMBER: 37,125
; REFERENCE/DOCKET NUMBER: 3935.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 867 0123
; TELEFAX: 212 867 0298
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 677 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-522-269B-3

Query Match 78.4%; Score 29; DB 1; Length 677;
Best Local Similarity 71.4%; Pred. No. 1.3e+03;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLHS 7
DB 212 YSSHLHN 218

RESULT 34
US-09-294-923-3
; Sequence 3, Application US/09294923
; Patent No. 6197566
; GENERAL INFORMATION:
; APPLICANT: Knapp, Inge Helmer
; APPLICANT: Hjort, Carsten M.
; APPLICANT: Halkier, Torben
; APPLICANT: Kofod, Lene Venke
; TITLE OF INVENTION: An Alpha-Galactosidase Enzyme
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6197566o No. 6197566disk of No. 6197566th America, Inc.
; STREET: 405 Lexington Avenue, Suite 6400
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/294,923
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/522,269
; FILING DATE: 12-SEP-1995
; ATTORNEY/AGENT INFORMATION:
```

```
;
; NAME: Gregg, Valeta A.
; REGISTRATION NUMBER: 37,125
; REFERENCE/DOCKET NUMBER: 3935.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 867 0123
; TELEFAX: 212 867 0298
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 677 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-294-923-3

Query Match 78.4%; Score 29; DB 2; Length 677;
Best Local Similarity 71.4%; Pred. No. 1.3e+03;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLHS 7
DB 212 YSSHLHN 218

RESULT 35
US-09-291-922-2
; Sequence 2, Application US/09291922
; Patent No. 6383776
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Hitz, Bill
; APPLICANT: Kinney, Tony
; APPLICANT: Tingey, Scott
; TITLE OF INVENTION: Plant Sugar Transport Proteins
; FILE REFERENCE: BB-1163
; CURRENT APPLICATION NUMBER: US/09/291,922
; CURRENT FILING DATE: 1999-04-14
; EARLIER APPLICATION NUMBER: 60/083,044
; EARLIER FILING DATE: April 24, 1998
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 2
; LENGTH: 747
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (129)
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (133)..(134)
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (144)
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (178)
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (207)
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (218)
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (220)
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (236)
; US-09-291-922-2

Query Match 78.4%; Score 29; DB 2; Length 747;
Best Local Similarity 71.4%; Pred. No. 1.4e+03;
```

Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YSSNLHS 7

Db 368 YEDNLHS 374

RESULT 36

US-08-137-117D-118  
; Sequence 118, Application US/08137117D  
; Patent No. 5795965  
; GENERAL INFORMATION:  
; APPLICANT: TSUCHIYA, Masayuki  
; APPLICANT: SATO, Koh  
; APPLICANT: BENDIG, Mary  
; APPLICANT: JONES, Steven  
; APPLICANT: SALDANHA, Jose  
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN  
; TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR  
; NUMBER OF SEQUENCES: 158  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 3000 K Street, N.W., Suite 500  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20007-5109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/137,117D  
; FILING DATE: 20-DEC-1993  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/JP92/00544  
; FILING DATE: 24-APR-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 4-32084  
; FILING DATE: 19-FEB-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 3-95476  
; FILING DATE: 25-APR-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: WEGNER, Harold C.  
; REGISTRATION NUMBER: 25,258  
; REFERENCE/DOCKET NUMBER: 53466/126/AAOK  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)672-5300  
; TELEFAX: (202)672-5399  
; TELEX: 904136

INFORMATION FOR SEQ ID NO: 118:

SEQUENCE CHARACTERISTICS:

LENGTH: 7 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-137-117D-118

Query Match 75.7%; Score 28; DB 1; Length 7;  
Best Local Similarity 71.4%; Pred. No. 4.6e+05;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSNLHS 7

Db 1 YTSRLHS 7

RESULT 37

US-08-480-434-78  
; Sequence 78, Application US/08480434

; Patent No. 5811248  
; GENERAL INFORMATION:  
; APPLICANT: Charles C. Diclow, et al.  
; TITLE OF INVENTION: ATHEROSCLEROTIC PLAQUE SPECIFIC ANTIGENS,  
; TITLE OF INVENTION: ANTIBODIES THERETO, AND USES THEREOF  
; NUMBER OF SEQUENCES: 88  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.24  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/480,434  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Albert P. Halluin  
; REGISTRATION NUMBER: 25,227  
; REFERENCE/DOCKET NUMBER: 7606-053  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 854-3660  
; TELEFAX: (415) 854-3694  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 78:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: DNA (genomic)  
; MOLECULE TYPE: N  
; HYPOTHETICAL: N  
; ANTI-SENSE: N  
; US-08-480-434-78

Query Match 75.7%; Score 28; DB 1; Length 7;  
Best Local Similarity 71.4%; Pred. No. 4.6e+05;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSNLHS 7

Db 1 YASRLHS 7

RESULT 38

US-08-436-717-118  
; Sequence 118, Application US/08436717  
; Patent No. 5817790  
; GENERAL INFORMATION:  
; APPLICANT: TSUCHIYA, Masayuki  
; APPLICANT: SATO, Koh  
; APPLICANT: BENDIG, Mary  
; APPLICANT: JONES, Steven  
; APPLICANT: SALDANHA, Jose  
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN  
; TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR  
; NUMBER OF SEQUENCES: 158  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 3000 K Street, N.W., Suite 500  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20007-5109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/436,717  
FILING DATE:  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/137,117  
FILING DATE: 20-DEC-1993  
APPLICATION NUMBER: WO PCT/JP92/00544  
FILING DATE: 24-APR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 4-32084  
FILING DATE: 19-FEB-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 3-95476  
FILING DATE: 25-APR-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: WEGNER, Harold C.  
REGISTRATION NUMBER: 25,258  
REFERENCE/DOCKET NUMBER: 53466/126/AARK  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 118:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-436-717-118

Query Match 75.7%; Score 28; DB 1; Length 7;  
Best Local Similarity 71.4%; Pred. No. 4.6e+05;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSNLHS 7  
|:|:|:|  
DB 1 YTSRLHS 7

RESULT 39  
US-08-053-451B-78  
Sequence 78, Application US/08053451B  
Patent No. 595584  
GENERAL INFORMATION:  
APPLICANT: Chen, Francis W.  
APPLICANT: Ditlow, Charles C.  
APPLICANT: Calenoff, Emanuel  
TITLE OF INVENTION: ATHEROSCLEROTIC PLAQUE SPECIFIC  
TITLE OF INVENTION: ANTIGENS, ANTIBODIES THERETO, AND USES THEREOF  
NUMBER OF SEQUENCES: 176  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/053,451B  
FILING DATE: 26-APR-1993  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Halluin, Albert P.  
REGISTRATION NUMBER: 25,227  
REFERENCE/DOCKET NUMBER: 7606-033-999

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-854-3660  
TELEFAX: 415-854-3694  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 78:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: DNA  
HYPOTHETICAL: N  
ANTI-SENSE: N  
US-08-053-451B-78

Query Match 75.7%; Score 28; DB 1; Length 7;  
Best Local Similarity 71.4%; Pred. No. 4.6e+05;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSNLHS 7  
|:|:|:|  
DB 1 YASRLHS 7

RESULT 40  
US-08-649-100-13  
Sequence 13, Application US/08649100  
Patent No. 6114507  
GENERAL INFORMATION:  
APPLICANT: SHIRAKAWA, KAMON  
APPLICANT: MATSUE, TOMOKAZU  
APPLICANT: NAGATA, SHIGEKAZU  
APPLICANT: CO, MAN SUNG  
APPLICANT: VASQUEZ, MAXIMILIANO  
TITLE OF INVENTION: ANTI-FAS LIGAND ANTIBODY AND ASSAY  
TITLE OF INVENTION: METHOD USING THE ANTI-FAS LIGAND ANTIBODY  
NUMBER OF SEQUENCES: 41  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH  
STREET: PO BOX 747  
CITY: FALLS CHURCH  
STATE: VA  
COUNTRY: USA  
ZIP: 22040-0747  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/649,100  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: MURPHY JR, GERALD M  
REGISTRATION NUMBER: 28,977  
REFERENCE/DOCKET NUMBER: 1110-160  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 205-8000  
TELEFAX: (703) 205-8050  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-649-100-13

Query Match 75.7%; Score 28; DB 2; Length 7;  
Best Local Similarity 71.4%; Pred. No. 4.6e+05;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSNLS 7  
|:| |||  
Db 1 YTSRLHS 7

RESULT 41  
US-08-649-100-29  
; Sequence 29, Application US/08649100  
; Patent No. 6114507  
; GENERAL INFORMATION:  
; APPLICANT: SHIRAKAWA, KAMON  
; APPLICANT: MATSUE, TOMOKAZU  
; APPLICANT: NAGATA, SHIGEKAZU  
; APPLICANT: CO, MAN SUNG  
; APPLICANT: VASQUEZ, MAXIMILIANO  
; TITLE OF INVENTION: ANTI-FAS LIGAND ANTIBODY AND ASSAY  
; TITLE OF INVENTION: METHOD USING THE ANTI-FAS LIGAND ANTIBODY  
; NUMBER OF SEQUENCES: 41  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH  
; STREET: PO BOX 747  
; CITY: FALLS CHURCH  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22040-0747  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/649,100  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MURPHY JR, GERALD M  
; REGISTRATION NUMBER: 28,977  
; REFERENCE/DOCKET NUMBER: 1110-160  
; TELEPHONE: (703) 205-8000  
; TELEFAX: (703) 205-8050  
; INFORMATION FOR SEQ ID NO: 29:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-649-100-29

Query Match 75.7%; Score 28; DB 2; Length 7;  
Best Local Similarity 71.4%; Pred. No. 4.6e+05;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSNLS 7  
|:| |||  
Db 1 YTSRLHS 7

RESULT 42  
US-09-563-222C-39  
; Sequence 39, Application US/09563222C  
; Patent No. 6696620  
; GENERAL INFORMATION:  
; APPLICANT: EPICYTE PHARMACEUTICALS, INC.  
; APPLICANT: HIATT, ANDREW C.  
; APPLICANT: HEIN, NICH B.  
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN PLANT CELLS  
; FILE REFERENCE: 068904-0501  
; CURRENT APPLICATION NUMBER: US/09/563,222C  
; CURRENT FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: PCT/US01/14349  
; PRIOR FILING DATE: 2001-05-02

; PRIOR APPLICATION NUMBER: 09/563,222  
; PRIOR FILING DATE: 2000-05-02  
; NUMBER OF SEQ ID NOS: 182  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 39  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-563-222C-39

Query Match 75.7%; Score 28; DB 2; Length 7;  
Best Local Similarity 71.4%; Pred. No. 4.6e+05;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSNLS 7  
|:| |||  
Db 1 YASRLHS 7

RESULT 43  
US-08-525-539A-14  
; Sequence 14, Application US/08525539A  
; Patent No. 6309636  
; GENERAL INFORMATION:  
; APPLICANT: DO COUTO, FERNANDO J.R.  
; APPLICANT: CERIANI, ROBERTO L.  
; APPLICANT: PETERSON, JERRY A.  
; TITLE OF INVENTION: RECOMBINANT PEPTIDES DERIVED FROM THE  
; TITLE OF INVENTION: MG3 ANTI-BA46 ANTIBODY, METHODS OF USE THEREOF, AND  
; TITLE OF INVENTION: METHODS OF HUMANIZING ANTIBODY PEPTIDES  
; NUMBER OF SEQUENCES: 81  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 755 Page Mill Road  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA: US/08/525,539A  
; APPLICATION NUMBER: US/08/525,539A  
; FILING DATE: 14-SEP-1995  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: DYLAN, TYLER  
; REGISTRATION NUMBER: 37,612  
; REFERENCE/DOCKET NUMBER: 27633-20001.21  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 813-5600  
; TELEFAX: (415) 494-0792  
; TELEX: 706141  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 32 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-525-539A-14

Query Match 75.7%; Score 28; DB 2; Length 32;  
Best Local Similarity 71.4%; Pred. No. 91;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSNLS 7  
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Db 1 YTSRLHS 7

RESULT 44



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US-09-134-000C-5271
; Sequence 5271, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5271
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-5271

Query Match      75.7%; Score 28; DB 2; Length 98;
Best Local Similarity 57.1%; Pred. No. 2.8e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 YSSNLHS 7
DB      54 YANLHA 60

RESULT 45
US-09-248-796A-19786
; Sequence 19786, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 19786
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-19786

Query Match      75.7%; Score 28; DB 2; Length 99;
Best Local Similarity 83.3%; Pred. No. 2.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 YSSNLH 6
DB      23 YSSSLH 28

RESULT 46
US-09-199-149-10
; Sequence 10, Application US/09199149
; Patent No. 6160099
; GENERAL INFORMATION:
; APPLICANT: Jonak, Zdenka L.
; APPLICANT: Taylor, Alexander H.
; APPLICANT: Trulli Jr., Stephen H.
; TITLE OF INVENTION: Humanized Monoclonal Antibodies
; FILE REFERENCE: P50860
; CURRENT APPLICATION NUMBER: US/09/199,149
; CURRENT FILING DATE: 1998-11-24

US-09-134-000C-5271
; Sequence 5271, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5271
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-5271

Query Match      75.7%; Score 28; DB 2; Length 98;
Best Local Similarity 57.1%; Pred. No. 2.8e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 YSSNLHS 7
DB      54 YANLHA 60

RESULT 45
US-09-248-796A-19786
; Sequence 19786, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 19786
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-19786

Query Match      75.7%; Score 28; DB 2; Length 99;
Best Local Similarity 83.3%; Pred. No. 2.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 YSSNLH 6
DB      23 YSSSLH 28

RESULT 46
US-09-199-149-10
; Sequence 10, Application US/09199149
; Patent No. 6160099
; GENERAL INFORMATION:
; APPLICANT: Jonak, Zdenka L.
; APPLICANT: Taylor, Alexander H.
; APPLICANT: Trulli Jr., Stephen H.
; TITLE OF INVENTION: Humanized Monoclonal Antibodies
; FILE REFERENCE: P50860
; CURRENT APPLICATION NUMBER: US/09/199,149
; CURRENT FILING DATE: 1998-11-24

US-09-199-149-29
; Sequence 29, Application US/09199149
; Patent No. 6160099
; GENERAL INFORMATION:
; APPLICANT: Jonak, Zdenka L.
; APPLICANT: Taylor, Alexander H.
; APPLICANT: Trulli Jr., Stephen H.
; APPLICANT: Johanson, Kyung O.
; TITLE OF INVENTION: Humanized Monoclonal Antibodies
; FILE REFERENCE: P50860
; CURRENT APPLICATION NUMBER: US/09/199,149
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
; LENGTH: 102
; TYPE: PRT
; ORGANISM: human and murine cells
US-09-199-149-29

Query Match      75.7%; Score 28; DB 2; Length 102;
Best Local Similarity 71.4%; Pred. No. 2.9e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 YSSNLHS 7
DB      50 YTSTLHS 56

RESULT 47
US-09-199-149-29
; Sequence 29, Application US/09199149
; Patent No. 6160099
; GENERAL INFORMATION:
; APPLICANT: Jonak, Zdenka L.
; APPLICANT: Taylor, Alexander H.
; APPLICANT: Trulli Jr., Stephen H.
; APPLICANT: Johanson, Kyung O.
; TITLE OF INVENTION: Humanized Monoclonal Antibodies
; FILE REFERENCE: P50860
; CURRENT APPLICATION NUMBER: US/09/199,149
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
; LENGTH: 102
; TYPE: PRT
; ORGANISM: human and murine cells
US-09-199-149-29

Query Match      75.7%; Score 28; DB 2; Length 102;
Best Local Similarity 71.4%; Pred. No. 2.9e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 YSSNLHS 7
DB      50 YTSTLHS 56

RESULT 48
US-09-199-149-31
; Sequence 31, Application US/09199149
; Patent No. 6160099
; GENERAL INFORMATION:
; APPLICANT: Jonak, Zdenka L.
; APPLICANT: Taylor, Alexander H.
; APPLICANT: Trulli Jr., Stephen H.
; APPLICANT: Johanson, Kyung O.
; TITLE OF INVENTION: Humanized Monoclonal Antibodies
; FILE REFERENCE: P50860
; CURRENT APPLICATION NUMBER: US/09/199,149
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 31
; LENGTH: 105
; TYPE: PRT
; ORGANISM: human and murine cells
US-09-199-149-31

Query Match      75.7%; Score 28; DB 2; Length 105;
Best Local Similarity 71.4%; Pred. No. 3e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 YSSNLHS 7
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Db 50 YSTLHS 56  
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## RESULT 49

US-08-458-516-8  
; Sequence 8, Application US/08458516  
; Patent No. 5777085  
; GENERAL INFORMATION:  
; APPLICANT: Co, Man Sung  
; APPLICANT: Tso, J. Yun  
; TITLE OF INVENTION: Humanized Antibodies Reactive with  
; TITLE OF INVENTION: GPIIB/IIIA  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: William M. Smith  
; STREET: One Market Plaza, Steuart Tower, Suite 2000  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94105  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/458,516  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/059,159  
; FILING DATE: 03-MAY-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M.  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 11823-37-3  
; TELEPHONE: 415-326-2400  
; TELEFAX: 415-326-2422  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 107 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-458-516-8

Query Match 75.7%; Score 28; DB 1; Length 107;  
Best Local Similarity 71.4%; Pred. No. 3.1e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSNLHS 7  
|.|.||||  
Db 50 YSTLHS 56

## RESULT 50

US-08-458-516-9  
; Sequence 9, Application US/08458516  
; Patent No. 5777085  
; GENERAL INFORMATION:  
; APPLICANT: Co, Man Sung  
; APPLICANT: Tso, J. Yun  
; TITLE OF INVENTION: Humanized Antibodies Reactive with  
; TITLE OF INVENTION: GPIIB/IIIA  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: William M. Smith  
; STREET: One Market Plaza, Steuart Tower, Suite 2000  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA

ZIP: 94105  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/458,516  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/059,159  
; FILING DATE: 03-MAY-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M.  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 11823-37-3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-326-2400  
; TELEFAX: 415-326-2422  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 107 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-458-516-9

Query Match 75.7%; Score 28; DB 1; Length 107;  
Best Local Similarity 71.4%; Pred. No. 3.1e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSNLHS 7  
|.|.||||  
Db 50 YSTLHS 56

Search completed: April 6, 2006, 09:00:31  
Job time : 18.3729 secs

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 6, 2006, 09:13:24 ; Search time 56.5932 Seconds  
(without alignments)  
51.681 Million cell updates

Title: US-10-089-500-7  
Perfect score: 37  
Sequence: 1 YSSNLHS 7

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

**Total number of hits satisfying chosen parameters: 1867569**

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                  Maximum Match 10%
                  Listing first 10

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Database : Published Applications_AA_Main.*
1: /cn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
3: /cn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
4: /cn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
5: /cn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
6: /cn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	#	Length	DB	ID	Description	
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2	37	100.0	128	3	US-09-764-304-19	Sequence 19, Appl		
3	37	100.0	128	4	US-10-265-713-10	Sequence 10, Appl		
4	37	100.0	128	4	US-10-265-713-19	Sequence 19, Appl		
5	37	100.0	128	4	US-10-166-626-10	Sequence 10, Appl		
6	37	100.0	128	4	US-10-166-626-19	Sequence 19, Appl		
7	34	91.9	107	4	US-10-741-657A-16	Sequence 16, Appl		
8	34	91.9	2207	4	US-10-437-963-189767	Sequence 189767,		
9	33	89.2	91	4	US-10-424-599-201107	Sequence 201107,		
10	33	89.2	303	4	US-10-424-599-208863	Sequence 208863,		
11	33	89.2	306	4	US-10-425-114-49629	Sequence 49629, A		
12	33	89.2	474	3	US-09-823-829-24	Sequence 24, Appl		
13	33	89.2	503	4	US-10-437-963-197006	Sequence 24, Appl		
14	32	86.5	57	4	US-10-425-115-227775	Sequence 227775,		
15	32	86.5	49	4	US-10-424-599-190057	Sequence 190057,		
16	32	86.5	500	3	US-09-970-367-2	Sequence 2, Appl		
17	32	86.5	500	6	US-11-072-129-2	Sequence 2, Appl		
18	31	83.8	61	4	US-10-425-113-316851	Sequence 316851,		
19	31	83.8	277	4	US-10-282-122A-53384	Sequence 53384, A		
20	31	83.8	347	3	US-09-816-028A-17	Sequence 17, Appl		
21	31	83.8	347	4	US-10-303-161-17	Sequence 17, Appl		
22	31	83.8	347	4	US-10-303-118-17	Sequence 17, Appl		
23	31	83.8	347	4	US-10-303-128-17	Sequence 17, Appl		
24	31	83.8	347	4	US-10-303-134-17	Sequence 17, Appl		
25	31	83.8	347	4	US-10-303-162-17	Sequence 17, Appl		
26	31	83.8	347	4	US-10-820-536-17	Sequence 17, Appl		
27	31	83.8	347	4	US-10-845-408-17	Sequence 17, Appl		

101	29	78.4	108	4	US-10-683-815-19	Sequence 19, Appl	174	28	75.7	107	4	US-10-460-595-7	Sequence 7, Appl
102	29	78.4	129	4	US-10-425-115-270390	Sequence 270390,	175	28	75.7	107	4	US-10-410-962-51	Sequence 51, Appl
103	29	78.4	142	4	US-10-424-599-176914	Sequence 176914,	176	28	75.7	107	4	US-10-410-962-52	Sequence 52, Appl
104	29	78.4	174	4	US-10-424-599-222757	Sequence 222757,	177	28	75.7	107	4	US-10-411-049-51	Sequence 51, Appl
105	29	78.4	184	4	US-10-424-599-155429	Sequence 155429,	178	28	75.7	107	4	US-10-411-049-52	Sequence 52, Appl
106	29	78.4	200	4	US-10-424-599-219260	Sequence 219260,	179	28	75.7	107	4	US-10-389-679-10	Sequence 10, Appl
107	29	78.4	214	4	US-10-683-815-6	Sequence 6, Appli	180	28	75.7	107	4	US-10-410-930-51	Sequence 51, Appl
108	29	78.4	309	4	US-10-425-115-336076	Sequence 336076,	181	28	75.7	107	4	US-10-410-930-52	Sequence 52, Appl
109	29	78.4	301	4	US-10-424-599-206384	Sequence 206384,	182	28	75.7	107	4	US-10-410-937-51	Sequence 51, Appl
110	29	78.4	334	3	US-09-165-522-14	Sequence 14, Appl	183	28	75.7	107	4	US-10-410-997-52	Sequence 52, Appl
111	29	78.4	405	4	US-10-369-493-13353	Sequence 13353, A	184	28	75.7	107	4	US-10-411-012-51	Sequence 51, Appl
112	29	78.4	463	4	US-10-424-599-222758	Sequence 222758,	185	28	75.7	107	4	US-10-411-012-52	Sequence 52, Appl
113	29	78.4	468	4	US-10-425-115-206421	Sequence 206421,	186	28	75.7	107	4	US-10-287-994-51	Sequence 51, Appl
114	29	78.4	478	4	US-10-437-963-142690	Sequence 142690,	187	28	75.7	107	4	US-10-287-994-52	Sequence 52, Appl
115	29	78.4	497	4	US-10-724-972A-4825	Sequence 4825, Ap	188	28	75.7	107	4	US-10-410-913-51	Sequence 51, Appl
116	29	78.4	502	6	US-11-097-143-27660	Sequence 27660, A	189	28	75.7	107	4	US-10-410-913-52	Sequence 52, Appl
117	29	78.4	503	4	US-10-437-963-141183	Sequence 141183,	190	28	75.7	107	5	US-10-835-641-16	Sequence 16, Appl
118	29	78.4	504	4	US-10-259-194A-174	Sequence 174, App	191	28	75.7	107	5	US-10-473-977-69	Sequence 69, Appl
119	29	78.4	525	4	US-10-437-963-109554	Sequence 109554,	192	28	75.7	107	5	US-10-410-980-51	Sequence 51, Appl
120	29	78.4	554	4	US-10-322-281-136	Sequence 136, App	193	28	75.7	107	5	US-10-410-980-52	Sequence 52, Appl
121	29	78.4	560	4	US-10-425-115-206001	Sequence 206001,	194	28	75.7	107	5	US-10-985-299-4	Sequence 4, Appli
122	29	78.4	563	4	US-10-425-114-56898	Sequence 56898, A	195	28	75.7	107	5	US-10-410-897-51	Sequence 51, Appl
123	29	78.4	663	4	US-10-322-281-133	Sequence 133, App	196	28	75.7	107	5	US-10-410-897-52	Sequence 52, Appl
124	29	78.4	682	4	US-10-461-194-136	Sequence 136, App	197	28	75.7	107	5	US-10-492-261-51	Sequence 51, Appl
125	29	78.4	685	4	US-10-461-194-104	Sequence 104, App	198	28	75.7	107	5	US-10-492-261-52	Sequence 52, Appl
126	29	78.4	745	4	US-10-310-154-718	Sequence 718, App	199	28	75.7	107	5	US-10-837-904-115	Sequence 115, App
127	29	78.4	747	4	US-10-051-903-2	Sequence 2, Appli	200	28	75.7	107	5	US-10-938-992-17	Sequence 17, Appl
128	29	78.4	747	4	US-10-051-909-2	Sequence 2, Appli	201	28	75.7	108	3	US-09-905-243-73	Sequence 73, Appl
129	29	78.4	800	4	US-10-051-909-32	Sequence 32, Appl	202	28	75.7	108	4	US-10-140-555-4	Sequence 4, Appli
130	29	78.4	867	5	US-10-450-763-37629	Sequence 37629, A	203	28	75.7	108	4	US-10-141-908-7	Sequence 7, Appli
131	29	78.4	1231	4	US-10-437-963-189622	Sequence 189622,	204	28	75.7	108	4	US-10-141-908-14	Sequence 14, Appl
132	29	78.4	2105	4	US-10-369-493-7002	Sequence 7002, Ap	205	28	75.7	108	6	US-11-099-331-73	Sequence 73, Appl
133	29	78.4	2105	4	US-10-369-493-7003	Sequence 7003, Ap	206	28	75.7	109	3	US-09-929-665-21	Sequence 21, Appl
134	29	78.4	2105	4	US-10-369-493-7004	Sequence 7004, Ap	207	28	75.7	109	3	US-09-929-546-21	Sequence 21, Appl
135	28	75.7	7	3	US-09-563-222-39	Sequence 39, Appl	208	28	75.7	109	5	US-10-763-424-68	Sequence 68, Appl
136	28	75.7	7	4	US-10-140-555-9	Sequence 9, Appli	209	28	75.7	109	5	US-10-763-539-68	Sequence 68, Appl
137	28	75.7	7	4	US-10-783-950-39	Sequence 39, Appl	210	28	75.7	111	4	US-10-424-599-257944	Sequence 257944,
138	28	75.7	8	5	US-10-473-977-19	Sequence 19, Appl	211	28	75.7	113	4	US-10-425-115-213535	Sequence 213535,
139	28	75.7	10	5	US-10-808-187-716	Sequence 716, App	212	28	75.7	117	4	US-10-767-701-54571	Sequence 54571, A
140	28	75.7	10	5	US-10-807-807-716	Sequence 716, App	213	28	75.7	123	4	US-10-425-115-321650	Sequence 321650,
141	28	75.7	15	5	US-10-985-210-4	Sequence 4, Appli	214	28	75.7	126	5	US-10-837-904-64	Sequence 64, Appl
142	28	75.7	31	4	US-10-080-254-66	Sequence 66, Appl	215	28	75.7	126	5	US-10-837-904-68	Sequence 68, Appl
143	28	75.7	31	4	US-10-242-355-610	Sequence 610, App	216	28	75.7	126	5	US-10-450-763-49639	Sequence 49639, A
144	28	75.7	32	3	US-09-956-208A-14	Sequence 14, Appl	217	28	75.7	127	4	US-10-084-139-2	Sequence 2, Appli
145	28	75.7	32	5	US-10-965-616-14	Sequence 14, Appl	218	28	75.7	127	4	US-10-084-139-6	Sequence 6, Appli
146	28	75.7	37	4	US-10-425-115-309402	Sequence 309402,	219	28	75.7	127	5	US-10-268-883-5	Sequence 5, Appli
147	28	75.7	40	4	US-10-424-599-240198	Sequence 240198,	220	28	75.7	127	5	US-10-837-904-29	Sequence 29, Appl
148	28	75.7	48	4	US-10-425-115-232506	Sequence 232506,	221	28	75.7	127	5	US-10-837-904-37	Sequence 37, Appl
149	28	75.7	52	5	US-10-808-187-1545	Sequence 1545, Ap	222	28	75.7	128	4	US-10-424-599-176181	Sequence 176181,
150	28	75.7	52	5	US-10-807-807-1545	Sequence 1545, Ap	223	28	75.7	129	4	US-10-767-701-37591	Sequence 37591, A
151	28	75.7	66	4	US-10-425-115-244828	Sequence 244828,	224	28	75.7	131	2	US-08-779-784-21	Sequence 21, Appl
152	28	75.7	66	4	US-10-425-115-337968	Sequence 337968,	225	28	75.7	131	4	US-10-010-729-64	Sequence 64, Appl
153	28	75.7	68	4	US-10-425-115-193927	Sequence 193927,	226	28	75.7	173	4	US-10-425-115-50529	Sequence 50529, A
154	28	75.7	75	4	US-10-424-599-249630	Sequence 249630,	227	28	75.7	174	4	US-10-425-115-237673	Sequence 237673,
155	28	75.7	79	4	US-10-437-963-151349	Sequence 151349,	228	28	75.7	177	4	US-10-424-599-236231	Sequence 236231,
156	28	75.7	85	4	US-10-425-115-304040	Sequence 304040,	229	28	75.7	205	4	US-10-424-599-191185	Sequence 191185,
157	28	75.7	91	4	US-10-408-765A-2732	Sequence 2732, Ap	230	28	75.7	206	3	US-09-906-226-48	Sequence 48, Appl
158	28	75.7	93	4	US-10-424-599-231085	Sequence 231085,	231	28	75.7	213	4	US-10-437-963-134300	Sequence 134300,
159	28	75.7	96	4	US-10-424-599-281287	Sequence 281287,	232	28	75.7	214	3	US-09-754-998-1	Sequence 1, Appli
160	28	75.7	97	4	US-10-767-701-42030	Sequence 42030, A	233	28	75.7	214	3	US-09-940-166A-2	Sequence 2, Appli
161	28	75.7	99	4	US-10-425-115-235730	Sequence 235730,	234	28	75.7	214	3	US-09-811-384-11	Sequence 11, Appl
162	28	75.7	102	4	US-10-141-908-10	Sequence 10, Appl	235	28	75.7	214	4	US-10-411-037-55	Sequence 55, Appl
163	28	75.7	102	4	US-10-141-908-29	Sequence 29, Appl	236	28	75.7	214	4	US-10-404-286-11	Sequence 11, Appl
164	28	75.7	105	4	US-10-141-908-31	Sequence 31, Appl	237	28	75.7	214	4	US-10-411-026-55	Sequence 55, Appl
165	28	75.7	106	4	US-10-424-599-163008	Sequence 163008,	238	28	75.7	214	4	US-10-410-962-55	Sequence 55, Appl
166	28	75.7	107	4	US-10-011-931-4	Sequence 4, Appli	239	28	75.7	214	4	US-10-411-049-55	Sequence 55, Appl
167	28	75.7	107	4	US-10-269-010-2	Sequence 2, Appli	240	28	75.7	214	4	US-10-410-930-55	Sequence 55, Appl
168	28	75.7	107	4	US-10-268-883-6	Sequence 6, Appli	241	28	75.7	214	4	US-10-410-937-55	Sequence 55, Appl
169	28	75.7	107	4	US-10-310-674A-34	Sequence 34, Appl	242	28	75.7	214	4	US-10-411-012-55	Sequence 55, Appl
170	28	75.7	107	4	US-10-411-037-51	Sequence 51, Appl	243	28	75.7	214	4	US-10-287-994-52	Sequence 52, Appl
171	28	75.7	107	4	US-10-411-037-52	Sequence 52, Appl	244	28	75.7	214	4	US-10-762-967-2	Sequence 2, Appli
172	28	75.7	107	4	US-10-411-026-51	Sequence 51, Appl	245	28	75.7	214	4	US-10-410-913-55	Sequence 55, Appl
173	28	75.7	107	4	US-10-411-026-52	Sequence 52, Appl	246	28	75.7	214	5	US-10-835-641-24	Sequence 24, Appl

247	28	75.7	214	5	US-10-410-980-55	Sequence 55, Appl	320	28	75.7	652	4	US-10-296-085A-120	Sequence 120, App
248	28	75.7	214	5	US-10-410-897-55	Sequence 55, Appl	321	28	75.7	656	4	US-10-296-085A-39	Sequence 39, Appl
249	28	75.7	214	5	US-10-492-261-55	Sequence 55, Appl	322	28	75.7	657	4	US-10-296-085A-68	Sequence 68, Appl
250	28	75.7	214	6	US-11-077-717-2	Sequence 2, Appl	323	28	75.7	664	3	US-09-841-132-401	Sequence 401, App
251	28	75.7	218	4	US-10-437-963-166640	Sequence 166640,	324	28	75.7	664	4	US-10-282-122A-54796	Sequence 54796, A
252	28	75.7	220	4	US-10-424-599-212902	Sequence 212902,	325	28	75.7	664	5	US-10-872-155-401	Sequence 401, App
253	28	75.7	233	4	US-10-660-128-9	Sequence 9, Appl	326	28	75.7	666	4	US-10-289-762-409	Sequence 409, App
254	28	75.7	233	5	US-10-835-641-25	Sequence 25, Appl	327	28	75.7	674	4	US-10-369-433-12648	Sequence 12648, A
255	28	75.7	237	3	US-09-940-166A-6	Sequence 6, Appl	328	28	75.7	676	4	US-10-282-122A-53321	Sequence 53321, A
256	28	75.7	237	4	US-10-227-694-1	Sequence 1, Appl	329	28	75.7	696	4	US-10-451-467A-502	Sequence 502, App
257	28	75.7	237	4	US-10-762-967-6	Sequence 6, Appl	330	28	75.7	698	4	US-10-425-115-292839	Sequence 292839,
258	28	75.7	237	5	US-10-754-212-2	Sequence 2, Appl	331	28	75.7	701	4	US-10-437-963-107364	Sequence 107364,
259	28	75.7	237	6	US-11-077-717-10	Sequence 10, Appl	332	28	75.7	750	4	US-10-425-115-291998	Sequence 291998,
260	28	75.7	250	4	US-10-767-701-4745	Sequence 4745, A	333	28	75.7	786	4	US-10-002-344A-221	Sequence 221, App
261	28	75.7	255	3	US-09-764-877-1843	Sequence 1843, Ap	334	28	75.7	786	5	US-10-958-862-221	Sequence 221, App
262	28	75.7	255	4	US-10-242-515-1843	Sequence 1843, Ap	335	28	75.7	787	4	US-10-424-599-267111	Sequence 267111,
263	28	75.7	257	4	US-10-296-115-1323	Sequence 1323, Ap	336	28	75.7	869	4	US-10-437-963-189803	Sequence 189803,
264	28	75.7	261	4	US-10-295-403-26	Sequence 26, Appl	337	28	75.7	893	4	US-10-334-143-27	Sequence 27, Appl
265	28	75.7	261	4	US-10-225-066A-996	Sequence 996, App	338	28	75.7	895	4	US-10-296-085A-19	Sequence 19, Appl
266	28	75.7	261	4	US-10-225-067-52	Sequence 52, Appl	339	28	75.7	895	4	US-10-296-085A-20	Sequence 20, Appl
267	28	75.7	261	4	US-10-374-780A-198	Sequence 198, App	340	28	75.7	895	4	US-10-296-085A-27	Sequence 27, Appl
268	28	75.7	261	4	US-10-412-699B-642	Sequence 642, App	341	28	75.7	895	5	US-10-496-179-4	Sequence 4, Appl
269	28	75.7	261	5	US-10-732-923-5360	Sequence 5360, Ap	342	28	75.7	896	4	US-10-296-085A-17	Sequence 17, Appl
270	28	75.7	261	5	US-10-225-066A-996	Sequence 996, App	343	28	75.7	896	4	US-10-296-085A-18	Sequence 18, Appl
271	28	75.7	267	3	US-09-738-626-3398	Sequence 3398, Ap	344	28	75.7	896	4	US-10-296-085A-26	Sequence 26, Appl
272	28	75.7	267	3	US-10-494-672-42	Sequence 42, Appl	345	28	75.7	896	5	US-10-496-179-2	Sequence 2, Appl
273	28	75.7	267	5	US-10-721-922A-166	Sequence 166, App	346	28	75.7	896	5	US-10-496-179-3	Sequence 3, Appl
274	28	75.7	271	4	US-10-425-115-216083	Sequence 216083,	347	28	75.7	899	4	US-10-296-085A-28	Sequence 28, Appl
275	28	75.7	274	3	US-09-813-659-30	Sequence 30, Appl	348	28	75.7	899	5	US-10-496-179-5	Sequence 5, Appl
276	28	75.7	274	4	US-10-283-610A-30	Sequence 30, Appl	349	28	75.7	899	5	US-10-496-179-5	Sequence 5, Appl
277	28	75.7	281	5	US-10-507-617-49	Sequence 49, Appl	350	28	75.7	904	6	US-11-097-143-15351	Sequence 15351, A
278	28	75.7	287	5	US-10-507-617-52	Sequence 52, Appl	351	28	75.7	923	4	US-10-425-115-292583	Sequence 292583,
279	28	75.7	287	6	US-11-097-143-18204	Sequence 18204, A	352	28	75.7	1030	3	US-09-894-159-72	Sequence 72, Appl
280	28	75.7	299	4	US-10-424-599-212900	Sequence 212900,	353	28	75.7	1040	4	US-10-211-462-157	Sequence 157, App
281	28	75.7	301	4	US-10-425-114-54946	Sequence 54946, A	354	28	75.7	1093	3	US-09-894-159-71	Sequence 71, Appl
282	28	75.7	302	3	US-09-813-659-18	Sequence 18, Appl	355	28	75.7	1175	4	US-10-259-194A-314	Sequence 314, App
283	28	75.7	302	3	US-09-813-659-32	Sequence 32, Appl	356	28	75.7	1330	4	US-10-282-122A-54113	Sequence 54113, A
284	28	75.7	302	4	US-10-283-610A-18	Sequence 18, Appl	357	28	75.7	1382	5	US-10-831-070-188	Sequence 188, App
285	28	75.7	302	4	US-10-283-610A-32	Sequence 32, Appl	358	28	75.7	1422	5	US-08-424-550B-86	Sequence 86, Appl
286	28	75.7	318	5	US-10-774-385A-2585	Sequence 2585, Ap	359	28	75.7	1534	5	US-10-732-923-8754	Sequence 8754, Ap
287	28	75.7	391	4	US-10-369-493-6132	Sequence 6132, Ap	360	28	75.7	1534	6	US-11-097-143-7836	Sequence 7836, Ap
288	28	75.7	393	4	US-10-425-114-68386	Sequence 68386, A	361	28	75.7	2887	3	US-09-742-153-8	Sequence 8, Appl
289	28	75.7	421	4	US-10-288-762-932	Sequence 932, App	362	28	73.0	15	4	US-10-662-651A-22	Sequence 22, Appl
290	28	75.7	422	4	US-10-437-963-134266	Sequence 134266,	363	27	73.0	16	3	US-09-776-490-49	Sequence 49, Appl
291	28	75.7	426	4	US-10-282-122A-52492	Sequence 52492, A	364	27	73.0	16	3	US-09-776-491-17	Sequence 17, Appl
292	28	75.7	440	4	US-10-174-693-290	Sequence 290, App	365	27	73.0	19	5	US-10-821-544-47	Sequence 47, Appl
293	28	75.7	453	4	US-10-425-114-43641	Sequence 43641, A	366	27	73.0	21	6	US-11-065-970-16	Sequence 16, Appl
294	28	75.7	453	6	US-11-097-143-32808	Sequence 32808, A	367	27	73.0	31	5	US-10-918-015A-14	Sequence 14, Appl
295	28	75.7	470	4	US-10-424-599-170929	Sequence 170929,	368	27	73.0	33	4	US-10-425-115-288374	Sequence 288374,
296	28	75.7	475	5	US-10-732-923-10198	Sequence 10198, A	369	27	73.0	36	3	US-09-864-761-44129	Sequence 44129, A
297	28	75.7	477	6	US-11-097-143-27585	Sequence 27585, A	370	27	73.0	48	4	US-10-437-963-141723	Sequence 141723,
298	28	75.7	482	4	US-10-425-114-55313	Sequence 55313, A	371	27	73.0	49	5	US-10-450-763-57247	Sequence 57247, A
299	28	75.7	500	4	US-10-437-963-141185	Sequence 141185,	372	27	73.0	51	4	US-10-424-599-156713	Sequence 156713,
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301	28	75.7	504	4	US-10-207-653-348	Sequence 348, App	374	27	73.0	53	3	US-09-864-761-43593	Sequence 43593, A
302	28	75.7	504	5	US-10-627-556-113	Sequence 113, App	375	27	73.0	54	4	US-10-381-906-97	Sequence 97, Appl
303	28	75.7	518	5	US-10-739-930-6764	Sequence 6764, Ap	376	27	73.0	54	4	US-10-381-906-98	Sequence 98, Appl
304	28	75.7	529	4	US-10-437-963-149806	Sequence 149806,	377	27	73.0	57	4	US-10-424-599-216091	Sequence 216091,
305	28	75.7	530	5	US-10-899-557-14	Sequence 14, Appl	378	27	73.0	57	4	US-10-425-115-217834	Sequence 217834,
306	28	75.7	555	4	US-10-107-991B-3	Sequence 3, Appl	379	27	73.0	58	4	US-10-425-115-248246	Sequence 248246,
307	28	75.7	555	5	US-10-627-556-444	Sequence 444, App	380	27	73.0	66	4	US-10-425-115-348889	Sequence 348889,
308	28	75.7	555	5	US-10-627-556-512	Sequence 512, App	381	27	73.0	67	3	US-09-985-153-132	Sequence 132, App
309	28	75.7	601	3	US-09-480-236-1	Sequence 1, Appl	382	27	73.0	68	4	US-10-425-115-287708	Sequence 287708,
310	28	75.7	606	4	US-10-074-978A-117	Sequence 117, App	383	27	73.0	69	4	US-10-437-963-173172	Sequence 173172,
311	28	75.7	627	4	US-10-222-100-3	Sequence 3, Appl	384	27	73.0	71	4	US-10-425-115-264031	Sequence 264031,
312	28	75.7	637	4	US-10-296-085A-16	Sequence 16, Appl	385	27	73.0	73	4	US-10-425-115-264031	Sequence 198079,
313	28	75.7	638	4	US-10-296-085A-21	Sequence 21, Appl	386	27	73.0	73	4	US-10-424-599-198079	Sequence 198079,
314	28	75.7	642	4	US-10-296-085A-38	Sequence 38, Appl	387	27	73.0	74	4	US-10-424-599-194517	Sequence 194517,
315	28	75.7	642	5	US-10-496-179-6	Sequence 6, Appl	388	27	73.0	74	5	US-10-424-599-160751	Sequence 160751,
316	28	75.7	643	4	US-10-296-085A-69	Sequence 69, Appl	389	27	73.0	75	4	US-10-501-282-3962	Sequence 3962, Ap
317	28	75.7	643	5	US-10-496-179-1	Sequence 1, Appl	390	27	73.0	75	4	US-10-425-115-275877	Sequence 275877,
318	28	75.7	647	5	US-10-496-179-3	Sequence 3, Appl	391	27	73.0	76	4	US-10-424-599-285339	Sequence 285339,
319	28	75.7	651	4	US-10-821-273-6	Sequence 6, Appl	392	27	73.0	77	4	US-10-424-599-258847	Sequence 258847,
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393	27	73.0	80	4	US-10-425-115-313734	Sequence 313734,	466	27	73.0	164	4	US-10-425-115-346283	Sequence 346283,
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395	27	73.0	84	4	US-10-425-115-328768	Sequence 328768,	468	27	73.0	165	5	US-10-732-923-5064	Sequence 5064, Ap
396	27	73.0	84	4	US-10-630-590-193	Sequence 193,	469	27	73.0	165	5	US-10-732-923-5076	Sequence 5076, Ap
397	27	73.0	84	5	US-10-789-102-292	Sequence 292, App	470	27	73.0	165	5	US-10-732-923-5101	Sequence 5101, Ap
398	27	73.0	86	4	US-10-425-115-353161	Sequence 353161,	471	27	73.0	165	5	US-10-450-763-35967	Sequence 35967, A
399	27	73.0	87	4	US-10-032-2018-97	Sequence 97, Appl	472	27	73.0	167	4	US-10-282-122A-77787	Sequence 77787, A
400	27	73.0	88	4	US-10-767-701-31919	Sequence 31919, A	473	27	73.0	171	4	US-10-425-115-350270	Sequence 350270,
401	27	73.0	90	4	US-10-425-115-292649	Sequence 292649,	474	27	73.0	172	4	US-10-424-955A-2	Sequence 2, Appli
402	27	73.0	91	4	US-10-437-963-147071	Sequence 147071,	475	27	73.0	172	4	US-10-424-955A-7	Sequence 7, Appli
403	27	73.0	92	4	US-10-630-590-38	Sequence 38, Appl	476	27	73.0	172	4	US-10-424-955A-7	Sequence 9, Appli
404	27	73.0	92	4	US-10-424-599-263294	Sequence 263294,	477	27	73.0	172	5	US-10-982-514-9	Sequence 9, Appli
405	27	73.0	92	5	US-10-789-102-137	Sequence 137, App	478	27	73.0	172	5	US-10-450-763-50120	Sequence 50120, A
406	27	73.0	94	4	US-10-425-115-36708	Sequence 36708,	479	27	73.0	174	4	US-10-381-906-177	Sequence 177, App
407	27	73.0	94	4	US-10-425-115-331441	Sequence 331441,	480	27	73.0	178	4	US-10-029-386-32858	Sequence 32858, A
408	27	73.0	95	4	US-10-424-599-239060	Sequence 239060,	481	27	73.0	178	5	US-10-774-355A-2284	Sequence 2284, Ap
409	27	73.0	95	4	US-10-425-115-320705	Sequence 320705,	482	27	73.0	180	4	US-10-451-467A-394	Sequence 394, App
410	27	73.0	98	6	US-11-021-949-134	Sequence 134, App	483	27	73.0	183	4	US-10-092-900A-260	Sequence 260, App
411	27	73.0	98	6	US-11-021-928A-31	Sequence 31, Appl	484	27	73.0	185	4	US-10-425-115-193022	Sequence 193022,
412	27	73.0	99	4	US-10-029-386-30335	Sequence 30335, A	485	27	73.0	190	4	US-10-016-447-16	Sequence 16, Appl
413	27	73.0	99	4	US-10-424-599-175045	Sequence 175045,	486	27	73.0	190	5	US-10-739-930-8193	Sequence 8193, Ap
414	27	73.0	99	6	US-11-021-949-332	Sequence 332, App	487	27	73.0	192	4	US-10-724-972A-6697	Sequence 6697, Ap
415	27	73.0	99	6	US-11-021-928A-219	Sequence 219, App	488	27	73.0	193	4	US-10-192-988-21	Sequence 21, Appl
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417	27	73.0	105	4	US-10-108-260A-2932	Sequence 2932, Ap	490	27	73.0	201	4	US-10-724-972A-4643	Sequence 4643, Ap
418	27	73.0	105	4	US-10-424-599-171740	Sequence 171740,	491	27	73.0	202	4	US-10-424-599-210175	Sequence 210175,
419	27	73.0	105	4	US-10-425-114-46719	Sequence 46719, A	492	27	73.0	202	4	US-10-424-599-211916	Sequence 211916,
420	27	73.0	105	4	US-10-425-115-241180	Sequence 241180,	493	27	73.0	203	4	US-10-282-122A-56440	Sequence 56440, A
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422	27	73.0	106	4	US-10-424-599-197250	Sequence 197250,	495	27	73.0	205	3	US-09-817-814-10	Sequence 10, Appl
423	27	73.0	108	4	US-10-425-115-285002	Sequence 285002,	496	27	73.0	205	3	US-09-817-814-11	Sequence 11, Appl
424	27	73.0	109	4	US-10-424-599-234700	Sequence 234700,	497	27	73.0	205	4	US-10-174-394-9	Sequence 9, Appli
425	27	73.0	117	4	US-10-424-955A-10	Sequence 10, Appl	498	27	73.0	205	4	US-10-174-394-10	Sequence 10, Appl
426	27	73.0	117	4	US-10-424-599-250470	Sequence 250470,	499	27	73.0	205	4	US-10-174-394-11	Sequence 11, Appl
427	27	73.0	118	4	US-10-425-115-266056	Sequence 266056,	500	27	73.0	205	5	US-10-948-588-9	Sequence 9, Appli
428	27	73.0	119	4	US-10-424-955A-11	Sequence 11, Appl	501	27	73.0	205	5	US-10-948-588-10	Sequence 10, Appl
429	27	73.0	119	4	US-10-437-963-177294	Sequence 177294,	502	27	73.0	205	5	US-10-948-588-11	Sequence 11, Appl
430	27	73.0	119	4	US-10-425-115-242733	Sequence 242733,	503	27	73.0	208	3	US-09-822-485-12	Sequence 12, Appl
431	27	73.0	123	4	US-10-425-115-338695	Sequence 338695,	504	27	73.0	208	3	US-09-750-963-7	Sequence 7, Appli
432	27	73.0	123	4	US-10-767-701-437616	Sequence 437616,	505	27	73.0	208	3	US-09-902-773A-8	Sequence 8, Appli
433	27	73.0	123	5	US-10-856-499-728	Sequence 728, App	506	27	73.0	208	3	US-09-805-805-3	Sequence 3, Appli
434	27	73.0	125	4	US-10-424-955A-12	Sequence 12, Appl	507	27	73.0	208	3	US-09-805-805-4	Sequence 4, Appli
435	27	73.0	125	4	US-10-424-955A-13	Sequence 13, Appl	508	27	73.0	208	3	US-09-805-805-5	Sequence 5, Appli
436	27	73.0	126	4	US-10-425-115-337343	Sequence 337343,	509	27	73.0	208	3	US-09-251-263-7	Sequence 7, Appli
437	27	73.0	127	4	US-10-424-955A-9	Sequence 9, Appli	510	27	73.0	208	3	US-09-251-263-8	Sequence 8, Appli
438	27	73.0	127	5	US-10-982-514-12	Sequence 12, Appl	511	27	73.0	208	3	US-09-817-814-12	Sequence 12, Appl
439	27	73.0	127	5	US-10-982-514-13	Sequence 13, Appl	512	27	73.0	208	3	US-09-425-021-17	Sequence 17, Appl
440	27	73.0	127	5	US-10-982-514-15	Sequence 15, Appl	513	27	73.0	208	3	US-09-345-373-18	Sequence 18, Appl
441	27	73.0	138	4	US-10-982-514-15	Sequence 15, Appl	514	27	73.0	208	4	US-10-005-646-5	Sequence 5, Appli
442	27	73.0	138	4	US-10-424-599-185723	Sequence 185723,	515	27	73.0	208	4	US-10-005-646-8	Sequence 8, Appli
443	27	73.0	139	4	US-10-424-599-202202	Sequence 202202,	516	27	73.0	208	4	US-10-131-965-3	Sequence 3, Appli
444	27	73.0	141	3	US-09-901-938-19	Sequence 19, Appl	517	27	73.0	208	4	US-10-212-357-3	Sequence 3, Appli
445	27	73.0	141	4	US-10-379-334-19	Sequence 19, Appl	518	27	73.0	208	4	US-10-212-357-10	Sequence 10, Appl
446	27	73.0	142	4	US-10-424-955A-27	Sequence 27, Appl	519	27	73.0	208	4	US-10-212-357-11	Sequence 11, Appl
447	27	73.0	145	4	US-10-424-955A-5	Sequence 5, Appli	520	27	73.0	208	4	US-10-081-347-34	Sequence 34, Appl
448	27	73.0	145	4	US-10-424-599-155503	Sequence 155503,	521	27	73.0	208	4	US-10-075-446-18	Sequence 18, Appl
449	27	73.0	145	4	US-10-389-821-14	Sequence 14, Appl	522	27	73.0	208	4	US-10-189-360-18	Sequence 18, Appl
450	27	73.0	145	5	US-10-982-514-10	Sequence 10, Appl	523	27	73.0	208	4	US-10-192-988-12	Sequence 12, Appl
451	27	73.0	145	5	US-10-982-514-11	Sequence 11, Appl	524	27	73.0	208	4	US-10-374-207-12	Sequence 12, Appl
452	27	73.0	145	5	US-10-982-514-14	Sequence 14, Appl	525	27	73.0	208	4	US-10-174-394-12	Sequence 12, Appl
453	27	73.0	149	5	US-10-450-763-53321	Sequence 53321, A	526	27	73.0	208	4	US-10-035-212-18	Sequence 18, Appl
454	27	73.0	151	5	US-10-450-763-60711	Sequence 60711, A	527	27	73.0	208	4	US-10-347-177-7	Sequence 7, Appli
455	27	73.0	152	5	US-10-982-514-16	Sequence 16, Appl	528	27	73.0	208	4	US-10-424-955A-1	Sequence 1, Appli
456	27	73.0	157	5	US-10-982-514-17	Sequence 17, Appl	529	27	73.0	208	4	US-10-424-955A-3	Sequence 3, Appli
457	27	73.0	158	4	US-10-437-963-105318	Sequence 105318,	530	27	73.0	208	4	US-10-424-955A-29	Sequence 29, Appl
458	27	73.0	160	4	US-10-176-372-13	Sequence 13, Appl	531	27	73.0	208	4	US-10-424-955A-30	Sequence 30, Appl
459	27	73.0	161	4	US-10-176-372-2	Sequence 2, Appli	532	27	73.0	208	4	US-10-424-955A-31	Sequence 31, Appl
460	27	73.0	161	4	US-10-176-372-10	Sequence 10, Appl	533	27	73.0	208	4	US-10-662-455-3	Sequence 3, Appli
461	27	73.0	161	4	US-10-176-372-11	Sequence 11, Appl	534	27	73.0	208	4	US-10-662-455-4	Sequence 4, Appli
462	27	73.0	161	4	US-10-176-372-12	Sequence 12, Appl	535	27	73.0	208	4	US-10-037-922-34	Sequence 34, Appli
463	27	73.0	161	4	US-10-424-955A-8	Sequence 8, Appli	536	27	73.0	208	4	US-10-690-019-7	Sequence 7, Appli
464	27	73.0	164	4	US-10-424-955A-6	Sequence 6, Appli	537	27	73.0	208	4	US-10-450-859-4	Sequence 4, Appli
465	27	73.0	164	4	US-10-389-821-18	Sequence 18, Appl	538	27	73.0	208	4		

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541	27	73.0	208	5	US-10-935-228-8	Sequence 8, Appl	614	27	73.0	300	5	US-10-774-355A-2592	Sequence 2592, Ap
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543	27	73.0	208	5	US-10-901-210-18	Sequence 18, Appl	616	27	73.0	306	4	US-10-425-114-59731	Sequence 59731, A
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547	27	73.0	208	5	US-10-982-514-8	Sequence 8, Appl	620	27	73.0	313	4	US-10-425-114-43180	Sequence 43180, A
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550	27	73.0	208	5	US-10-991-224-6	Sequence 6, Appl	623	27	73.0	314	4	US-10-113-944-461	Sequence 461, App
551	27	73.0	208	6	US-11-027-948-9	Sequence 9, Appl	624	27	73.0	314	4	US-10-276-732-1	Sequence 1, Appl
552	27	73.0	208	6	US-11-027-948-10	Sequence 10, Appl	625	27	73.0	314	4	US-10-433-238-12	Sequence 12, Appl
553	27	73.0	208	6	US-11-027-948-11	Sequence 11, Appl	626	27	73.0	314	4	US-10-313-354-21	Sequence 21, Appl
554	27	73.0	208	6	US-11-027-948-12	Sequence 12, Appl	627	27	73.0	315	5	US-10-774-355A-2465	Sequence 2465, Ap
555	27	73.0	216	4	US-10-424-599-199938	Sequence 199938, A	628	27	73.0	315	4	US-10-425-114-49525	Sequence 49525, A
556	27	73.0	216	5	US-10-918-015A-17	Sequence 17, Appl	629	27	73.0	317	5	US-10-425-114-49525	Sequence 49525, A
557	27	73.0	217	4	US-10-425-115-246237	Sequence 246237, A	630	27	73.0	317	5	US-10-774-355A-1426	Sequence 1426, Ap
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561	27	73.0	226	4	US-10-225-066A-1058	Sequence 1058, Ap	634	27	73.0	318	4	US-10-425-114-53396	Sequence 53396, A
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564	27	73.0	230	4	US-10-425-115-285272	Sequence 285272, A	637	27	73.0	321	4	US-10-381-906-195	Sequence 195, App
565	27	73.0	233	4	US-10-425-114-57272	Sequence 57272, A	638	27	73.0	323	4	US-10-312-273-131	Sequence 131, App
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567	27	73.0	233	4	US-10-425-115-308296	Sequence 308296, A	640	27	73.0	328	4	US-10-289-762-637	Sequence 637, App
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569	27	73.0	237	3	US-09-864-761-37992	Sequence 37992, A	642	27	73.0	329	3	US-10-225-066A-318	Sequence 15, Appl
570	27	73.0	238	4	US-10-437-963-23806	Sequence 23806, A	643	27	73.0	339	4	US-10-374-780A-2634	Sequence 318, App
571	27	73.0	240	4	US-10-264-049-2202	Sequence 2202, Ap	644	27	73.0	339	5	US-10-225-066A-318	Sequence 2, Appl
572	27	73.0	243	4	US-10-424-599-213244	Sequence 213244, A	645	27	73.0	340	3	US-09-740-027-2	Sequence 318, App
573	27	73.0	243	6	US-11-021-949-136	Sequence 136, App	646	27	73.0	340	4	US-10-274-968-2	Sequence 2, Appl
574	27	73.0	244	4	US-10-425-115-304305	Sequence 33, Appl	647	27	73.0	340	6	US-11-043-932-2	Sequence 2, Appl
575	27	73.0	244	4	US-10-289-762-1891	Sequence 1891, Ap	648	27	73.0	343	5	US-10-450-763-51727	Sequence 51727, A
576	27	73.0	245	4	US-10-369-493-15370	Sequence 15370, A	649	27	73.0	347	5	US-10-732-923-2358	Sequence 2358, Ap
577	27	73.0	246	4	US-10-369-493-15737	Sequence 15737, A	650	27	73.0	355	6	US-10-732-923-2358	Sequence 318, App
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580	27	73.0	251	4	US-10-102-806-496	Sequence 496, App	653	27	73.0	358	4	US-10-274-968-4	Sequence 4, Appl
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582	27	73.0	252	4	US-10-437-963-199512	Sequence 199512, A	655	27	73.0	358	4	US-10-648-593-209	Sequence 209, App
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592	27	73.0	262	5	US-10-732-923-18886	Sequence 18886, A	665	27	73.0	397	4	US-10-214-446-34	Sequence 34, Appl
593	27	73.0	271	4	US-10-276-732-2	Sequence 2, Appl	666	27	73.0	400	4	US-10-381-906-191	Sequence 191, App
594	27	73.0	273	4	US-10-108-260A-2625	Sequence 2625, Ap	667	27	73.0	414	5	US-10-732-923-23987	Sequence 23987, A
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597	27	73.0	277	5	US-10-425-115-350835	Sequence 350835, A	670	27	73.0	434	4	US-10-001-843-179	Sequence 179, App
598	27	73.0	279	5	US-10-425-115-350835	Sequence 350835, A	671	27	73.0	434	6	US-11-097-143-33483	Sequence 33483, A
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603	27	73.0	286	5	US-10-617-320-4083	Sequence 4083, Ap	676	27	73.0	444	6	US-11-097-143-33483	Sequence 33483, A
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691	27	73.0	525	5	US-10-732-923-23396	Sequence 23396, A	764	27	73.0	990	5	US-10-220-335-266	Sequence 266, App
692	27	73.0	525	5	US-09-712-363-156	Sequence 156, App	765	27	73.0	1025	5	US-10-879-638-19	Sequence 19, Appl
693	27	73.0	527	4	US-10-080-170-348	Sequence 348, App	766	27	73.0	1066	3	US-09-280-197-5	Sequence 5, Appl
694	27	73.0	527	4	US-10-080-170-348	Sequence 348, App	767	27	73.0	1066	3	US-09-423-126-3	Sequence 3, Appl
695	27	73.0	527	4	US-10-468-356-348	Sequence 348, App	768	27	73.0	1066	4	US-10-448-139-5	Sequence 5, Appl
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698	27	73.0	536	4	US-10-425-115-193029	Sequence 193029, A	771	27	73.0	1070	3	US-09-423-126-4	Sequence 4, Appl
699	27	73.0	537	4	US-10-425-115-193026	Sequence 193026, A	772	27	73.0	1070	4	US-10-448-139-6	Sequence 6, Appl
700	27	73.0	538	5	US-10-831-070-234	Sequence 234, App	773	27	73.0	1070	5	US-10-879-638-4	Sequence 4, Appl
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702	27	73.0	547	4	US-10-425-114-63176	Sequence 63176, A	775	27	73.0	1156	4	US-10-369-493-6128	Sequence 6128, App
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704	27	73.0	553	4	US-10-425-114-59266	Sequence 59266, A	777	27	73.0	1235	5	US-10-918-015A-16	Sequence 16, Appl
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990 26 70.3 167 4 US-10-425-115-200966 Sequence 200966,  
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994 26 70.3 174 3 US-09-809-391-526 Sequence 526, App  
995 26 70.3 174 3 US-09-882-171-526 Sequence 526, App  
996 26 70.3 174 4 US-10-164-861-526 Sequence 526, App  
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## ALIGNMENTS

RESULT 1  
US-09-764-304-10  
; Sequence 10, Application US/09764304  
; Patent No. US20020026036A1  
; GENERAL INFORMATION:  
; APPLICANT: SHITARA, KENYA  
; APPLICANT: HANAI, NOBUO  
; APPLICANT: HASEGAWA, MAMORU  
; APPLICANT: MIYAJI, HIROMASA  
; APPLICANT: KUWANA, YOSHIHISA  
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY  
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; OTHER INFORMATION: variable region  
US-09-764-304-19

Query Match 100.0%; Score 37; DB 3; Length 128;  
Best Local Similarity 100.0%; Pred. No. 24;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSSNLHS 7  
Db 70 YSSNLHS 76  
US-10-265-713-10  
; Sequence 10, Application US/10265713  
; Publication No. US20030095964A1  
; GENERAL INFORMATION:  
; APPLICANT: SHITARA, KENYA  
; APPLICANT: HANAI, NOBUO  
; APPLICANT: HASEGAWA, MAMORU  
; APPLICANT: MIYAJI, HIROMASA  
; APPLICANT: KUWANA, YOSHIHISA  
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY  
; FILE REFERENCE: 249-101  
; CURRENT APPLICATION NUMBER: US/10/265,713  
; CURRENT FILING DATE: 2002-10-08  
; PRIOR APPLICATION NUMBER: US/09/225,322  
; PRIOR FILING DATE: 1999-01-05  
; PRIOR APPLICATION NUMBER: US 08/454,680  
; PRIOR FILING DATE: 1995-05-31  
; PRIOR APPLICATION NUMBER: US 08/408,133  
; PRIOR FILING DATE: 1995-03-21  
; PRIOR APPLICATION NUMBER: US 08/292,178  
; PRIOR FILING DATE: 1994-08-17  
; PRIOR APPLICATION NUMBER: US07/947,674  
; PRIOR FILING DATE: 1992-09-17  
; PRIOR APPLICATION NUMBER: JP 3-238375  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 10  
; LENGTH: 128  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: cdna KM-641  
US-09-764-304-10

Query Match 100.0%; Score 37; DB 3; Length 128;  
Best Local Similarity 100.0%; Pred. No. 24;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSSNLHS 7  
Db 70 YSSNLHS 76

RESULT 2  
US-09-764-304-19  
; Sequence 19, Application US/09764304  
; Patent No. US20020026036A1  
; GENERAL INFORMATION:  
; APPLICANT: SHITARA, KENYA  
; APPLICANT: HANAI, NOBUO  
; APPLICANT: HASEGAWA, MAMORU  
; APPLICANT: MIYAJI, HIROMASA  
; APPLICANT: KUWANA, YOSHIHISA  
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY  
; FILE REFERENCE: 249-101  
; CURRENT APPLICATION NUMBER: US/09/764,304  
; CURRENT FILING DATE: 2001-01-19  
; EARLIER APPLICATION NUMBER: 09/225,322  
; EARLIER FILING DATE: 1999-01-05  
; EARLIER APPLICATION NUMBER: US 08/454,680  
; EARLIER FILING DATE: 1995-05-31  
; EARLIER APPLICATION NUMBER: US 08/408,133  
; EARLIER FILING DATE: 1995-03-21  
; EARLIER APPLICATION NUMBER: US 08/292,178  
; EARLIER FILING DATE: 1994-08-17  
; EARLIER APPLICATION NUMBER: US07/947,674  
; EARLIER FILING DATE: 1992-09-17  
; EARLIER APPLICATION NUMBER: JP 3-238375  
; EARLIER FILING DATE: 1991-09-18  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 19  
; LENGTH: 128  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: light chain  
; OTHER INFORMATION: variable region  
US-09-764-304-19

Query Match 100.0%; Score 37; DB 3; Length 128;  
Best Local Similarity 100.0%; Pred. No. 24;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSSNLHS 7  
Db 70 YSSNLHS 76  
US-10-265-713-10  
; Sequence 10, Application US/10265713  
; Publication No. US20030095964A1  
; GENERAL INFORMATION:  
; APPLICANT: SHITARA, KENYA  
; APPLICANT: HANAI, NOBUO  
; APPLICANT: HASEGAWA, MAMORU  
; APPLICANT: MIYAJI, HIROMASA  
; APPLICANT: KUWANA, YOSHIHISA  
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY  
; FILE REFERENCE: 249-101  
; CURRENT APPLICATION NUMBER: US/10/265,713  
; CURRENT FILING DATE: 2002-10-08  
; PRIOR APPLICATION NUMBER: US/09/225,322  
; PRIOR FILING DATE: 1999-01-05  
; PRIOR APPLICATION NUMBER: US 08/454,680  
; PRIOR FILING DATE: 1995-05-31  
; PRIOR APPLICATION NUMBER: US 08/408,133  
; PRIOR FILING DATE: 1995-03-21  
; PRIOR APPLICATION NUMBER: US 08/292,178  
; PRIOR FILING DATE: 1994-08-17  
; PRIOR APPLICATION NUMBER: US07/947,674  
; PRIOR FILING DATE: 1992-09-17  
; PRIOR APPLICATION NUMBER: JP 3-238375  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 10  
; LENGTH: 128  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: cdna KM-641  
US-09-764-304-10

Query Match 100.0%; Score 37; DB 3; Length 128;  
Best Local Similarity 100.0%; Pred. No. 24;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSSNLHS 7  
Db 70 YSSNLHS 76

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; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: cdna KM-641
US-10-265-713-10

Query Match      100.0%; Score 37; DB 4; Length 128;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YSSNLHS 7
        |||||
DB      70 YSSNLHS 76

RESULT 4
US-10-265-713-19
; Sequence 19, Application US/10265713
; Publication No. US2003095964A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/10/265,713
; CURRENT FILING DATE: 2002-10-08
; PRIOR APPLICATION NUMBER: US/09/225,322
; PRIOR FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: US 08/454,680
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
; PRIOR APPLICATION NUMBER: US07/947,674
; PRIOR FILING DATE: 1992-09-17
; PRIOR APPLICATION NUMBER: JP 3-238375
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:light chain
US-10-265-713-19

Query Match      100.0%; Score 37; DB 4; Length 128;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YSSNLHS 7
        |||||
DB      70 YSSNLHS 76

RESULT 5
US-10-166-626-10
; Sequence 10, Application US/10166626
; Publication No. US20030166876A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
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; APPLICANT: MIYAJI, HIROMASA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/10/166,626
; PRIOR FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: US/09/225,322B
; PRIOR FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: US 08/454,680
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
; PRIOR APPLICATION NUMBER: US07/947,674
; PRIOR FILING DATE: 1992-09-17
; PRIOR APPLICATION NUMBER: JP 3-238375
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: cdna KM-641
US-10-166-626-10

Query Match      100.0%; Score 37; DB 4; Length 128;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YSSNLHS 7
        |||||
DB      70 YSSNLHS 76

RESULT 6
US-10-166-626-19
; Sequence 19, Application US/10166626
; Publication No. US20030166876A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUWANA, YOSHIIISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/10/166,626
; CURRENT FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: US/09/225,322B
; PRIOR FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: US 08/454,680
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
; PRIOR APPLICATION NUMBER: US07/947,674
; PRIOR FILING DATE: 1992-09-17
; PRIOR APPLICATION NUMBER: JP 3-238375
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:variable region
US-10-166-626-19
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Query Match 100.0%; Score 37; DB 4; Length 128;  
Best Local Similarity 100.0%; Pred. No. 24;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLHS 7  
|:|||||  
DB 70 YSSNLHS 76

RESULT 7  
US-10-741-657A-16  
; Sequence 16, Application US/10741657A  
; Publication No. US20040197325A1  
; GENERAL INFORMATION:  
; APPLICANT: Protein Design Labs  
; TITLE OF INVENTION: ANTIBODIES AGAINST GPR64 AND USES THEREOF  
; FILE REFERENCE: 05882.0177.NPUS01  
; CURRENT APPLICATION NUMBER: US/10/741,657A  
; CURRENT FILING DATE: 2003-12-19  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 16  
; LENGTH: 107  
; TYPE: PRT  
; ORGANISM: Mus sp.  
US-10-741-657A-16

Query Match 91.9%; Score 34; DB 4; Length 107;  
Best Local Similarity 85.7%; Pred. No. 75;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLHS 7  
|:|||||  
DB 50 YTSNLHS 56

RESULT 8  
US-10-437-963-189767  
; Sequence 189767, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 189767  
; LENGTH: 2207  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)..(2207)  
; OTHER INFORMATION: unsure at all Xaa locations  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_86244C.1.pap  
US-10-437-963-189767

Query Match 91.9%; Score 34; DB 4; Length 2207;  
Best Local Similarity 85.7%; Pred. No. 1.5e+03;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLHS 7

DB 850 YSNLHS 856  
|:|||||

RESULT 9  
US-10-424-599-201107  
; Sequence 201107, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa Thomas J  
; APPLICANT: Kovalic David K  
; APPLICANT: Zhou Yihua  
; APPLICANT: Cao Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 201107  
; LENGTH: 91  
; TYPE: PRT  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_23625C.1.pap  
US-10-424-599-201107

Query Match 89.2%; Score 33; DB 4; Length 91;  
Best Local Similarity 85.7%; Pred. No. 99;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLHS 7  
|:|||||  
DB 8 FSSNLHS 14

RESULT 10  
US-10-424-599-208863  
; Sequence 208863, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa Thomas J  
; APPLICANT: Kovalic David K  
; APPLICANT: Zhou Yihua  
; APPLICANT: Cao Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 208863  
; LENGTH: 303  
; TYPE: PRT  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_30631C.1.pap  
US-10-424-599-208863

Query Match 89.2%; Score 33; DB 4; Length 303;  
Best Local Similarity 85.7%; Pred. No. 3.3e+02;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLHS 7  
|:|||||  
DB 9 FSSNLHS 15

RESULT 11  
US-10-425-114-49629  
; Sequence 49629, Application US/10425114  
; Publication No. US20040034888A1  
; GENERAL INFORMATION:

; APPLICANT: Liu, Jingdong  
; APPLICANT: Zhou Yihua  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Screen, Steven E  
; APPLICANT: Tabaska, Jack E  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53313)B  
; CURRENT APPLICATION NUMBER: US/10/425,114  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 73128  
; SEQ ID NO 49629  
; LENGTH: 306  
; TYPE: PRT  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: 700739771\_FLI.pep  
US-10-425-114-49629

Query Match 89.2%; Score 33; DB 4; Length 306;  
Best Local Similarity 85.7%; Pred. No. 3.3e+02;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLHS 7  
:|||||  
DB 12 FSSNLHS 18

RESULT 12  
US-09-823-829-24  
; Sequence 24, Application US/09823829  
; Patent No. US20020146697A1  
; GENERAL INFORMATION:  
; APPLICANT: Yamamoto, Satoshi  
; APPLICANT: Nakamura, Shoko  
; APPLICANT: Suzuki, Makoto  
; APPLICANT: Kasai, Hiroaki  
; APPLICANT: Hamada, Tohru  
; TITLE OF INVENTION: METHOD FOR IDENTIFICATION AND DETECTION OF MICROORGANISMS  
; TITLE OF INVENTION: USING GYRASE GENE AS AN INDICATOR  
; FILE REFERENCE: 12817-004001  
; CURRENT APPLICATION NUMBER: US/09/823,829  
; CURRENT FILING DATE: 2001-03-30  
; PRIOR APPLICATION NUMBER: US 09/208,688  
; PRIOR FILING DATE: 1998-12-10  
; PRIOR APPLICATION NUMBER: JP 97/343316  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 82  
; SOFTWARE: Patentin version 2.0  
; SEQ ID NO 24  
; LENGTH: 474  
; TYPE: PRT  
; ORGANISM: Cytophaga lytica  
US-09-823-829-24

Query Match 89.2%; Score 33; DB 3; Length 474;  
Best Local Similarity 85.7%; Pred. No. 5.1e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSNLHS 7  
:|||||  
DB 164 YSNNLHS 170

RESULT 13  
US-10-437-963-197006  
; Sequence 197006, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 197006  
; LENGTH: 503  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_92805C.1.pep  
US-10-437-963-197006

Query Match 89.2%; Score 33; DB 4; Length 503;  
Best Local Similarity 100.0%; Pred. No. 5.4e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLH 6  
:|||||  
DB 84 YSSNLH 89

RESULT 14  
US-10-425-115-227775  
; Sequence 227775, Application US/10425115  
; Publication No. US20040214272A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants  
; FILE REFERENCE: 38-21(53222)B  
; CURRENT APPLICATION NUMBER: US/10/425,115  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 369326  
; SEQ ID NO 227775  
; LENGTH: 47  
; TYPE: PRT  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: MRT4577\_139326C.1.pep  
US-10-425-115-227775

Query Match 86.5%; Score 32; DB 4; Length 47;  
Best Local Similarity 85.7%; Pred. No. 79;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLHS 7  
:|||||  
DB 12 HSSNLHS 18

RESULT 15  
US-10-424-599-190057  
; Sequence 190057, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J  
; APPLICANT: Kovalic, David K  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599

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; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 190057
; LENGTH: 59
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_142640C.1.pap
US-10-424-599-190057

Query Match      86.5%; Score 32; DB 4; Length 59;
Best Local Similarity 85.7%; Pred. No. 1e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLHS 7
   |||:||||
Db 9 YSSSLHS 15

RESULT 16
US-09-970-367-2
; Sequence 2, Application US/09970367
; Publication No. US20030106092A1
; GENERAL INFORMATION:
; APPLICANT: Davis, Eric L.
; APPLICANT: Goellner, Melissa
; TITLE OF INVENTION: ENDOGLUCANASE GENE PROMOTER UPREGULATED BY NEMATODES
; FILE REFERENCE: 5051.587
; CURRENT APPLICATION NUMBER: US/09/970,367
; CURRENT FILING DATE: 2001-10-02
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 2
; LENGTH: 500
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
US-09-970-367-2

Query Match      86.5%; Score 32; DB 3; Length 500;
Best Local Similarity 85.7%; Pred. No. 8.4e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLHS 7
   |||:||||
Db 228 YSSSLHS 234

RESULT 17
US-11-072-129-2
; Sequence 2, Application US/11072129
; Publication No. US20050166285A1
; GENERAL INFORMATION:
; APPLICANT: Davis, Eric L.
; APPLICANT: Goellner, Melissa
; TITLE OF INVENTION: ENDOGLUCANASE GENE PROMOTER UPREGULATED BY NEMATODES
; FILE REFERENCE: 5051.587
; CURRENT APPLICATION NUMBER: US/11/072,129
; CURRENT FILING DATE: 2005-03-04
; PRIOR APPLICATION NUMBER: US/09/970,367
; PRIOR FILING DATE: 2001-10-02
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 2
; LENGTH: 500
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
US-11-072-129-2

Query Match      86.5%; Score 32; DB 6; Length 500;
Best Local Similarity 85.7%; Pred. No. 8.4e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLHS 7
   |||:||||
Db 228 YSSSLHS 234

; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 190057
; LENGTH: 59
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_142640C.1.pap
US-10-424-599-190057

Query Match      86.5%; Score 32; DB 4; Length 59;
Best Local Similarity 85.7%; Pred. No. 1e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLHS 7
   |||:||||
Db 9 YSSSLHS 15

RESULT 18
US-10-425-115-316851
; Sequence 316851, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 316851
; LENGTH: 61
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_5203C.1.pap
US-10-425-115-316851

Query Match      83.8%; Score 31; DB 4; Length 61;
Best Local Similarity 85.7%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSNLHS 7
   |||:||||
Db 52 YSINLHS 58

RESULT 19
US-10-282-122A-53384
; Sequence 53384, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
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; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 53384
; LENGTH: 277
; TYPE: PRT
; ORGANISM: Clostridium difficile
US-10-282-122A-53384

Query Match      83.8%; Score 31; DB 4; Length 277;
Best Local Similarity 83.3%; Pred. No. 7.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 YSSNLH 6
      |||||
Db      94 YSNIH 99

RESULT 20
US-09-816-028A-17
; Sequence 17, Application US/09816028A
; Patent No. US20020042369A1
; GENERAL INFORMATION:
; APPLICANT: Wakarchuk, Michel
; APPLICANT: National Research Council of Canada
; TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of
; TITLE OF INVENTION: Gangliosides and Ganglioside Mimics
; FILE REFERENCE: 019633-000111US
; CURRENT APPLICATION NUMBER: US/09/816,028A
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/118,213
; PRIOR FILING DATE: 1999-02-01
; PRIOR APPLICATION NUMBER: US 09/495,406
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 347
; TYPE: PRT
; ORGANISM: Campylobacter jejuni
; FEATURE:
; OTHER INFORMATION: beta-1,4 N-acetylgalactosaminyl (GalNAc)
; OTHER INFORMATION: transferase from C. jejuni strain OH4384 (ORF 5a)
; OTHER INFORMATION: of lipooligosaccharide (LOS) biosynthesis locus)
US-09-816-028A-17

Query Match      83.8%; Score 31; DB 3; Length 347;
Best Local Similarity 71.4%; Pred. No. 9e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 YSSNLH 7
      |||||
Db      268 FSSNIHS 274

RESULT 21
US-10-303-161-17
; Sequence 17, Application US/10303161
; Publication No. US20030148459A1
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Michel
; APPLICANT: Wakarchuk, Warren W.
; APPLICANT: National Research Council of Canada
; TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of
; TITLE OF INVENTION: Gangliosides and Ganglioside Mimics
; FILE REFERENCE: 019633-000111US
; CURRENT APPLICATION NUMBER: US/10/303,161
; CURRENT FILING DATE: 2002-11-21

; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 53384
; LENGTH: 277
; TYPE: PRT
; ORGANISM: Clostridium difficile
US-10-282-122A-53384

Query Match      83.8%; Score 31; DB 4; Length 277;
Best Local Similarity 83.3%; Pred. No. 7.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 YSSNLH 6
      |||||
Db      94 YSNIH 99

RESULT 20
US-09-816-028A-17
; Sequence 17, Application US/09816028A
; Patent No. US20020042369A1
; GENERAL INFORMATION:
; APPLICANT: Wakarchuk, Michel
; APPLICANT: National Research Council of Canada
; TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of
; TITLE OF INVENTION: Gangliosides and Ganglioside Mimics
; FILE REFERENCE: 019633-000111US
; CURRENT APPLICATION NUMBER: US/09/816,028A
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/118,213
; PRIOR FILING DATE: 1999-02-01
; PRIOR APPLICATION NUMBER: US 09/495,406
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 347
; TYPE: PRT
; ORGANISM: Campylobacter jejuni
; FEATURE:
; OTHER INFORMATION: beta-1,4 N-acetylgalactosaminyl (GalNAc)
; OTHER INFORMATION: transferase from C. jejuni strain OH4384 (ORF 5a)
; OTHER INFORMATION: of lipooligosaccharide (LOS) biosynthesis locus)
US-09-816-028A-17

Query Match      83.8%; Score 31; DB 3; Length 347;
Best Local Similarity 71.4%; Pred. No. 9e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 YSSNLH 7
      |||||
Db      268 FSSNIHS 274

RESULT 21
US-10-303-161-17
; Sequence 17, Application US/10303161
; Publication No. US20030148459A1
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Michel
; APPLICANT: Wakarchuk, Warren W.
; APPLICANT: National Research Council of Canada
; TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of
; TITLE OF INVENTION: Gangliosides and Ganglioside Mimics
; FILE REFERENCE: 019633-000111US
; CURRENT APPLICATION NUMBER: US/10/303,161
; CURRENT FILING DATE: 2002-11-21

; PRIOR APPLICATION NUMBER: US/09/816,028
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US/09/816,028
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/118,213
; PRIOR FILING DATE: 1999-02-01
; PRIOR APPLICATION NUMBER: US 09/495,406
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 347
; TYPE: PRT
; ORGANISM: Campylobacter jejuni
; FEATURE:
; OTHER INFORMATION: beta-1,4 N-acetylgalactosaminyl (GalNAc)
; OTHER INFORMATION: transferase from C. jejuni strain OH4384 (ORF 5a)
; OTHER INFORMATION: of lipooligosaccharide (LOS) biosynthesis locus)
US-10-303-118-17

Query Match      83.8%; Score 31; DB 4; Length 347;
Best Local Similarity 71.4%; Pred. No. 9e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 YSSNLH 7
      |||||
Db      268 FSSNIHS 274

RESULT 22
US-10-303-118-17
; Sequence 17, Application US/10303118
; Publication No. US20030157655A1
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Michel
; APPLICANT: Wakarchuk, Warren W.
; APPLICANT: National Research Council of Canada
; TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of
; TITLE OF INVENTION: Gangliosides and Ganglioside Mimics
; FILE REFERENCE: 019633-000111US
; CURRENT APPLICATION NUMBER: US/10/303,118
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US/09/816,028
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/118,213
; PRIOR FILING DATE: 1999-02-01
; PRIOR APPLICATION NUMBER: US 09/495,406
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 347
; TYPE: PRT
; ORGANISM: Campylobacter jejuni
; FEATURE:
; OTHER INFORMATION: beta-1,4 N-acetylgalactosaminyl (GalNAc)
; OTHER INFORMATION: transferase from C. jejuni strain OH4384 (ORF 5a)
; OTHER INFORMATION: of lipooligosaccharide (LOS) biosynthesis locus)
US-10-303-118-17

Query Match      83.8%; Score 31; DB 4; Length 347;
Best Local Similarity 71.4%; Pred. No. 9e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 YSSNLH 7
      |||||
Db      268 FSSNIHS 274

RESULT 23
US-10-303-128-17
; Sequence 17, Application US/10303128
; Publication No. US20030157656A1
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Michel
```

;; APPLICANT: Wakarchuk, Warren W.  
;; APPLICANT: National Research Council of Canada  
;; TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of  
;; TITLE OF INVENTION: Gangliosides and Ganglioside Mimics  
;; FILE REFERENCE: 019633-000111US  
;; CURRENT APPLICATION NUMBER: US/10/303,128  
;; CURRENT FILING DATE: 2002-11-21  
;; PRIOR APPLICATION NUMBER: US/09/816,028  
;; PRIOR FILING DATE: 2001-03-21  
;; PRIOR APPLICATION NUMBER: US 60/118,213  
;; PRIOR FILING DATE: 1999-02-01  
;; PRIOR APPLICATION NUMBER: US 09/495,406  
;; PRIOR FILING DATE: 2000-01-31  
;; NUMBER OF SEQ ID NOS: 49  
;; SOFTWARE: PatentIn Ver. 2.1  
;; SEQ ID NO 17  
;; LENGTH: 347  
;; TYPE: PRT  
;; ORGANISM: Campylobacter jejuni  
;; FEATURE:  
;; OTHER INFORMATION: beta-1,4 N-acetylgalactosaminyl (GalNAc)  
;; OTHER INFORMATION: transferase from C. jejuni strain OH4384 (ORF 5a  
;; OTHER INFORMATION: of lipooligosaccharide (LOS) biosynthesis locus)  
US-10-303-128-17

Query Match 83.8%; Score 31; DB 4; Length 347;  
Best Local Similarity 71.4%; Pred. No. 9e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLHS 7  
:|:|:|:  
Db 268 FSSNIHS 274

RESULT 24  
US-10-303-134-17  
;; Sequence 17, Application US/10303134  
;; Publication No. US20030157657A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Gilbert, Michel  
;; APPLICANT: Wakarchuk, Warren W.  
;; APPLICANT: National Research Council of Canada  
;; TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of  
;; TITLE OF INVENTION: Gangliosides and Ganglioside Mimics  
;; FILE REFERENCE: 019633-000111US  
;; CURRENT APPLICATION NUMBER: US/10/303,134  
;; CURRENT FILING DATE: 2002-11-21  
;; PRIOR APPLICATION NUMBER: US/09/816,028  
;; PRIOR FILING DATE: 2001-03-21  
;; PRIOR APPLICATION NUMBER: US 60/118,213  
;; PRIOR FILING DATE: 1999-02-01  
;; PRIOR APPLICATION NUMBER: US 09/495,406  
;; PRIOR FILING DATE: 2000-01-31  
;; NUMBER OF SEQ ID NOS: 49  
;; SOFTWARE: PatentIn Ver. 2.1  
;; SEQ ID NO 17  
;; LENGTH: 347  
;; TYPE: PRT  
;; ORGANISM: Campylobacter jejuni  
;; FEATURE:  
;; OTHER INFORMATION: beta-1,4 N-acetylgalactosaminyl (GalNAc)  
;; OTHER INFORMATION: transferase from C. jejuni strain OH4384 (ORF 5a  
;; OTHER INFORMATION: of lipooligosaccharide (LOS) biosynthesis locus)  
US-10-303-134-17

Query Match 83.8%; Score 31; DB 4; Length 347;  
Best Local Similarity 71.4%; Pred. No. 9e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLHS 7  
:|:|:|:  
Db 268 FSSNIHS 274

RESULT 25  
US-10-303-162-17  
;; Sequence 17, Application US/10303162  
;; Publication No. US20030157658A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Gilbert, Michel  
;; APPLICANT: Wakarchuk, Warren W.  
;; APPLICANT: National Research Council of Canada  
;; TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of  
;; TITLE OF INVENTION: Gangliosides and Ganglioside Mimics  
;; FILE REFERENCE: 019633-000111US  
;; CURRENT APPLICATION NUMBER: US/10/303,162  
;; CURRENT FILING DATE: 2002-11-21  
;; PRIOR APPLICATION NUMBER: US/09/816,028  
;; PRIOR FILING DATE: 2001-03-21  
;; PRIOR APPLICATION NUMBER: US 60/118,213  
;; PRIOR FILING DATE: 1999-02-01  
;; PRIOR APPLICATION NUMBER: US 09/495,406  
;; PRIOR FILING DATE: 2000-01-31  
;; NUMBER OF SEQ ID NOS: 49  
;; SOFTWARE: PatentIn Ver. 2.1  
;; SEQ ID NO 17  
;; LENGTH: 347  
;; TYPE: PRT  
;; ORGANISM: Campylobacter jejuni  
;; FEATURE:  
;; OTHER INFORMATION: beta-1,4 N-acetylgalactosaminyl (GalNAc)  
;; OTHER INFORMATION: transferase from C. jejuni strain OH4384 (ORF 5a  
;; OTHER INFORMATION: of lipooligosaccharide (LOS) biosynthesis locus)  
US-10-303-162-17

Query Match 83.8%; Score 31; DB 4; Length 347;  
Best Local Similarity 71.4%; Pred. No. 9e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLHS 7  
:|:|:|:  
Db 268 FSSNIHS 274

RESULT 26  
US-10-820-536-17  
;; Sequence 17, Application US/10820536  
;; Publication No. US20040203103A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Gilbert, Michel  
;; APPLICANT: Wakarchuk, Warren W.  
;; APPLICANT: National Research Council of Canada  
;; TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of  
;; TITLE OF INVENTION: Gangliosides and Ganglioside Mimics  
;; FILE REFERENCE: 019633-000111US  
;; CURRENT APPLICATION NUMBER: US/10/820,536  
;; CURRENT FILING DATE: 2004-04-07  
;; PRIOR APPLICATION NUMBER: 10/303,128  
;; PRIOR FILING DATE: 2002-11-21  
;; PRIOR APPLICATION NUMBER: US/09/816,028  
;; PRIOR FILING DATE: 2001-03-21  
;; PRIOR APPLICATION NUMBER: US 60/118,213  
;; PRIOR FILING DATE: 1999-02-01  
;; PRIOR APPLICATION NUMBER: US 09/495,406  
;; PRIOR FILING DATE: 2000-01-31  
;; NUMBER OF SEQ ID NOS: 49  
;; SOFTWARE: PatentIn Ver. 2.1  
;; SEQ ID NO 17  
;; LENGTH: 347  
;; TYPE: PRT  
;; ORGANISM: Campylobacter jejuni  
;; FEATURE:  
;; OTHER INFORMATION: beta-1,4 N-acetylgalactosaminyl (GalNAc)  
;; OTHER INFORMATION: transferase from C. jejuni strain OH4384 (ORF 5a  
;; OTHER INFORMATION: of lipooligosaccharide (LOS) biosynthesis locus)  
US-10-820-536-17



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Query Match      83.8%; Score 31; DB 4; Length 347;
Best Local Similarity 71.4%; Pred. No. 9e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLS 7
   :|||:|
Db 268 FSSNIHS 274

RESULT 27
US-10-845-408-17
; Sequence 17, Application US/10845408
; Publication No. US20040203112A1
; GENERAL INFORMATION:
; APPLICANT: Wakarchuk, Warren W.
; APPLICANT: National Research Council of Canada
; TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of
; TITLE OF INVENTION: Gangliosides and Ganglioside Mimics
; FILE REFERENCE: 019633-000111US
; CURRENT APPLICATION NUMBER: US/10/845,408
; CURRENT FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: US/09/816,028
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/118,213
; PRIOR FILING DATE: 1999-02-01
; PRIOR APPLICATION NUMBER: US 09/495,406
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 347
; TYPE: PRT
; ORGANISM: Campylobacter jejuni
; FEATURE:
; OTHER INFORMATION: beta-1,4 N-acetylgalactosaminyl (GalNAC)
; OTHER INFORMATION: transferase from C. jejuni strain OH4384 (ORF 5a
; OTHER INFORMATION: of lipooligosaccharide (LOS) biosynthesis locus)
US-10-845-408-17

Query Match      83.8%; Score 31; DB 4; Length 347;
Best Local Similarity 71.4%; Pred. No. 9e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLS 7
   :|||:|
Db 268 FSSNIHS 274

RESULT 28
US-10-845-412-17
; Sequence 17, Application US/10845412
; Publication No. US20040203113A1
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Michel
; APPLICANT: National Research Council of Canada
; TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of
; TITLE OF INVENTION: Gangliosides and Ganglioside Mimics
; FILE REFERENCE: 019633-000111US
; CURRENT APPLICATION NUMBER: US/10/845,412
; CURRENT FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: US/10/303,128
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US/09/816,028
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/118,213
; PRIOR FILING DATE: 1999-02-01
; PRIOR APPLICATION NUMBER: US 09/495,406
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.1

Query Match      83.8%; Score 31; DB 4; Length 347;
Best Local Similarity 71.4%; Pred. No. 9e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLS 7
   :|||:|
Db 268 FSSNIHS 274

RESULT 29
US-10-846-219-17
; Sequence 17, Application US/10846219
; Publication No. US20040219638A1
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Michel
; APPLICANT: Wakarchuk, Warren W.
; APPLICANT: National Research Council of Canada
; TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of
; TITLE OF INVENTION: Gangliosides and Ganglioside Mimics
; FILE REFERENCE: 019633-000111US
; CURRENT APPLICATION NUMBER: US/10/846,219
; CURRENT FILING DATE: 2004-05-14
; PRIOR APPLICATION NUMBER: US/09/816,028
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/118,213
; PRIOR FILING DATE: 1999-02-01
; PRIOR APPLICATION NUMBER: US 09/495,406
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 347
; TYPE: PRT
; ORGANISM: Campylobacter jejuni
; FEATURE:
; OTHER INFORMATION: beta-1,4 N-acetylgalactosaminyl (GalNAC)
; OTHER INFORMATION: transferase from C. jejuni strain OH4384 (ORF 5a
; OTHER INFORMATION: of lipooligosaccharide (LOS) biosynthesis locus)
US-10-846-219-17

Query Match      83.8%; Score 31; DB 5; Length 347;
Best Local Similarity 71.4%; Pred. No. 9e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLS 7
   :|||:|
Db 268 FSSNIHS 274

RESULT 30
US-10-821-604-17
; Sequence 17, Application US/10821604
; Publication No. US20040229263A1
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Michel
; APPLICANT: Wakarchuk, Warren W.
; APPLICANT: National Research Council of Canada
; TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of
; TITLE OF INVENTION: Gangliosides and Ganglioside Mimics
; FILE REFERENCE: 019633-000111US
; CURRENT APPLICATION NUMBER: US/10/821,604
; CURRENT FILING DATE: 2004-04-08
; PRIOR APPLICATION NUMBER: 10/303,128
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; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US/09/816,028
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/118,213
; PRIOR FILING DATE: 1999-02-01
; PRIOR APPLICATION NUMBER: US 09/495,406
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 347
; TYPE: PRT
; ORGANISM: Campylobacter jejuni
; FEATURE:
; OTHER INFORMATION: beta-1,4 N-acetylgalactosaminyl (GalNAC)
; OTHER INFORMATION: transferase from C. jejuni strain OH4384 (ORF 5a
; OTHER INFORMATION: of lipooligosaccharide (LOS) biosynthesis locus)
US-10-821-573-17

Query Match      83.8%; Score 31; DB 5; Length 347;
Best Local Similarity 71.4%; Pred. No. 9e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLSHS 7
Db 268 FSSNIHS 274

RESULT 31
US-10-847-983-17
; Sequence 17, Application US/10847983
; Publication No. US20040229272A1
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Michel
; APPLICANT: Wakarchuk, Warren W.
; APPLICANT: National Research Council of Canada
; TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of
; TITLE OF INVENTION: Gangliosides and Ganglioside Mimics
; FILE REFERENCE: 019633-000111US
; CURRENT APPLICATION NUMBER: US/10/847,983
; CURRENT FILING DATE: 2004-05-17
; PRIOR APPLICATION NUMBER: US/09/816,028
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/118,213
; PRIOR FILING DATE: 1999-02-01
; PRIOR APPLICATION NUMBER: US 09/495,406
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 347
; TYPE: PRT
; ORGANISM: Campylobacter jejuni
; FEATURE:
; OTHER INFORMATION: beta-1,4 N-acetylgalactosaminyl (GalNAC)
; OTHER INFORMATION: transferase from C. jejuni strain OH4384 (ORF 5a
; OTHER INFORMATION: of lipooligosaccharide (LOS) biosynthesis locus)
US-10-847-983-17

Query Match      83.8%; Score 31; DB 5; Length 347;
Best Local Similarity 71.4%; Pred. No. 9e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLSHS 7
Db 268 FSSNIHS 274

RESULT 32
US-10-821-573-17
; Sequence 17, Application US/10821573
; Publication No. US20040229313A1
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Michel
; APPLICANT: Wakarchuk, Warren W.
; APPLICANT: National Research Council of Canada
; TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of
; TITLE OF INVENTION: Gangliosides and Ganglioside Mimics
; FILE REFERENCE: 019633-000111US
; CURRENT APPLICATION NUMBER: US/10/821,573
; CURRENT FILING DATE: 2004-04-08
; PRIOR APPLICATION NUMBER: US/09/816,028
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US/09/816,028
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/118,213
; PRIOR FILING DATE: 1999-02-01
; PRIOR APPLICATION NUMBER: US 09/495,406
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 347
; TYPE: PRT
; ORGANISM: Campylobacter jejuni
; FEATURE:
; OTHER INFORMATION: beta-1,4 N-acetylgalactosaminyl (GalNAC)
; OTHER INFORMATION: transferase from C. jejuni strain OH4384 (ORF 5a
; OTHER INFORMATION: of lipooligosaccharide (LOS) biosynthesis locus)
US-10-821-573-17

Query Match      83.8%; Score 31; DB 5; Length 347;
Best Local Similarity 71.4%; Pred. No. 9e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLSHS 7
Db 268 FSSNIHS 274

RESULT 33
US-10-850-807-17
; Sequence 17, Application US/10850807
; Publication No. US20040259140A1
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Michel
; APPLICANT: Wakarchuk, Warren W.
; APPLICANT: National Research Council of Canada
; TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of
; TITLE OF INVENTION: Gangliosides and Ganglioside Mimics
; FILE REFERENCE: 019633-000111US
; CURRENT APPLICATION NUMBER: US/10/850,807
; CURRENT FILING DATE: 2004-05-21
; PRIOR APPLICATION NUMBER: US/09/816,028
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/118,213
; PRIOR FILING DATE: 1999-02-01
; PRIOR APPLICATION NUMBER: US 09/495,406
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 347
; TYPE: PRT
; ORGANISM: Campylobacter jejuni
; FEATURE:
; OTHER INFORMATION: beta-1,4 N-acetylgalactosaminyl (GalNAC)
; OTHER INFORMATION: transferase from C. jejuni strain OH4384 (ORF 5a
; OTHER INFORMATION: of lipooligosaccharide (LOS) biosynthesis locus)
US-10-850-807-17

Query Match      83.8%; Score 31; DB 5; Length 347;
Best Local Similarity 71.4%; Pred. No. 9e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLSHS 7
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Db          268 FSSNIHS 274
          :|||:|
RESULT 34
US-10-850-125-17
; Sequence 17, Application US/10850125
; Publication No. US20040259203A1
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Michel
; APPLICANT: Wakarchuk, Warren W.
; APPLICANT: National Research Council of Canada
; TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of
; TITLE OF INVENTION: Gangliosides and Ganglioside Mimics
; FILE REFERENCE: 019633-000111US
; CURRENT APPLICATION NUMBER: US/10/850,125
; CURRENT FILING DATE: 2004-05-19
; PRIOR APPLICATION NUMBER: US/09/816,028
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/118,213
; PRIOR FILING DATE: 1999-02-01
; PRIOR APPLICATION NUMBER: US 09/495,406
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 17
; LENGTH: 347
; TYPE: PRT
; ORGANISM: Campylobacter jejuni
; FEATURE:
; OTHER INFORMATION: beta-1,4 N-acetylgalactosaminyl (GalNAC)
; OTHER INFORMATION: transferase from C. jejuni strain OH4384 (ORF 5a
; OTHER INFORMATION: of lipooligosaccharide (LOS) biosynthesis locus)
US-10-850-125-17

Query Match          83.8%; Score 31; DB 5; Length 347;
Best Local Similarity 71.4%; Pred. No. 9e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy          1 YSSNLHS 7
          :|||:|
Db          268 FSSNIHS 274

RESULT 35
US-10-830-825-17
; Sequence 17, Application US/10830825
; Publication No. US20040265875A1
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Michel
; APPLICANT: Wakarchuk, Warren W.
; APPLICANT: National Research Council of Canada
; TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of
; TITLE OF INVENTION: Gangliosides and Ganglioside Mimics
; FILE REFERENCE: 019633-000111US
; CURRENT APPLICATION NUMBER: US/10/830,825
; CURRENT FILING DATE: 2004-04-24
; PRIOR APPLICATION NUMBER: US/09/816,028
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/118,213
; PRIOR FILING DATE: 1999-02-01
; PRIOR APPLICATION NUMBER: US 09/495,406
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 17
; LENGTH: 347
; TYPE: PRT
; ORGANISM: Campylobacter jejuni
; FEATURE:
; OTHER INFORMATION: beta-1,4 N-acetylgalactosaminyl (GalNAC)
; OTHER INFORMATION: transferase from C. jejuni strain OH4384 (ORF 5a
; OTHER INFORMATION: of lipooligosaccharide (LOS) biosynthesis locus)
US-10-830-825-17

Query Match          83.8%; Score 31; DB 5; Length 347;
Best Local Similarity 71.4%; Pred. No. 9e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy          1 YSSNLHS 7
          :|||:|
Db          268 FSSNIHS 274

RESULT 36
US-10-962-334-17
; Sequence 17, Application US/10962334
; Publication No. US20050048630A1
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Michel
; APPLICANT: Wakarchuk, Warren W.
; APPLICANT: National Research Council of Canada
; TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of
; TITLE OF INVENTION: Gangliosides and Ganglioside Mimics
; FILE REFERENCE: 019633-000111US
; CURRENT APPLICATION NUMBER: US/10/962,334
; CURRENT FILING DATE: 2004-10-08
; PRIOR APPLICATION NUMBER: US/09/816,028
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/118,213
; PRIOR FILING DATE: 1999-02-01
; PRIOR APPLICATION NUMBER: US 09/495,406
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 17
; LENGTH: 347
; TYPE: PRT
; ORGANISM: Campylobacter jejuni
; FEATURE:
; OTHER INFORMATION: beta-1,4 N-acetylgalactosaminyl (GalNAC)
; OTHER INFORMATION: transferase from C. jejuni strain OH4384 (ORF 5a
; OTHER INFORMATION: of lipooligosaccharide (LOS) biosynthesis locus)
US-10-962-334-17

Query Match          83.8%; Score 31; DB 5; Length 347;
Best Local Similarity 71.4%; Pred. No. 9e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy          1 YSSNLHS 7
          :|||:|
Db          268 FSSNIHS 274

RESULT 37
US-10-830-997-17
; Sequence 17, Application US/10830997
; Publication No. US20050064550A1
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Michel
; APPLICANT: Wakarchuk, Warren W.
; APPLICANT: National Research Council of Canada
; TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of
; TITLE OF INVENTION: Gangliosides and Ganglioside Mimics
; FILE REFERENCE: 019633-000111US
; CURRENT APPLICATION NUMBER: US/10/830,997
; CURRENT FILING DATE: 2004-04-22
; PRIOR APPLICATION NUMBER: US/10/303,128
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US/09/816,028
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/118,213
; PRIOR FILING DATE: 1999-02-01
; PRIOR APPLICATION NUMBER: US 09/495,406
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 49
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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 347
; TYPE: PRT
; ORGANISM: Campylobacter jejuni
; FEATURE:
; OTHER INFORMATION: beta-1,4 N-acetylgalactosaminyl (GalNAC)
; OTHER INFORMATION: transferase from C. jejuni strain OH4384 (ORF 5a
; OTHER INFORMATION: of lipooligosaccharide (LOS) biosynthesis locus)
US-10-830-997-17

Query Match      83.8%; Score 31; DB 5; Length 347;
Best Local Similarity 71.4%; Pred. No. 9e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 5; Conservative 2;

QY 1 YSSNLHS 7
   :|||:||
Db 268 FSSNIHS 274

RESULT 38
US-10-962-235-17
; Sequence 17, Application US/10962235
; Publication No. US20050084891A1
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Michel
; APPLICANT: Wakarchuk, Warren W.
; APPLICANT: National Research Council of Canada
; TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of
; TITLE OF INVENTION: Gangliosides and Ganglioside Mimics
; FILE REFERENCE: 019633-000111US
; CURRENT APPLICATION NUMBER: US/10/962,235
; CURRENT FILING DATE: 2004-10-08
; PRIOR FILING DATE: 2001-03-21
; PRIOR FILING DATE: 2001-03-21
; PRIOR FILING DATE: 2001-03-21
; PRIOR FILING DATE: 1999-02-01
; PRIOR FILING DATE: 1999-02-01
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 347
; TYPE: PRT
; ORGANISM: Campylobacter jejuni
; FEATURE:
; OTHER INFORMATION: beta-1,4 N-acetylgalactosaminyl (GalNAC)
; OTHER INFORMATION: transferase from C. jejuni strain OH4384 (ORF 5a
; OTHER INFORMATION: of lipooligosaccharide (LOS) biosynthesis locus)
US-10-962-235-17

Query Match      83.8%; Score 31; DB 5; Length 347;
Best Local Similarity 71.4%; Pred. No. 9e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 5; Conservative 2;

QY 1 YSSNLHS 7
   :|||:||
Db 268 FSSNIHS 274

RESULT 39
US-10-961-882-17
; Sequence 17, Application US/10961882
; Publication No. US20050227248A1
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Michel
; APPLICANT: Wakarchuk, Warren W.
; APPLICANT: National Research Council of Canada
; TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of
; TITLE OF INVENTION: Gangliosides and Ganglioside Mimics
; FILE REFERENCE: 019633-000111US
; CURRENT APPLICATION NUMBER: US/10/961,882
; CURRENT FILING DATE: 2004-10-08
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; PRIOR APPLICATION NUMBER: US/09/816,028
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/118,213
; PRIOR FILING DATE: 1999-02-01
; PRIOR APPLICATION NUMBER: US 09/495,406
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 347
; TYPE: PRT
; ORGANISM: Campylobacter jejuni
; FEATURE:
; OTHER INFORMATION: beta-1,4 N-acetylgalactosaminyl (GalNAC)
; OTHER INFORMATION: transferase from C. jejuni strain OH4384 (ORF 5a
; OTHER INFORMATION: of lipooligosaccharide (LOS) biosynthesis locus)
US-10-961-882-17

Query Match      83.8%; Score 31; DB 5; Length 347;
Best Local Similarity 71.4%; Pred. No. 9e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 5; Conservative 2;

QY 1 YSSNLHS 7
   :|||:||
Db 268 FSSNIHS 274

RESULT 40
US-10-425-115-320203
; Sequence 320203, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 320203
; LENGTH: 385
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_55091C.1.pap
US-10-425-115-320203

Query Match      83.8%; Score 31; DB 4; Length 385;
Best Local Similarity 85.7%; Pred. No. 1e+03; Mismatches 1; Indels 0; Gaps 0;
Matches 6; Conservative 0;

QY 1 YSSNLHS 7
   :|||:||
Db 165 YSSNOHS 171

RESULT 41
US-10-739-930-7620
; Sequence 7620, Application US/10739930
; Publication No. US20040216190A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
; TITLE OF INVENTION: PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53377)B
; CURRENT APPLICATION NUMBER: US/10/739,930
; CURRENT FILING DATE: 2003-12-18
; NUMBER OF SEQ ID NOS: 11088
; SEQ ID NO 7620
; LENGTH: 385
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; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: ZEAMA-23APR03-C21375_2.p
US-10-739-930-7620

Query Match      83.8%; Score 31; DB 5; Length 385;
Best Local Similarity 85.7%; Pred. No. 1e+03;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSNLHS 7
Db 165 YSSNQHS 171

RESULT 42
US-10-425-114-49028
; Sequence 49028, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 49028
; LENGTH: 392
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 700726516_FLI.pep
US-10-425-114-49028

Query Match      83.8%; Score 31; DB 4; Length 392;
Best Local Similarity 85.7%; Pred. No. 1e+03;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSNLHS 7
Db 195 YSSGLHS 201

RESULT 43
US-10-425-114-64369
; Sequence 64369, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 64369
; LENGTH: 407
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3689-224-H11_FLI.pep
US-10-425-114-64369

Query Match      83.8%; Score 31; DB 4; Length 407;
Best Local Similarity 85.7%; Pred. No. 1.1e+03;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSNLHS 7
Db 187 YSSNQHS 193

RESULT 44
US-10-424-599-285570
; Sequence 285570, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 285570
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_9989C.1.pap
US-10-424-599-285570

Query Match      83.8%; Score 31; DB 4; Length 442;
Best Local Similarity 85.7%; Pred. No. 1.1e+03;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSNLHS 7
Db 25 YSSNRHS 31

RESULT 45
US-10-425-115-192258
; Sequence 192258, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 192258
; LENGTH: 501
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_106925C.1.pap
US-10-425-115-192258

Query Match      83.8%; Score 31; DB 4; Length 501;
Best Local Similarity 85.7%; Pred. No. 1.3e+03;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSNLHS 7
Db 477 YSSRLHS 483
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RESULT 46  
 US-10-424-599-231545  
 ; Sequence 231545, Application US/10424599  
 ; Publication No. US20040031072A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: La Rosa, Thomas J  
 ; APPLICANT: Kovalic, David K  
 ; APPLICANT: Zhou, Yihua  
 ; APPLICANT: Cao, Yongwei  
 ; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
 ; FILE REFERENCE: 38-21(53223)B  
 ; CURRENT FILING DATE: 2003-04-28  
 ; CURRENT APPLICATION NUMBER: US/10/424,599  
 ; NUMBER OF SEQ ID NOS: 285684  
 ; SEQ ID NO 231545  
 ; LENGTH: 529  
 ; TYPE: PRT  
 ; ORGANISM: Glycine max  
 ; FEATURE:  
 ; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_51106C.1.pep  
 US-10-424-599-231545  
 Query Match 83.8%; Score 31; DB 4; Length 529;  
 Best Local Similarity 85.7%; Pred. No. 1.4e+03;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Qy 1 YSSNLHS 7  
 Db 332 YSSGLHS 338  
 RESULT 47  
 US-10-425-115-242547  
 ; Sequence 242547, Application US/10425115  
 ; Publication No. US20040214272A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: La Rosa, Thomas J.  
 ; APPLICANT: Kovalic, David K.  
 ; APPLICANT: Zhou, Yihua  
 ; APPLICANT: Cao, Yongwei  
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
 ; TITLE OF INVENTION: Plants  
 ; FILE REFERENCE: 38-21(53222)B  
 ; CURRENT APPLICATION NUMBER: US/10/425,115  
 ; CURRENT FILING DATE: 2003-04-28  
 ; NUMBER OF SEQ ID NOS: 369326  
 ; SEQ ID NO 242547  
 ; LENGTH: 62  
 ; TYPE: PRT  
 ; ORGANISM: Zea mays  
 ; FEATURE:  
 ; OTHER INFORMATION: Clone ID: MRT4577\_152789C.1.pep  
 US-10-425-115-242547  
 Query Match 81.1%; Score 30; DB 4; Length 62;  
 Best Local Similarity 83.3%; Pred. No. 2.5e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 YSSNLH 6  
 Db 40 YSTNLH 45  
 RESULT 48  
 US-10-424-599-264246  
 ; Sequence 264246, Application US/10424599  
 ; Publication No. US20040031072A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: La Rosa, Thomas J  
 ; APPLICANT: Kovalic, David K  
 ; APPLICANT: Zhou, Yihua  
 ; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
 ; FILE REFERENCE: 38-21(53223)B  
 ; CURRENT FILING DATE: 2003-04-28  
 ; CURRENT APPLICATION NUMBER: US/10/424,599  
 ; NUMBER OF SEQ ID NOS: 285684  
 ; SEQ ID NO 231545  
 ; LENGTH: 529  
 ; TYPE: PRT  
 ; ORGANISM: Glycine max  
 ; FEATURE:  
 ; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_51106C.1.pep  
 US-10-424-599-264246  
 Query Match 81.1%; Score 30; DB 4; Length 74;  
 Best Local Similarity 71.4%; Pred. No. 3e+02;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 Qy 1 YSSNLHS 7  
 Db 15 YSNHIS 21  
 RESULT 49  
 US-10-425-115-223534  
 ; Sequence 223534, Application US/10425115  
 ; Publication No. US20040214272A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: La Rosa, Thomas J.  
 ; APPLICANT: Kovalic, David K.  
 ; APPLICANT: Zhou, Yihua  
 ; APPLICANT: Cao, Yongwei  
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
 ; TITLE OF INVENTION: Plants  
 ; FILE REFERENCE: 38-21(53222)B  
 ; CURRENT APPLICATION NUMBER: US/10/425,115  
 ; CURRENT FILING DATE: 2003-04-28  
 ; NUMBER OF SEQ ID NOS: 369326  
 ; SEQ ID NO 223534  
 ; LENGTH: 79  
 ; TYPE: PRT  
 ; ORGANISM: Zea mays  
 ; FEATURE:  
 ; OTHER INFORMATION: Clone ID: MRT4577\_135452C.1.pep  
 US-10-425-115-223534  
 Query Match 81.1%; Score 30; DB 4; Length 79;  
 Best Local Similarity 83.3%; Pred. No. 3.2e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 YSSNLH 6  
 Db 33 YSTNLH 38  
 RESULT 50  
 US-10-425-115-193189  
 ; Sequence 193189, Application US/10425115  
 ; Publication No. US20040214272A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: La Rosa, Thomas J.  
 ; APPLICANT: Kovalic, David K.  
 ; APPLICANT: Zhou, Yihua  
 ; APPLICANT: Cao, Yongwei  
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
 ; TITLE OF INVENTION: Plants  
 ; FILE REFERENCE: 38-21(53222)B  
 ; CURRENT APPLICATION NUMBER: US/10/425,115  
 ; CURRENT FILING DATE: 2003-04-28  
 ; NUMBER OF SEQ ID NOS: 369326  
 ; SEQ ID NO 193189  
 ; LENGTH: 81

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; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_107772C.1.pap
US-10-425-115-193189

Query Match      81.1%; Score 30; DB 4; Length 81;
Best Local Similarity 83.3%; Pred. No. 3.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 YSSNLH 6
      ||:||
Db      68 YSANTLH 73

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OM protein - protein search, using sw model

Run on: April 6, 2006, 09:13:32 ; Search time 7.11864 Seconds

(without alignments)  
30.672 Million cell updates/sec

Title: US-10-089-500-7

Perfect score: 37

Sequence: 1 YSNLHS 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 184161 seqs, 31191982 residues

Total number of hits satisfying chosen parameters: 184161

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Published Applications AA New:\*

1: /SIDSS/ptodata/2/pubpaa/US08\_NEW\_PUB\_PEP.\*  
2: /SIDSS/ptodata/2/pubpaa/US06\_NEW\_PUB\_PEP.\*  
3: /SIDSS/ptodata/2/pubpaa/US07\_NEW\_PUB\_PEP.\*  
4: /SIDSS/ptodata/2/pubpaa/PCT\_NEW\_PUB\_PEP.\*  
5: /SIDSS/ptodata/2/pubpaa/US05\_NEW\_PUB\_PEP.\*  
6: /SIDSS/ptodata/2/pubpaa/US10\_NEW\_PUB\_PEP.\*  
7: /SIDSS/ptodata/2/pubpaa/US11\_NEW\_PUB\_PEP.\*  
8: /SIDSS/ptodata/2/pubpaa/US60\_NEW\_PUB\_PEP.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	IDB	Description
1	37	100.0	7	6	US-10-473-037-7 Sequence 7, Appli
2	37	100.0	108	6	US-10-473-037-10 Sequence 10, Appli
3	37	100.0	108	6	US-10-473-037-50 Sequence 50, Appli
4	37	100.0	128	6	US-10-473-037-2 Sequence 2, Appli
5	37	100.0	128	7	US-11-228-293-10 Sequence 10, Appli
6	37	100.0	128	7	US-11-228-293-19 Sequence 19, Appli
7	37	100.0	128	7	US-11-228-319-10 Sequence 10, Appli
8	37	100.0	128	7	US-11-228-319-19 Sequence 19, Appli
9	31	83.8	380	6	US-10-467-657-7258 Sequence 7258, Ap
10	30	81.1	256	7	US-11-096-568A-21861 Sequence 21861, A
11	30	81.1	323	7	US-11-096-568A-21860 Sequence 21860, A
12	30	81.1	468	7	US-11-096-568A-11620 Sequence 11620, A
13	30	81.1	470	7	US-11-096-568A-21859 Sequence 21859, A
14	30	81.1	471	7	US-11-096-568A-11619 Sequence 11619, A
15	30	81.1	502	7	US-11-096-568A-11618 Sequence 11618, A
16	30	81.1	1943	7	US-11-122-396-5 Sequence 5, Appli
17	29	78.4	99	7	US-11-195-095-14 Sequence 14, Appli
18	29	78.4	138	6	US-10-667-295-45 Sequence 45, Appli
19	29	78.4	138	7	US-11-172-740-2478 Sequence 2478, Ap
20	29	78.4	334	7	US-11-180-044-14 Sequence 14, Appli
21	29	78.4	376	7	US-11-096-568A-20218 Sequence 20218, A
22	29	78.4	392	7	US-11-096-568A-29662 Sequence 29662, A
23	29	78.4	409	7	US-11-096-568A-29661 Sequence 29661, A
24	29	78.4	496	6	US-10-793-626-1386 Sequence 1386, Ap
25	29	78.4	510	7	US-11-096-568A-29660 Sequence 29660, A

26	29	78.4	747	7	US-11-210-316-2 Sequence 2, Appli
27	28	75.7	7	6	US-10-999-866-56 Sequence 56, Appli
28	28	75.7	7	7	US-11-009-939-39 Sequence 39, Appli
29	28	75.7	10	7	US-11-004-399-1409 Sequence 1409, Ap
30	28	75.7	52	7	US-11-004-399-2238 Sequence 2238, Ap
31	28	75.7	107	6	US-10-999-866-43 Sequence 43, Appli
32	28	75.7	107	6	US-10-946-836A-10 Sequence 10, Appli
33	28	75.7	107	6	US-10-988-207-10 Sequence 10, Appli
34	28	75.7	107	6	US-11-183-205-51 Sequence 51, Appli
35	28	75.7	107	7	US-11-183-205-52 Sequence 52, Appli
36	28	75.7	108	7	US-11-009-939-37 Sequence 37, Appli
37	28	75.7	109	7	US-11-096-074-52 Sequence 52, Appli
38	28	75.7	109	7	US-11-095-822-52 Sequence 52, Appli
39	28	75.7	127	7	US-11-083-872-5 Sequence 5, Appli
40	28	75.7	214	7	US-11-025-712-11 Sequence 11, Appli
41	28	75.7	214	7	US-11-173-564-1 Sequence 1, Appli
42	28	75.7	214	7	US-11-183-205-55 Sequence 55, Appli
43	28	75.7	228	7	US-11-087-099-7721 Sequence 7721, Ap
44	28	75.7	315	7	US-11-096-568A-23186 Sequence 23186, A
45	28	75.7	537	7	US-11-098-686-10170 Sequence 10170, A
46	28	75.7	562	7	US-11-096-568A-27962 Sequence 27962, A
47	28	75.7	570	7	US-11-096-568A-27961 Sequence 27961, A
48	27	73.0	21	7	US-11-167-636-16 Sequence 16, Appli
49	27	73.0	76	7	US-11-096-568A-30950 Sequence 30950, A
50	27	73.0	84	6	US-10-485-788A-809 Sequence 809, App
51	27	73.0	84	6	US-11-053-076-193 Sequence 193, App
52	27	73.0	92	6	US-10-485-788A-673 Sequence 673, App
53	27	73.0	92	7	US-11-053-076-38 Sequence 38, Appli
54	27	73.0	99	7	US-11-096-568A-4734 Sequence 4734, Ap
55	27	73.0	182	6	US-10-467-657-4548 Sequence 4548, Ap
56	27	73.0	192	6	US-10-485-517-406 Sequence 406, App
57	27	73.0	192	6	US-10-793-626-2000 Sequence 2000, Ap
58	27	73.0	192	6	US-10-793-626-2304 Sequence 2304, Ap
59	27	73.0	196	6	US-10-793-626-2014 Sequence 2014, Ap
60	27	73.0	208	7	US-11-238-936-13 Sequence 13, Appli
61	27	73.0	210	7	US-11-096-568A-22927 Sequence 22927, A
62	27	73.0	271	7	US-11-058-817A-6 Sequence 4, Appli
63	27	73.0	272	7	US-11-058-817A-6 Sequence 6, Appli
64	27	73.0	306	7	US-11-096-568A-22926 Sequence 22926, A
65	27	73.0	314	7	US-11-058-817A-2 Sequence 2, Appli
66	27	73.0	347	7	US-11-087-099-4743 Sequence 4743, Ap
67	27	73.0	358	7	US-11-072-175-209 Sequence 209, App
68	27	73.0	360	7	US-11-087-099-10644 Sequence 10644, A
69	27	73.0	375	7	US-11-096-568A-13090 Sequence 13090, A
70	27	73.0	376	7	US-11-096-568A-30761 Sequence 30761, A
71	27	73.0	387	7	US-11-096-568A-6334 Sequence 6334, Ap
72	27	73.0	396	7	US-11-096-568A-30760 Sequence 30760, A
73	27	73.0	471	7	US-11-096-568A-13089 Sequence 13089, A
74	27	73.0	498	7	US-11-096-568A-30759 Sequence 30759, A
75	27	73.0	532	7	US-11-087-099-11945 Sequence 11945, A
76	27	73.0	633	6	US-10-467-657-3440 Sequence 3440, Ap
77	27	73.0	633	6	US-10-467-657-4632 Sequence 4632, Ap
78	27	73.0	902	7	US-11-072-512-2987 Sequence 2987, Ap
79	26	70.3	7	6	US-10-507-662-13 Sequence 13, Appli
80	26	70.3	20	7	US-11-188-187A-19 Sequence 19, Appli
81	26	70.3	20	7	US-11-188-187A-20 Sequence 20, Appli
82	26	70.3	66	7	US-11-096-568A-11449 Sequence 11449, A
83	26	70.3	87	7	US-11-096-568A-11448 Sequence 11448, A
84	26	70.3	109	7	US-11-096-568A-11447 Sequence 11447, A
85	26	70.3	111	6	US-10-507-662-37 Sequence 37, Appli
86	26	70.3	111	6	US-10-507-662-38 Sequence 38, Appli
87	26	70.3	111	7	US-11-020-772-17 Sequence 17, Appli
88	26	70.3	111	7	US-11-020-772-18 Sequence 18, Appli
89	26	70.3	111	7	US-11-076-728-17 Sequence 17, Appli
90	26	70.3	111	7	US-11-076-728-18 Sequence 18, Appli
91	26	70.3	112	7	US/11/020 Sequence 24, Appli
92	26	70.3	112	7	US-11-076-728-24 Sequence 24, Appli
93	26	70.3	126	6	US-10-501-035-225 Sequence 225, App
94	26	70.3	129	7	US-11-188-187A-2 Sequence 2, Appli
95	26	70.3	153	7	US-11-031-206-58 Sequence 58, Appli
96	26	70.3	173	7	US-11-096-568A-12090 Sequence 12090, A
97	26	70.3	180	7	US-11-223-294-1 Sequence 1, Appli
98	26	70.3	185	7	US-11-096-568A-14259 Sequence 14259, A

99	26	70.3	196	7	US-11-223-294-8	Sequence 8, Appli	172	25	67.6	110	6	US-10-648-816-8	Sequence 8, Appli
100	26	70.3	211	7	US-11-087-093-4812	Sequence 4812, Ap	173	25	67.6	113	7	US-11-076-395-16	Sequence 16, Appl
101	26	70.3	212	7	US-11-087-099-3006	Sequence 3006, Ap	174	25	67.6	113	7	US-11-076-395-21	Sequence 21, Appl
102	26	70.3	215	7	US-11-087-099-2832	Sequence 2832, Ap	175	25	67.6	113	7	US-11-076-395-70	Sequence 70, Appl
103	26	70.3	216	7	US-11-087-099-11649	Sequence 11649, A	176	25	67.6	127	7	US-11-096-568A-26718	Sequence 26718, A
104	26	70.3	225	6	US-10-467-657-3570	Sequence 3570, Ap	177	25	67.6	132	6	US-10-980-459-38	Sequence 38, Appl
105	26	70.3	226	6	US-10-467-657-6458	Sequence 6458, Ap	178	25	67.6	132	6	US-10-980-459-40	Sequence 40, Appl
106	26	70.3	226	6	US-10-467-657-8404	Sequence 8404, Ap	179	25	67.6	132	7	US-11-096-568A-26717	Sequence 26717, A
107	26	70.3	241	7	US-11-106-820-15	Sequence 15, Appl	180	25	67.6	133	7	US-11-098-686-10341	Sequence 10341, A
108	26	70.3	241	7	US-11-190-364-14	Sequence 14, Appl	181	25	67.6	134	6	US-10-980-459-34	Sequence 34, Appl
109	26	70.3	241	7	US-11-147-780-14	Sequence 14, Appl	182	25	67.6	134	7	US-11-052-554A-88	Sequence 88, Appl
110	26	70.3	245	7	US-11-054-515-1291	Sequence 1291, Ap	183	25	67.6	136	6	US-10-842-206-16	Sequence 16, Appl
111	26	70.3	245	7	US-11-266-444-1291	Sequence 1291, Ap	184	25	67.6	136	6	US-10-842-206-18	Sequence 18, Appl
112	26	70.3	250	7	US-11-113-837-2	Sequence 2, Appli	185	25	67.6	138	6	US-10-842-206-10	Sequence 10, Appl
113	26	70.3	267	7	US-11-087-099-9190	Sequence 9190, Ap	186	25	67.6	149	6	US-10-980-459-36	Sequence 36, Appl
114	26	70.3	272	6	US-10-853-807A-40	Sequence 40, Appl	187	25	67.6	155	6	US-10-842-206-12	Sequence 12, Appl
115	26	70.3	292	6	US-10-793-626-2636	Sequence 2636, Ap	188	25	67.6	157	7	US-11-096-568A-32742	Sequence 32742, A
116	26	70.3	311	7	US-11-096-568A-5368	Sequence 5368, Ap	189	25	67.6	158	6	US-10-842-206-20	Sequence 20, Appl
117	26	70.3	336	7	US-11-096-568A-5367	Sequence 5367, Ap	190	25	67.6	158	6	US-10-980-459-4	Sequence 4, Appli
118	26	70.3	345	7	US-11-096-568A-6152	Sequence 6152, Ap	191	25	67.6	160	7	US-11-096-568A-32741	Sequence 32741, A
119	26	70.3	372	7	US-11-096-568A-5366	Sequence 5366, Ap	192	25	67.6	169	7	US-11-096-568A-6494	Sequence 6494, Ap
120	26	70.3	389	6	US-10-257-143B-4	Sequence 4, Appli	193	25	67.6	170	7	US-11-172-740-2013	Sequence 2013, Ap
121	26	70.3	423	7	US-11-098-686-11089	Sequence 11089, A	194	25	67.6	171	7	US-11-096-568A-32740	Sequence 32740, A
122	26	70.3	439	6	US-11-031-206-60	Sequence 60, Appl	195	25	67.6	171	7	US-11-172-740-2012	Sequence 2012, Ap
123	26	70.3	443	6	US-10-793-626-1200	Sequence 1200, Ap	196	25	67.6	172	7	US-11-087-099-501	Sequence 501, App
124	26	70.3	445	6	US-10-793-626-2844	Sequence 2844, Ap	197	25	67.6	179	6	US-10-842-206-6	Sequence 6, Appli
125	26	70.3	485	7	US-11-165-211-47	Sequence 47, Appl	198	25	67.6	179	6	US-10-842-206-24	Sequence 24, Appl
126	26	70.3	485	7	US-11-165-226-57	Sequence 57, Appl	199	25	67.6	179	6	US-10-980-459-7	Sequence 7, Appli
127	26	70.3	507	7	US-11-033-039-96	Sequence 96, Appl	200	25	67.6	179	6	US-10-980-459-10	Sequence 10, Appl
128	26	70.3	550	7	US-11-113-837-17	Sequence 17, Appl	201	25	67.6	183	6	US-10-842-206-14	Sequence 14, Appl
129	26	70.3	580	7	US-11-072-512-2103	Sequence 2103, Ap	202	25	67.6	185	6	US-10-842-206-8	Sequence 8, Appli
130	26	70.3	635	7	US-11-113-837-16	Sequence 16, Appl	203	25	67.6	188	6	US-10-842-206-40	Sequence 40, Appl
131	26	70.3	665	6	US-10-506-454-407	Sequence 407, App	204	25	67.6	188	6	US-10-980-459-32	Sequence 32, Appl
132	26	70.3	709	7	US-11-074-176-158	Sequence 158, App	205	25	67.6	197	6	US-11-096-568A-6015	Sequence 6015, Ap
133	26	70.3	892	7	US-11-237-600-4	Sequence 4, Appli	206	25	67.6	197	6	US-10-842-206-39	Sequence 39, Appl
134	26	70.3	925	6	US-10-453-372-1124	Sequence 1124, Ap	207	25	67.6	197	7	US-11-096-568A-29604	Sequence 29604, A
135	26	70.3	966	6	US-10-877-346-32	Sequence 32, Appl	208	25	67.6	198	6	US-10-793-626-2188	Sequence 2188, Ap
136	26	70.3	972	6	US-10-453-372-1128	Sequence 1128, Ap	209	25	67.6	199	6	US-10-647-072-2	Sequence 2, Appli
137	26	70.3	1168	6	US-10-509-422-2	Sequence 2, Appli	210	25	67.6	200	6	US-10-842-206-38	Sequence 38, Appl
138	26	70.3	1613	6	US-10-055-877-145	Sequence 145, App	211	25	67.6	200	6	US-10-980-459-28	Sequence 28, Appl
139	26	70.3	1637	6	US-10-055-877-144	Sequence 144, App	212	25	67.6	201	7	US-11-094-519A-45	Sequence 45, Appl
140	26	70.3	1735	6	US-10-495-083-3	Sequence 3, Appli	213	25	67.6	201	6	US-10-842-206-37	Sequence 37, Appl
141	26	70.3	2223	6	US-10-895-064-388	Sequence 388, App	214	25	67.6	203	6	US-10-980-459-26	Sequence 26, Appl
142	26	70.3	2723	7	US-11-129-741-388	Sequence 388, App	215	25	67.6	203	6	US-10-842-206-37	Sequence 37, Appl
143	26	70.3	2723	7	US-11-129-741-3318	Sequence 3318, Ap	216	25	67.6	206	6	US-10-055-877-192	Sequence 192, App
144	26	70.3	3069	7	US-11-235-732-2	Sequence 2, Appli	217	25	67.6	207	7	US-11-072-512-2278	Sequence 2278, Ap
145	26	70.3	3095	7	US-11-235-732-4	Sequence 4, Appli	218	25	67.6	209	6	US-10-980-459-24	Sequence 24, Appl
146	26	70.3	3100	7	US-11-235-732-7	Sequence 7, Appli	219	25	67.6	210	7	US-11-087-099-1044	Sequence 1044, Ap
147	26	70.3	3567	6	US-10-453-372-1112	Sequence 1112, Ap	220	25	67.6	211	6	US-10-842-206-2	Sequence 2, Appli
148	26	70.3	8746	7	US-11-098-686-10232	Sequence 10232, A	221	25	67.6	211	6	US-10-842-206-4	Sequence 4, Appli
149	25	67.6	9	6	US-10-895-064-2180	Sequence 2180, Ap	222	25	67.6	211	6	US-10-842-206-22	Sequence 22, Appl
150	25	67.6	9	7	US-11-129-741-2180	Sequence 2180, Ap	223	25	67.6	211	6	US-10-842-206-36	Sequence 36, Appl
151	25	67.6	11	6	US-10-510-824-3	Sequence 3, Appli	224	25	67.6	211	6	US-10-980-459-2	Sequence 2, Appli
152	25	67.6	19	7	US-11-038-980-1	Sequence 1, Appli	225	25	67.6	211	6	US-10-980-459-22	Sequence 22, Appl
153	25	67.6	19	7	US-11-038-980-2	Sequence 2, Appli	226	25	67.6	211	7	US-11-216-660-2	Sequence 2, Appli
154	25	67.6	20	7	US-11-167-636-18	Sequence 18, Appl	227	25	67.6	214	6	US-10-793-626-1898	Sequence 1898, Ap
155	25	67.6	23	7	US-11-038-980-7	Sequence 7, Appli	228	25	67.6	218	6	US-10-506-454-886	Sequence 886, App
156	25	67.6	23	7	US-11-038-980-8	Sequence 8, Appli	229	25	67.6	222	6	US-10-793-626-1510	Sequence 1510, Ap
157	25	67.6	25	7	US-11-038-980-16	Sequence 16, Appl	230	25	67.6	223	6	US-10-793-626-1234	Sequence 1234, Ap
158	25	67.6	83	7	US-11-038-980-17	Sequence 17, Appl	231	25	67.6	224	6	US-10-793-626-1002	Sequence 1002, Ap
159	25	67.6	83	7	US-11-096-568A-32448	Sequence 32448, A	232	25	67.6	226	6	US-10-510-941-10	Sequence 10, Appl
160	25	67.6	88	7	US-11-004-393-2143	Sequence 2143, Ap	233	25	67.6	234	6	US-10-793-626-1380	Sequence 1380, Ap
161	25	67.6	164	25	US-11-096-568A-32447	Sequence 32447, A	234	25	67.6	244	7	US-11-096-568A-2924	Sequence 2924, Ap
162	25	67.6	108	7	US-11-208-422-7	Sequence 7, Appli	235	25	67.6	244	7	US-11-096-568A-2925	Sequence 2925, Ap
163	25	67.6	108	7	US-11-208-422-9	Sequence 9, Appli	236	25	67.6	245	7	US-11-096-568A-6014	Sequence 6014, Ap
164	25	67.6	108	7	US-11-208-422-11	Sequence 11, Appl	237	25	67.6	252	7	US-11-096-568A-6493	Sequence 6493, Ap
165	25	67.6	110	6	US-10-648-816-1	Sequence 1, Appli	238	25	67.6	265	7	US-11-096-568A-29603	Sequence 29603, A
166	25	67.6	110	6	US-10-648-816-2	Sequence 2, Appli	239	25	67.6	283	7	US-11-096-568A-6013	Sequence 6013, Ap
167	25	67.6	110	6	US-10-648-816-3	Sequence 3, Appli	240	25	67.6	292	7	US-11-096-568A-2922	Sequence 2922, Ap
168	25	67.6	110	6	US-10-648-816-4	Sequence 4, Appli	241	25	67.6	309	7	US-11-087-099-3288	Sequence 3288, Ap
169	25	67.6	110	6	US-10-648-816-5	Sequence 5, Appli	242	25	67.6	309	7	US-11-087-099-10759	Sequence 10759, A
170	25	67.6	110	6	US-10-648-816-6	Sequence 6, Appli	243	25	67.6	311	5	US-09-978-360A-800	Sequence 800, App
171	25	67.6	110	6	US-10-648-816-7	Sequence 7, Appli	244	25	67.6	317	7	US-11-096-568A-6492	Sequence 6492, Ap

245	25	67.6	332	7	US-11-172-740-1674	Sequence 1674, Ap	318	25	67.6	2602	6	US-10-453-372-716	Sequence 716, App
246	25	67.6	337	6	US-10-793-626-148	Sequence 148, App	319	25	67.6	2617	6	US-10-453-372-666	Sequence 666, App
247	25	67.6	337	6	US-10-793-626-156	Sequence 156, App	320	25	67.6	2617	6	US-10-453-372-732	Sequence 732, App
248	25	67.6	337	6	US-10-793-626-458	Sequence 458, App	321	25	67.6	2617	6	US-10-453-372-734	Sequence 734, App
249	25	67.6	337	6	US-10-793-626-1152	Sequence 1152, App	322	25	67.6	2617	6	US-10-453-372-736	Sequence 736, App
250	25	67.6	337	6	US-10-793-626-1158	Sequence 1198, Ap	323	25	67.6	2617	6	US-10-453-372-738	Sequence 738, App
251	25	67.6	337	6	US-10-793-626-1230	Sequence 1220, Ap	324	25	67.6	2617	6	US-10-453-372-740	Sequence 740, App
252	25	67.6	337	6	US-10-793-626-1384	Sequence 1384, Ap	325	25	67.6	2617	6	US-10-453-372-742	Sequence 742, App
253	25	67.6	337	6	US-10-793-626-2044	Sequence 2044, Ap	326	25	67.6	2617	6	US-10-453-372-744	Sequence 744, App
254	25	67.6	337	6	US-10-793-626-2154	Sequence 2154, Ap	327	25	67.6	2617	6	US-10-453-372-746	Sequence 746, App
255	25	67.6	337	6	US-10-793-626-2196	Sequence 2196, Ap	328	25	67.6	2617	6	US-10-453-372-748	Sequence 748, App
256	25	67.6	337	6	US-10-793-626-2786	Sequence 2786, Ap	329	25	67.6	2617	6	US-10-453-372-750	Sequence 750, App
257	25	67.6	344	7	US-11-174-816-46	Sequence 46, Appl	330	24	64.9	9	7	US-11-136-079-603	Sequence 603, App
258	25	67.6	344	7	US-11-174-816-47	Sequence 47, Appl	331	24	64.9	15	7	US-11-044-899-17	Sequence 17, Appl
259	25	67.6	344	7	US-11-174-816-62	Sequence 62, Appl	332	24	64.9	16	7	US-11-152-974A-208	Sequence 208, App
260	25	67.6	344	7	US-11-174-819-30	Sequence 30, Appl	333	24	64.9	16	7	US-11-153-143A-208	Sequence 208, App
261	25	67.6	344	7	US-11-174-819-32	Sequence 32, Appl	334	24	64.9	59	6	US-10-467-657-972	Sequence 972, App
262	25	67.6	344	7	US-11-174-819-81	Sequence 81, Appl	335	24	64.9	93	6	US-10-467-657-8150	Sequence 8150, Ap
263	25	67.6	357	7	US-11-096-568A-29602	Sequence 29602, A	336	24	64.9	96	7	US-11-096-568A-957	Sequence 957, App
264	25	67.6	368	7	US-11-096-568A-23842	Sequence 29842, A	337	24	64.9	106	7	US-11-096-568A-27368	Sequence 27368, A
265	25	67.6	379	7	US-11-087-099-4820	Sequence 4820, Ap	338	24	64.9	107	6	US-10-946-836A-16	Sequence 16, Appl
266	25	67.6	402	7	US-11-096-568A-25398	Sequence 25398, A	339	24	64.9	107	6	US-10-946-836A-18	Sequence 18, Appl
267	25	67.6	405	7	US-11-096-568A-1768	Sequence 1768, Ap	340	24	64.9	107	6	US-10-988-207-16	Sequence 16, Appl
268	25	67.6	406	7	US-11-096-568A-1767	Sequence 1767, Ap	341	24	64.9	107	6	US-10-988-207-18	Sequence 18, Appl
269	25	67.6	419	7	US-11-087-099-1147	Sequence 1147, Ap	342	24	64.9	107	6	US-10-988-207-25	Sequence 25, Appl
270	25	67.6	419	7	US-11-087-099-10715	Sequence 110715, A	343	24	64.9	108	6	US-10-988-207-25	Sequence 25, Appl
271	25	67.6	420	7	US-11-229-371-90	Sequence 90, Appl	344	24	64.9	109	7	US-11-023-366A-201	Sequence 201, App
272	25	67.6	420	7	US-11-228-923-90	Sequence 90, Appl	345	24	64.9	114	6	US-10-667-295-92	Sequence 92, Appl
273	25	67.6	420	7	US-11-228-875-90	Sequence 90, Appl	346	24	64.9	114	7	US-11-172-740-2477	Sequence 2477, Ap
274	25	67.6	425	7	US-11-096-568A-1766	Sequence 1766, Ap	347	24	64.9	120	7	US-11-098-686-11219	Sequence 11219, A
275	25	67.6	428	7	US-11-096-568A-25584	Sequence 25584, A	348	24	64.9	155	7	US-11-098-686-10463	Sequence 10463, A
276	25	67.6	431	6	US-10-995-561-807	Sequence 807, App	349	24	64.9	173	7	US-11-098-686-10463	Sequence 10463, A
277	25	67.6	431	6	US-10-995-561-808	Sequence 808, App	350	24	64.9	181	6	US-10-980-388-100	Sequence 100, App
278	25	67.6	431	6	US-11-186-284-161	Sequence 186, Ap	351	24	64.9	192	7	US-11-096-568A-18152	Sequence 18152, A
279	25	67.6	431	7	US-11-183-205-34	Sequence 34, Appl	352	24	64.9	224	7	US-11-096-568A-18151	Sequence 18151, A
280	25	67.6	460	7	US-11-182-016-28	Sequence 28, Appl	353	24	64.9	234	7	US-11-096-568A-32205	Sequence 32205, A
281	25	67.6	466	7	US-11-052-554A-22	Sequence 22, Appl	354	24	64.9	240	7	US-11-096-568A-32204	Sequence 32204, A
282	25	67.6	467	7	US-11-096-568A-25397	Sequence 25397, A	355	24	64.9	242	7	US-11-096-568A-32219	Sequence 32219, A
283	25	67.6	477	6	US-10-540-091-2	Sequence 2, Appl1	356	24	64.9	244	7	US-11-096-568A-2964	Sequence 2964, Ap
284	25	67.6	494	6	US-11-094-519A-35	Sequence 35, Appl	357	24	64.9	244	7	US-11-096-568A-2967	Sequence 2967, Ap
285	25	67.6	509	6	US-10-506-454-1111	Sequence 1111, Ap	358	24	64.9	244	7	US-11-172-740-896	Sequence 896, App
286	25	67.6	518	6	US-11-096-568A-25396	Sequence 25396, A	359	24	64.9	246	7	US-11-096-568A-32203	Sequence 32203, A
287	25	67.6	528	6	US-10-858-730-88	Sequence 88, Appl	360	24	64.9	256	7	US-11-096-568A-16584	Sequence 16584, A
288	25	67.6	528	6	US-10-858-730-89	Sequence 89, Appl	361	24	64.9	259	7	US-11-122-524-2	Sequence 2, Appl1
289	25	67.6	530	6	US-10-858-730-232	Sequence 232, App	362	24	64.9	260	6	US-10-055-877-166	Sequence 166, App
290	25	67.6	531	7	US-11-087-099-891	Sequence 891, App	363	24	64.9	261	6	US-10-055-877-164	Sequence 164, App
291	25	67.6	543	7	US-11-106-672A-10	Sequence 10, Appl	364	24	64.9	261	6	US-10-055-877-165	Sequence 165, App
292	25	67.6	543	7	US-11-057-732-6	Sequence 6, Appl1	365	24	64.9	261	7	US-11-177-506-31	Sequence 31, Appl
293	25	67.6	543	7	US-11-154-805A-5	Sequence 5, Appl1	366	24	64.9	263	7	US-11-096-568A-22718	Sequence 22718, A
294	25	67.6	556	7	US-11-072-512-3914	Sequence 3914, Ap	367	24	64.9	263	7	US-11-096-568A-23687	Sequence 23687, A
295	25	67.6	556	7	US-11-077-619-60	Sequence 60, Appl	368	24	64.9	268	7	US-11-055-822-936	Sequence 926, App
296	25	67.6	563	7	US-11-072-512-3392	Sequence 3392, Ap	369	24	64.9	277	7	US-11-126-817-54	Sequence 54, Appl
297	25	67.6	592	7	US-11-106-672A-14	Sequence 14, Appl	370	24	64.9	278	7	US-11-113-424-43	Sequence 43, Appl
298	25	67.6	622	7	US-11-098-686-11191	Sequence 11191, A	371	24	64.9	285	7	US-11-037-243-88	Sequence 88, Appl
299	25	67.6	642	7	US-11-098-686-10457	Sequence 10457, A	372	24	64.9	304	6	US-10-506-454-667	Sequence 667, App
300	25	67.6	686	7	US-11-051-724-46	Sequence 46, Appl	373	24	64.9	309	7	US-11-156-084-200	Sequence 200, App
301	25	67.6	686	7	US-11-051-724-48	Sequence 48, Appl	374	24	64.9	309	7	US-11-087-099-6874	Sequence 6874, Ap
302	25	67.6	686	7	US-11-051-724-50	Sequence 50, Appl	375	24	64.9	311	7	US-11-098-686-11245	Sequence 11245, A
303	25	67.6	686	7	US-11-051-724-52	Sequence 52, Appl	376	24	64.9	322	7	US-11-156-084-318	Sequence 318, App
304	25	67.6	756	7	US-11-072-175-218	Sequence 218, App	377	24	64.9	323	7	US-11-087-099-408	Sequence 408, App
305	25	67.6	773	7	US-11-124-367A-505	Sequence 505, App	378	24	64.9	327	7	US-11-096-568A-4231	Sequence 4231, Ap
306	25	67.6	773	7	US-11-124-367A-506	Sequence 506, App	379	24	64.9	340	7	US-11-098-686-10918	Sequence 10918, A
307	25	67.6	799	7	US-11-072-512-2929	Sequence 2929, Ap	380	24	64.9	340	7	US-11-087-099-5679	Sequence 5679, Ap
308	25	67.6	855	6	US-10-506-454-146	Sequence 146, App	381	24	64.9	340	7	US-11-087-099-9402	Sequence 9402, Ap
309	25	67.6	961	7	US-11-051-724-42	Sequence 42, Appl	382	24	64.9	342	6	US-10-980-388-118	Sequence 118, App
310	25	67.6	1085	6	US-10-523-477-13	Sequence 13, Appl	383	24	64.9	342	7	US-11-174-816-18	Sequence 18, Appl
311	25	67.6	1098	6	US-11-072-512-2475	Sequence 2475, Ap	384	24	64.9	342	7	US-11-174-819-71	Sequence 71, Appl
312	25	67.6	1115	6	US-10-055-877-160	Sequence 160, App	385	24	64.9	342	7	US-11-174-751-19	Sequence 19, Appl
313	25	67.6	1138	6	US-10-509-422-4	Sequence 4, Appl1	386	24	64.9	344	7	US-11-174-816-45	Sequence 45, Appl
314	25	67.6	1411	6	US-10-453-372-1106	Sequence 1106, Ap	387	24	64.9	344	7	US-11-174-819-28	Sequence 28, Appl
315	25	67.6	1436	6	US-10-453-372-1094	Sequence 1094, Ap	388	24	64.9	344	7	US-11-096-568A-5551	Sequence 5551, Ap
316	25	67.6	1591	6	US-10-453-372-1092	Sequence 1092, Ap	389	24	64.9	346	7	US-11-096-568A-7777	Sequence 7777, Ap
317	25	67.6	2593	6	US-10-453-372-718	Sequence 718, App	390	24	64.9	348	7	US-11-087-099-6269	Sequence 6269, Ap

391	24	64.9	349	7	US-11-123-893-13	Sequence 13, Appl	464	24	64.9	745	7	US-11-091-018-4	Sequence 4, Appl
392	24	64.9	349	7	US-11-096-568A-4230	Sequence 4230, Ap	465	24	64.9	747	6	US-10-492-835-8	Sequence 8, Appl
393	24	64.9	350	7	US-11-096-568A-48150	Sequence 18150, A	466	24	64.9	747	6	US-10-492-835-15	Sequence 15, Appl
394	24	64.9	359	7	US-11-087-099-10369	Sequence 10369, A	467	24	64.9	747	6	US-10-492-835-27	Sequence 27, Appl
395	24	64.9	363	7	US-11-096-568A-5550	Sequence 5550, Ap	468	24	64.9	748	6	US-10-492-835-12	Sequence 12, Appl
396	24	64.9	369	7	US-11-096-568A-5549	Sequence 5549, Ap	469	24	64.9	748	6	US-10-492-835-28	Sequence 28, Appl
397	24	64.9	373	7	US-11-096-568A-4229	Sequence 4229, Ap	470	24	64.9	756	7	US-11-096-568A-27530	Sequence 27530, A
398	24	64.9	379	7	US-11-096-568A-5264	Sequence 5264, Ap	471	24	64.9	763	7	US-11-087-039-8573	Sequence 8573, Ap
399	24	64.9	388	6	US-10-527-500-61	Sequence 61, Appl	472	24	64.9	765	6	US-10-821-234-1164	Sequence 1164, Ap
400	24	64.9	390	7	US-11-055-822-924	Sequence 924, Ap	473	24	64.9	792	6	US-10-467-657-6026	Sequence 6026, Ap
401	24	64.9	392	7	US-11-096-568A-5263	Sequence 5263, Ap	474	24	64.9	792	6	US-10-467-657-7528	Sequence 7528, Ap
402	24	64.9	401	7	US-11-096-568A-5262	Sequence 5262, Ap	475	24	64.9	792	7	US-11-103-957-92	Sequence 92, Appl
403	24	64.9	402	6	US-10-506-454-1143	Sequence 1143, Ap	476	24	64.9	809	7	US-11-091-018-2	Sequence 2, Appl
404	24	64.9	412	7	US-11-282-495-2	Sequence 2, Appl	477	24	64.9	811	7	US-11-072-512-3559	Sequence 3559, Ap
405	24	64.9	415	6	US-10-467-657-7774	Sequence 7774, Ap	478	24	64.9	814	7	US-11-096-568A-27529	Sequence 27529, A
406	24	64.9	417	6	US-10-506-454-424	Sequence 424, Ap	479	24	64.9	882	7	US-11-096-568A-31243	Sequence 31243, A
407	24	64.9	418	7	US-11-098-686-10385	Sequence 10385, A	480	24	64.9	914	7	US-11-087-099-6835	Sequence 6835, Ap
408	24	64.9	425	7	US-11-087-099-2316	Sequence 2316, Ap	481	24	64.9	919	7	US-11-096-568A-27465	Sequence 27465, Ap
409	24	64.9	432	7	US-11-169-041-140	Sequence 140, App	482	24	64.9	941	7	US-11-096-568A-29375	Sequence 29375, A
410	24	64.9	435	7	US-11-010-238-113	Sequence 113, App	483	24	64.9	952	7	US-11-087-039-3514	Sequence 3514, Ap
411	24	64.9	438	7	US-11-096-568A-11315	Sequence 11315, A	484	24	64.9	952	7	US-11-087-039-7009	Sequence 7009, Ap
412	24	64.9	441	6	US-10-821-234-1668	Sequence 1668, Ap	485	24	64.9	979	6	US-10-636-320-6	Sequence 6, Appl
413	24	64.9	442	7	US-11-096-568A-11314	Sequence 11314, A	486	24	64.9	988	7	US-11-096-568A-29775	Sequence 29775, A
414	24	64.9	453	7	US-11-096-568A-11313	Sequence 11313, A	487	24	64.9	1014	7	US-11-096-568A-29936	Sequence 29936, A
415	24	64.9	458	7	US-11-096-568A-7137	Sequence 7137, Ap	488	24	64.9	1015	7	US-11-096-568A-29935	Sequence 29935, A
416	24	64.9	461	7	US-11-096-568A-7136	Sequence 7136, Ap	489	24	64.9	1019	7	US-11-096-568A-29934	Sequence 29934, A
417	24	64.9	463	7	US-11-072-512-2880	Sequence 2880, Ap	490	24	64.9	1023	7	US-11-096-568A-27464	Sequence 27464, A
418	24	64.9	463	7	US-11-087-099-7012	Sequence 7012, Ap	491	24	64.9	1035	7	US-11-096-568A-27463	Sequence 27463, A
419	24	64.9	465	7	US-11-096-568A-16582	Sequence 16582, A	492	24	64.9	1050	7	US-11-096-568A-29374	Sequence 29374, A
420	24	64.9	467	7	US-11-096-568A-7776	Sequence 7776, Ap	493	24	64.9	1124	7	US-11-090-617-688	Sequence 688, App
421	24	64.9	468	7	US-11-087-099-9301	Sequence 9301, Ap	494	24	64.9	1132	7	US-11-096-568A-29373	Sequence 29373, A
422	24	64.9	469	7	US-11-096-568A-7775	Sequence 7775, Ap	495	24	64.9	1163	7	US-11-044-839-2	Sequence 2, Appl
423	24	64.9	472	7	US-11-150-845-48	Sequence 48, Appl	496	24	64.9	1163	7	US-11-044-839-30	Sequence 30, Appl
424	24	64.9	481	6	US-10-995-561-959	Sequence 959, App	497	24	64.9	1167	6	US-10-601-368-18	Sequence 18, Appl
425	24	64.9	490	7	US-11-096-568A-27963	Sequence 27963, A	498	24	64.9	1247	7	US-11-096-568A-29240	Sequence 29240, A
426	24	64.9	492	6	US-10-467-962B-51	Sequence 51, Appl	499	24	64.9	1254	7	US-11-096-568A-29335	Sequence 29335, A
427	24	64.9	492	6	US-10-501-035-359	Sequence 359, App	500	24	64.9	1302	7	US-11-004-057-6	Sequence 6, Appl
428	24	64.9	494	6	US-10-934-944-236	Sequence 236, App	501	24	64.9	1302	7	US-11-210-471-2	Sequence 2, Appl
429	24	64.9	494	7	US-11-116-881A-245	Sequence 245, App	502	24	64.9	1351	7	US-11-129-741-2937	Sequence 2937, Ap
430	24	64.9	495	7	US-11-072-512-2860	Sequence 2860, Ap	503	24	64.9	1351	7	US-11-129-741-3655	Sequence 3655, Ap
431	24	64.9	501	7	US-11-172-740-441	Sequence 441, App	504	24	64.9	1419	7	US-11-124-367A-324	Sequence 324, App
432	24	64.9	507	7	US-11-091-018-10	Sequence 10, Appl	505	24	64.9	1485	7	US-11-124-367A-320	Sequence 320, App
433	24	64.9	508	7	US-11-183-567A-1	Sequence 1, Appl	506	24	64.9	1485	7	US-11-169-041-181	Sequence 181, App
434	24	64.9	515	6	US-10-467-657-4680	Sequence 4680, Ap	507	24	64.9	1493	7	US-11-004-057-4	Sequence 4, Appl
435	24	64.9	516	7	US-11-052-554A-335	Sequence 335, App	508	24	64.9	1493	7	US-11-004-057-21	Sequence 21, Appl
436	24	64.9	516	7	US-11-096-568A-34183	Sequence 34183, A	509	24	64.9	1493	7	US-11-210-471-8	Sequence 8, Appl
437	24	64.9	526	7	US-11-096-568A-34182	Sequence 34182, A	510	24	64.9	1571	7	US-11-134-587B-13	Sequence 13, Appl
438	24	64.9	527	7	US-11-098-686-10607	Sequence 10607, A	511	24	64.9	1571	7	US-11-134-587B-12	Sequence 12, Appl
439	24	64.9	542	7	US-11-214-199-44	Sequence 44, Appl	512	24	64.9	1813	6	US-10-495-083-10	Sequence 10, Appl
440	24	64.9	552	7	US-11-232-408A-4	Sequence 4, Appl	513	24	64.9	1813	6	US-10-495-083-10	Sequence 10, Appl
441	24	64.9	576	7	US-11-098-686-10763	Sequence 10763, A	514	24	64.9	1910	7	US-11-134-587B-3	Sequence 3, Appl
442	24	64.9	583	7	US-11-096-568A-27885	Sequence 27885, A	515	24	64.9	1910	7	US-11-134-587B-2	Sequence 2, Appl
443	24	64.9	585	7	US-11-091-018-9	Sequence 9, Appl	516	24	64.9	2080	6	US-10-821-234-1640	Sequence 1640, Ap
444	24	64.9	599	7	US-11-087-099-447	Sequence 447, App	517	24	64.9	2250	6	US-10-922-232B-57	Sequence 57, Appl
445	24	64.9	619	7	US-11-096-568A-2576	Sequence 2576, Ap	518	24	64.9	4060	6	US-10-922-232B-55	Sequence 55, Appl
446	24	64.9	619	7	US-11-096-568A-28016	Sequence 28016, A	519	24	64.9	4060	6	US-10-922-232B-56	Sequence 56, Appl
447	24	64.9	626	7	US-11-098-686-10124	Sequence 10124, A	520	23	62.2	6738	7	US-11-033-039-324	Sequence 324, App
448	24	64.9	627	7	US-11-150-845-47	Sequence 47, Appl	521	23	62.2	11	7	US-11-203-251A-8	Sequence 8, Appl
449	24	64.9	642	7	US-11-072-175-172	Sequence 172, App	522	23	62.2	11	7	US-11-203-251A-73	Sequence 73, Appl
450	24	64.9	668	7	US-11-096-568A-31245	Sequence 31245, A	523	23	62.2	12	7	US-11-166-412-176	Sequence 176, App
451	24	64.9	671	7	US-11-096-568A-28178	Sequence 28178, A	524	23	62.2	14	7	US-11-033-039-340	Sequence 340, App
452	24	64.9	672	7	US-11-004-057-2	Sequence 2, Appl	525	23	62.2	15	6	US-10-895-064-2329	Sequence 2329, Ap
453	24	64.9	673	7	US-11-096-568A-28177	Sequence 28177, A	526	23	62.2	15	7	US-11-129-741-2229	Sequence 94, Appl
454	24	64.9	687	7	US-11-091-018-8	Sequence 6, Appl	527	23	62.2	20	7	US-11-247-423-94	Sequence 95, Appl
455	24	64.9	690	7	US-11-052-554A-99	Sequence 99, Appl	528	23	62.2	20	7	US-11-247-423-95	Sequence 96, Appl
456	24	64.9	690	7	US-11-096-568A-31244	Sequence 31244, A	529	23	62.2	20	7	US-11-247-423-96	Sequence 97, Appl
457	24	64.9	700	7	US-11-169-630-5	Sequence 5, Appl	530	23	62.2	20	7	US-11-247-423-97	Sequence 98, Appl
458	24	64.9	712	7	US-11-096-568A-29777	Sequence 29777, A	531	23	62.2	20	7	US-11-247-423-98	Sequence 99, Appl
459	24	64.9	715	7	US-11-096-568A-28176	Sequence 28176, A	532	23	62.2	20	7	US-11-247-423-99	Sequence 100, App
460	24	64.9	715	7	US-11-096-568A-29776	Sequence 29776, A	533	23	62.2	20	7	US-11-247-423-100	Sequence 104, App
461	24	64.9	742	7	US-11-127-877-43	Sequence 43, Appl	534	23	62.2	20	7	US-11-247-423-105	Sequence 105, App
462	24	64.9	743	7	US-11-096-568A-27531	Sequence 27531, A	535	23	62.2	20	7	US-11-167-636-63	Sequence 63, Appl
463	24	64.9	743	7			536	23	62.2	23	7		

537	23	62.2	34	7	US-11-112-277-6	Sequence 6, Appli	610	23	62.2	225	7	US-11-151-598-7	Sequence 7, Appli
538	23	62.2	34	7	US-11-112-277-38	Sequence 38, Appli	611	23	62.2	225	7	US-11-151-598-8	Sequence 8, Appli
539	23	62.2	34	7	US-11-151-598-10	Sequence 10, Appli	612	23	62.2	227	7	US-11-151-598-9	Sequence 9, Appli
540	23	62.2	34	7	US-11-151-598-12	Sequence 12, Appli	613	23	62.2	228	6	US-10-467-657-156	Sequence 156, App
541	23	62.2	35	7	US-11-112-277-7	Sequence 7, Appli	614	23	62.2	231	7	US-11-096-568A-16541	Sequence 16541, A
542	23	62.2	35	6	US-11-112-277-37	Sequence 37, Appli	615	23	62.2	235	7	US-11-159-597-2	Sequence 2, Appli
543	23	62.2	36	6	US-10-841-956A-1	Sequence 1, Appli	616	23	62.2	235	7	US-11-219-359-5	Sequence 5, Appli
544	23	62.2	36	7	US-11-029-003-1	Sequence 1, Appli	617	23	62.2	237	6	US-10-644-807-401	Sequence 401, App
545	23	62.2	36	7	US-11-187-687-22	Sequence 22, Appli	618	23	62.2	237	7	US-11-104-111-16	Sequence 16, Appli
546	23	62.2	37	7	US-11-112-277-33	Sequence 33, Appli	619	23	62.2	241	6	US-10-467-657-4474	Sequence 4474, Ap
547	23	62.2	38	7	US-11-151-598-4	Sequence 4, Appli	620	23	62.2	244	6	US-10-510-959-7	Sequence 7, Appli
548	23	62.2	44	6	US-10-729-121-52	Sequence 52, Appli	621	23	62.2	244	6	US-11-096-568A-5521	Sequence 5521, Ap
549	23	62.2	44	7	US-11-187-687-24	Sequence 24, Appli	622	23	62.2	245	6	US-10-644-807-215	Sequence 215, App
550	23	62.2	44	7	US-11-285-537-52	Sequence 52, Appli	623	23	62.2	245	6	US-10-644-807-305	Sequence 305, App
551	23	62.2	47	7	US-11-151-598-5	Sequence 5, Appli	624	23	62.2	251	6	US-10-510-959-6	Sequence 6, Appli
552	23	62.2	53	7	US-11-004-399-2805	Sequence 2805, Ap	625	23	62.2	251	6	US-10-510-959-10	Sequence 10, Appli
553	23	62.2	63	7	US-11-078-735-2	Sequence 2, Appli	626	23	62.2	252	6	US-10-510-959-4	Sequence 4, Appli
554	23	62.2	63	7	US-11-078-735-3	Sequence 3, Appli	627	23	62.2	252	6	US-10-510-959-8	Sequence 8, Appli
555	23	62.2	63	7	US-11-078-735-4	Sequence 4, Appli	628	23	62.2	252	6	US-10-510-959-11	Sequence 11, Appli
556	23	62.2	63	7	US-11-000-463-353	Sequence 353, App	629	23	62.2	255	6	US-10-467-657-6148	Sequence 6148, Ap
557	23	62.2	63	7	US-11-000-463-825	Sequence 825, App	630	23	62.2	255	6	US-10-467-657-7562	Sequence 7562, Ap
558	23	62.2	63	7	US-11-050-346-47	Sequence 47, Appli	631	23	62.2	257	6	US-10-793-626-3244	Sequence 3244, Ap
559	23	62.2	63	7	US-11-050-346-48	Sequence 48, Appli	632	23	62.2	257	6	US-11-074-176-220	Sequence 220, App
560	23	62.2	63	7	US-11-050-346-49	Sequence 49, Appli	633	23	62.2	261	7	US-11-096-568A-8861	Sequence 8861, Ap
561	23	62.2	63	7	US-11-103-077-2	Sequence 2, Appli	634	23	62.2	262	7	US-11-087-099-7815	Sequence 7815, Ap
562	23	62.2	63	7	US-11-103-077-3	Sequence 3, Appli	635	23	62.2	263	7	US-11-214-199-48	Sequence 48, Appli
563	23	62.2	63	7	US-11-103-077-4	Sequence 4, Appli	636	23	62.2	264	7	US-11-214-199-46	Sequence 46, Appli
564	23	62.2	81	7	US-11-020-772-9	Sequence 9, Appli	637	23	62.2	264	7	US-11-096-568A-14569	Sequence 14569, A
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566	23	62.2	89	7	US-11-120-308-104	Sequence 104, App	639	23	62.2	266	6	US-10-454-437-284	Sequence 284, App
567	23	62.2	89	7	US-11-120-308-112	Sequence 112, App	640	23	62.2	267	6	US-10-841-956A-4	Sequence 4, Appli
568	23	62.2	96	6	US-10-821-234-1351	Sequence 1351, App	641	23	62.2	267	7	US-11-151-598-2	Sequence 2, Appli
569	23	62.2	102	6	US-10-841-956A-18	Sequence 18, Appli	642	23	62.2	267	6	US-11-096-568A-33225	Sequence 33225, A
570	23	62.2	104	6	US-10-467-657-138	Sequence 138, App	643	23	62.2	269	6	US-10-841-956A-8	Sequence 8, Appli
571	23	62.2	104	6	US-10-467-657-6972	Sequence 6972, App	644	23	62.2	270	6	US-10-841-956A-5	Sequence 5, Appli
572	23	62.2	107	7	US-11-165-023-1	Sequence 1, Appli	645	23	62.2	275	7	US-11-096-568A-21684	Sequence 21684, A
573	23	62.2	107	7	US-11-165-023-2	Sequence 2, Appli	646	23	62.2	277	6	US-10-515-417-13	Sequence 13, Appli
574	23	62.2	107	7	US-11-165-023-3	Sequence 3, Appli	647	23	62.2	279	7	US-11-096-568A-8112	Sequence 8112, Ap
575	23	62.2	107	7	US-11-165-023-5	Sequence 5, Appli	648	23	62.2	281	6	US-10-821-234-1288	Sequence 1288, Ap
576	23	62.2	107	7	US-11-165-023-6	Sequence 6, Appli	649	23	62.2	281	6	US-10-841-956A-7	Sequence 7, Appli
577	23	62.2	107	7	US-11-098-686-10612	Sequence 10612, A	650	23	62.2	281	6	US-10-501-035-269	Sequence 269, App
578	23	62.2	107	7	US-11-203-251A-65	Sequence 65, Appli	651	23	62.2	281	7	US-11-077-272-2	Sequence 2, Appli
579	23	62.2	107	7	US-11-203-251A-69	Sequence 69, Appli	652	23	62.2	281	7	US-11-136-842-1	Sequence 1, Appli
580	23	62.2	107	7	US-11-203-253A-65	Sequence 65, Appli	653	23	62.2	281	7	US-11-136-079-5	Sequence 5, Appli
581	23	62.2	107	7	US-11-203-253A-69	Sequence 69, Appli	654	23	62.2	282	7	US-11-221-281-5	Sequence 5, Appli
582	23	62.2	108	7	US-11-165-023-4	Sequence 4, Appli	655	23	62.2	282	6	US-10-841-956A-6	Sequence 6, Appli
583	23	62.2	111	6	US-10-523-362-28	Sequence 28, Appli	656	23	62.2	282	7	US-11-096-568A-5326	Sequence 5326, Ap
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585	23	62.2	112	7	US-11-020-772-15	Sequence 15, Appli	658	23	62.2	283	7	US-11-096-568A-8111	Sequence 8111, Ap
586	23	62.2	112	7	US-11-076-728-14	Sequence 14, Appli	659	23	62.2	291	7	US-11-078-735-30	Sequence 30, Appli
587	23	62.2	112	7	US-11-076-728-15	Sequence 15, Appli	660	23	62.2	291	7	US-11-050-346-24	Sequence 24, Appli
588	23	62.2	113	7	US-11-073-605-8	Sequence 8, Appli	661	23	62.2	291	7	US-11-098-686-11384	Sequence 11384, A
589	23	62.2	113	7	US-11-140-284-20	Sequence 20, Appli	662	23	62.2	292	6	US-10-793-626-1434	Sequence 1434, Ap
590	23	62.2	119	7	US-11-096-568A-24863	Sequence 24863, A	663	23	62.2	293	6	US-10-841-956A-9	Sequence 9, Appli
591	23	62.2	129	7	US-11-052-554A-317	Sequence 317, App	664	23	62.2	293	7	US-11-096-568A-8860	Sequence 8860, Ap
592	23	62.2	129	7	US-11-072-512-2145	Sequence 2145, App	665	23	62.2	293	7	US-11-096-568A-8862	Sequence 8862, Ap
593	23	62.2	132	7	US-11-087-099-9089	Sequence 9089, Ap	666	23	62.2	297	7	US-11-146-428-102	Sequence 102, App
594	23	62.2	169	7	US-11-096-568A-14570	Sequence 14570, A	667	23	62.2	298	7	US-11-096-568A-8110	Sequence 8110, Ap
595	23	62.2	174	7	US-11-227-976-14	Sequence 14, Appli	668	23	62.2	301	7	US-11-152-569-10	Sequence 10, Appli
596	23	62.2	178	7	US-11-172-740-2277	Sequence 2277, Ap	669	23	62.2	304	7	US-11-096-568A-7821	Sequence 7821, Ap
597	23	62.2	186	7	US-11-096-568A-3471	Sequence 3471, Ap	670	23	62.2	308	7	US-11-087-039-9460	Sequence 9460, Ap
598	23	62.2	192	7	US-11-022-478-17	Sequence 17, Appli	671	23	62.2	308	7	US-11-096-568A-5325	Sequence 5325, Ap
599	23	62.2	199	7	US-11-096-568A-10724	Sequence 10724, A	672	23	62.2	309	7	US-11-096-568A-8187	Sequence 8187, Ap
600	23	62.2	210	7	US-11-096-568A-11265	Sequence 11265, A	673	23	62.2	317	7	US-11-096-568A-33224	Sequence 33224, A
601	23	62.2	213	6	US-10-841-956A-19	Sequence 19, Appli	674	23	62.2	317	7	US-11-172-740-1384	Sequence 1384, Ap
602	23	62.2	213	7	US-11-098-686-11144	Sequence 11144, A	675	23	62.2	317	7	US-11-096-568A-7394	Sequence 7394, Ap
603	23	62.2	213	7	US-11-096-568A-19284	Sequence 19284, A	676	23	62.2	318	7	US-11-096-568A-25812	Sequence 25812, A
604	23	62.2	213	7	US-11-096-568A-22424	Sequence 22424, A	677	23	62.2	318	7	US-11-096-568A-25812	Sequence 25812, A
605	23	62.2	213	7	US-11-172-740-954	Sequence 954, App	678	23	62.2	319	6	US-10-506-454-1036	Sequence 1036, Ap
606	23	62.2	218	7	US-11-096-568A-7822	Sequence 7822, App	679	23	62.2	324	7	US-11-096-568A-21907	Sequence 21907, A
607	23	62.2	220	7	US-11-151-598-1	Sequence 1, Appli	680	23	62.2	324	7	US-11-096-568A-28417	Sequence 28417, A
608	23	62.2	221	7	US-11-096-568A-5522	Sequence 5522, App	681	23	62.2	325	7	US-11-166-412-65	Sequence 65, Appli
609	23	62.2	223	6	US-10-454-437-286	Sequence 286, App	682	23	62.2	325	7	US-11-172-740-725	Sequence 725, App

683	23	62.2	326	7	US-11-096-568A-33223	Sequence 33223, A	756	23	62.2	456	7	US-11-059-867-4	Sequence 4, Appl
684	23	62.2	328	7	US-11-096-568A-28416	Sequence 28416, A	757	23	62.2	456	7	US-11-096-568A-20175	Sequence 20175, A
685	23	62.2	329	7	US-11-096-568A-16654	Sequence 16654, A	758	23	62.2	462	7	US-11-087-099-12028	Sequence 12028, A
686	23	62.2	329	7	US-11-172-740-1387	Sequence 1387, A	759	23	62.2	462	7	US-11-096-568A-12786	Sequence 12786, A
687	23	62.2	331	7	US-11-078-735-33	Sequence 33, Appl	760	23	62.2	465	7	US-11-098-686-10707	Sequence 10707, A
688	23	62.2	331	7	US-11-050-346-27	Sequence 27, Appl	761	23	62.2	466	7	US-11-072-512-2410	Sequence 2410, A
689	23	62.2	331	7	US-11-096-568A-28394	Sequence 28394, A	762	23	62.2	468	7	US-11-156-084-250	Sequence 250, A
690	23	62.2	332	7	US-11-078-735-51	Sequence 51, Appl	763	23	62.2	476	7	US-11-169-041-219	Sequence 219, A
691	23	62.2	332	7	US-11-050-346-41	Sequence 41, Appl	764	23	62.2	479	7	US-11-156-084-271	Sequence 271, A
692	23	62.2	332	7	US-11-103-077-24	Sequence 24, Appl	765	23	62.2	481	7	US-11-094-519A-27	Sequence 27, Appl
693	23	62.2	332	7	US-11-172-740-1388	Sequence 1388, A	766	23	62.2	484	7	US-11-078-735-43	Sequence 43, Appl
694	23	62.2	332	6	US-10-980-388-91	Sequence 91, Appl	767	23	62.2	484	7	US-11-050-346-37	Sequence 37, Appl
695	23	62.2	333	6	US-10-980-388-114	Sequence 114, Appl	768	23	62.2	484	7	US-11-096-568A-6203	Sequence 6203, A
696	23	62.2	335	7	US-11-096-568A-5324	Sequence 5324, A	769	23	62.2	487	6	US-10-980-722-2	Sequence 2, Appl
697	23	62.2	338	7	US-11-096-568A-16653	Sequence 16653, A	770	23	62.2	488	7	US-11-096-568A-6202	Sequence 6202, A
698	23	62.2	339	6	US-10-821-234-1085	Sequence 1085, A	771	23	62.2	499	7	US-11-096-568A-6201	Sequence 6201, A
699	23	62.2	340	7	US-11-096-568A-10723	Sequence 10723, A	772	23	62.2	501	7	US-11-096-568A-32216	Sequence 32216, A
700	23	62.2	341	7	US-11-072-512-3424	Sequence 3424, A	773	23	62.2	503	7	US-11-013-247A-4	Sequence 4, Appl
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702	23	62.2	344	7	US-11-096-568A-32172	Sequence 32172, A	775	23	62.2	504	7	US-11-072-512-3467	Sequence 3467, A
703	23	62.2	345	7	US-11-072-175-210	Sequence 210, Appl	776	23	62.2	506	7	US-11-053-100-37	Sequence 37, Appl
704	23	62.2	345	7	US-11-096-568A-28393	Sequence 28393, A	777	23	62.2	507	7	US-11-053-100-31	Sequence 31, Appl
705	23	62.2	347	7	US-11-096-568A-21906	Sequence 21906, A	778	23	62.2	507	7	US-11-053-100-34	Sequence 34, Appl
706	23	62.2	348	7	US-11-096-568A-8859	Sequence 8859, A	779	23	62.2	508	6	US-10-467-657-6928	Sequence 6928, A
707	23	62.2	349	7	US-11-096-568A-8186	Sequence 8186, A	780	23	62.2	513	6	US-10-821-234-1112	Sequence 1112, A
708	23	62.2	349	7	US-11-096-568A-28392	Sequence 28392, A	781	23	62.2	515	7	US-11-132-142-8	Sequence 8, Appl
709	23	62.2	350	7	US-11-096-568A-21683	Sequence 21683, A	782	23	62.2	517	7	US-11-135-603-8	Sequence 8, Appl
710	23	62.2	353	7	US-11-087-099-689	Sequence 689, A	783	23	62.2	524	6	US-10-501-930-7	Sequence 7, Appl
711	23	62.2	353	7	US-11-087-099-12054	Sequence 12054, A	784	23	62.2	528	6	US-10-864-758-7	Sequence 7, Appl
712	23	62.2	354	7	US-11-053-100-27	Sequence 27, Appl	785	23	62.2	529	6	US-10-501-930-5	Sequence 5, Appl
713	23	62.2	354	7	US-11-096-568A-22423	Sequence 22423, A	786	23	62.2	531	7	US-11-072-512-3442	Sequence 3442, A
714	23	62.2	356	7	US-11-053-100-36	Sequence 36, Appl	787	23	62.2	534	6	US-10-204-639-53	Sequence 53, Appl
715	23	62.2	356	7	US-11-087-099-2981	Sequence 2981, A	788	23	62.2	537	7	US-11-037-243-104	Sequence 104, Appl
716	23	62.2	357	7	US-11-053-100-30	Sequence 30, Appl	789	23	62.2	538	7	US-11-087-099-5646	Sequence 5646, A
717	23	62.2	357	7	US-11-053-100-33	Sequence 33, Appl	790	23	62.2	540	7	US-11-045-802-35	Sequence 35, Appl
718	23	62.2	358	6	US-10-995-561-547	Sequence 547, Appl	791	23	62.2	546	6	US-10-919-492-31	Sequence 31, Appl
719	23	62.2	360	7	US-11-096-568A-25811	Sequence 25811, A	792	23	62.2	552	7	US-11-074-176-204	Sequence 204, Appl
720	23	62.2	361	7	US-11-096-568A-25811	Sequence 25811, A	793	23	62.2	564	7	US-11-096-568A-29681	Sequence 29681, A
721	23	62.2	364	7	US-11-096-568A-7392	Sequence 7392, A	794	23	62.2	572	7	US-10-959-310-7	Sequence 7, Appl
722	23	62.2	364	7	US-11-096-568A-7820	Sequence 7820, A	795	23	62.2	575	6	US-10-959-310-8	Sequence 8, Appl
723	23	62.2	364	7	US-11-096-568A-10722	Sequence 10722, A	796	23	62.2	575	6	US-10-959-322-13	Sequence 13, Appl
724	23	62.2	366	7	US-11-072-512-2329	Sequence 2329, A	797	23	62.2	575	6	US-10-959-322-14	Sequence 14, Appl
725	23	62.2	366	7	US-11-172-740-1647	Sequence 1647, A	798	23	62.2	575	6	US-11-131-212-23	Sequence 23, Appl
726	23	62.2	367	6	US-10-821-234-985	Sequence 985, A	799	23	62.2	575	7	US-11-131-212-24	Sequence 24, Appl
727	23	62.2	369	7	US-11-078-735-38	Sequence 38, Appl	800	23	62.2	575	7	US-11-218-473-23	Sequence 23, Appl
728	23	62.2	369	7	US-11-050-346-32	Sequence 32, Appl	801	23	62.2	575	7	US-11-218-473-24	Sequence 24, Appl
729	23	62.2	369	7	US-11-096-568A-28415	Sequence 28415, A	802	23	62.2	575	7	US-11-240-579-23	Sequence 23, Appl
730	23	62.2	371	7	US-11-120-308-118	Sequence 118, A	803	23	62.2	575	7	US-11-240-579-24	Sequence 24, Appl
731	23	62.2	380	7	US-11-132-864-30	Sequence 30, Appl	804	23	62.2	579	7	US-11-072-512-2360	Sequence 2360, A
732	23	62.2	386	7	US-11-096-568A-28186	Sequence 28186, A	805	23	62.2	600	7	US-11-096-568A-32215	Sequence 32215, A
733	23	62.2	388	7	US-11-096-568A-21682	Sequence 21682, A	806	23	62.2	601	7	US-11-103-957-3	Sequence 3, Appl
734	23	62.2	391	7	US-11-105-172-4	Sequence 4, Appl	807	23	62.2	601	7	US-11-103-957-3	Sequence 3, Appl
735	23	62.2	392	7	US-11-096-568A-16652	Sequence 16652, A	808	23	62.2	601	6	US-10-921-793-4	Sequence 4, Appl
736	23	62.2	394	7	US-11-087-099-11753	Sequence 11753, A	809	23	62.2	610	6	US-10-921-793-4	Sequence 4, Appl
737	23	62.2	395	7	US-11-087-099-3016	Sequence 3016, A	810	23	62.2	610	6	US-10-931-198-4	Sequence 4, Appl
738	23	62.2	395	7	US-11-087-099-12132	Sequence 12132, A	811	23	62.2	610	6	US-10-942-042-4	Sequence 4, Appl
739	23	62.2	396	7	US-11-096-568A-28185	Sequence 28185, A	812	23	62.2	616	7	US-11-058-727-16	Sequence 16, Appl
740	23	62.2	398	7	US-11-087-099-366	Sequence 366, A	813	23	62.2	616	7	US-11-108-389-16	Sequence 16, Appl
741	23	62.2	400	7	US-11-087-099-11732	Sequence 11732, A	814	23	62.2	616	7	US-11-224-624-16	Sequence 16, Appl
742	23	62.2	400	7	US-11-096-568A-28184	Sequence 28184, A	815	23	62.2	619	7	US-11-087-099-396	Sequence 396, A
743	23	62.2	401	7	US-11-072-512-2680	Sequence 2680, A	816	23	62.2	619	7	US-11-087-099-12020	Sequence 12020, A
744	23	62.2	404	7	US-11-052-554A-344	Sequence 344, A	817	23	62.2	620	7	US-11-058-727-20	Sequence 20, Appl
745	23	62.2	408	7	US-11-096-568A-12788	Sequence 12788, A	818	23	62.2	620	7	US-11-108-389-20	Sequence 20, Appl
746	23	62.2	415	7	US-11-072-512-2624	Sequence 2624, A	819	23	62.2	620	7	US-11-224-624-20	Sequence 20, Appl
747	23	62.2	421	7	US-11-087-099-6184	Sequence 6184, A	820	23	62.2	620	7	US-11-087-099-4584	Sequence 4584, A
748	23	62.2	421	7	US-11-087-099-6540	Sequence 6540, A	821	23	62.2	635	7	US-11-096-568A-29628	Sequence 29628, A
749	23	62.2	421	7	US-11-087-099-7697	Sequence 7697, A	822	23	62.2	654	7	US-11-053-100-29	Sequence 29, A
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## ALIGNMENTS

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; GENERAL INFORMATION:
; APPLICANT: KYOWA HAKKO KOGYO CO., LTD.
; TITLE OF INVENTION: Agents for treatment of cancer using recombinant anti-GD3 antibody
; FILE REFERENCE: 11374WO1
; CURRENT APPLICATION NUMBER: US/10/473,037
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: JP2001-097483
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.0
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; LENGTH: 7
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-473-037-7
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; Publication No. US20050260206A1
; GENERAL INFORMATION:
; APPLICANT: KYOWA HAKKO KOGYO CO., LTD.
; TITLE OF INVENTION: Agents for treatment of cancer using recombinant anti-GD3 antibody
; FILE REFERENCE: 11374WO1
; CURRENT APPLICATION NUMBER: US/10/473,037
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: JP2001-097483
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; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Artificial Sequence
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US-10-473-037-10
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; APPLICANT: KYOWA HAKKO KOGYO CO., LTD.
; TITLE OF INVENTION: Agents for treatment of cancer using recombinant anti-GD3 antibody
; FILE REFERENCE: 11374WO1
; CURRENT APPLICATION NUMBER: US/10/473,037
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: JP2001-097483
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.0
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; ORGANISM: Mus musculus
US-10-473-037-50
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; GENERAL INFORMATION:
; APPLICANT: KYOWA HAKKO KOGYO CO., LTD.
; TITLE OF INVENTION: Agents for treatment of cancer using recombinant anti-GD3 antibody
; FILE REFERENCE: 11374WO1
; CURRENT APPLICATION NUMBER: US/10/473,037
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: JP2001-097483
; PRIOR FILING DATE: 2001-03-29
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; Publication No. US20060057139A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUWANA, YOSHISHI
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/11/228,293
; CURRENT FILING DATE: 2005-09-19
; PRIOR APPLICATION NUMBER: US/09/225,322
; PRIOR FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: US 08/454,680
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
; PRIOR APPLICATION NUMBER: US/07/947,674
; PRIOR FILING DATE: 1992-09-17
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US-11-228-293-10
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Best Local Similarity 100.0%; Pred. No. 0.54;
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; Publication No. US20060057139A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUWANA, YOSHISHI
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/11/228,293
; CURRENT FILING DATE: 2005-09-19
; PRIOR APPLICATION NUMBER: US/09/225,322
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; Sequence 10, Application US/11228319
; Publication No. US20060058512A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUWANA, YOSHISHI
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/11/228,319
; CURRENT FILING DATE: 2005-09-19
; PRIOR APPLICATION NUMBER: US/09/225,322
; PRIOR FILING DATE: 1999-01-05
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; PRIOR FILING DATE: 1995-05-31
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US-11-228-319-10
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; Sequence 19, Application US/11228319
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Publication No. US20060058512A1  
GENERAL INFORMATION:  
APPLICANT: SHITARA, KENYA  
APPLICANT: HANAI, NOBUO  
APPLICANT: HASEGAWA, MAMORU  
APPLICANT: MIYAJI, HIROMASA  
APPLICANT: KUMANA, YOSHIHISA  
TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY  
FILE REFERENCE: 249-101  
CURRENT APPLICATION NUMBER: US/11/228,319  
CURRENT FILING DATE: 2005-09-19  
PRIOR APPLICATION NUMBER: US/09/225,322  
PRIOR FILING DATE: 1999-01-05  
PRIOR APPLICATION NUMBER: US 08/454,680  
PRIOR FILING DATE: 1995-05-31  
PRIOR APPLICATION NUMBER: US 08/408,133  
PRIOR FILING DATE: 1995-03-21  
PRIOR APPLICATION NUMBER: US 08/292,178  
PRIOR FILING DATE: 1994-08-17  
PRIOR APPLICATION NUMBER: US07/947,674  
PRIOR FILING DATE: 1992-09-17  
PRIOR APPLICATION NUMBER: JP 3-238375  
PRIOR FILING DATE: 1991-09-18  
NUMBER OF SEQ ID NOS: 19  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 19  
LENGTH: 128  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:light chain  
OTHER INFORMATION: variable region  
US-11-228-319-19

Query Match 100.0%; Score 37; DB 7; Length 128;  
Best Local Similarity 100.0%; Pred. No. 0.54; Mismatches 0; Indels 0; Gaps 0;  
Matches 7; Conservative 0;

QY 1 YSSNLHS 7  
DB 70 YSSNLHS 76

RESULT 9  
US-10-467-657-7258  
Sequence 7258, Application US/10467657  
Publication No. US20050260581A1  
GENERAL INFORMATION:  
APPLICANT: CHIRON SpA  
APPLICANT: FONTANA Maria Rita  
APPLICANT: PIZZA Mariagrazia  
APPLICANT: MASIGNANI Vega  
APPLICANT: MONACI Elisabetta  
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS  
FILE REFERENCE:  
CURRENT APPLICATION NUMBER: US/10/467,657  
CURRENT FILING DATE: 2003-08-11  
PRIOR APPLICATION NUMBER: GB-0103424.8  
PRIOR FILING DATE: 2001-02-12  
NUMBER OF SEQ ID NOS: 9218  
SOFTWARE: SeqWin99, version 1.04  
SEQ ID NO 7258  
LENGTH: 380  
TYPE: PRT  
ORGANISM: Neisseria gonorrhoeae  
US-10-467-657-7258

Query Match 83.8%; Score 31; DB 6; Length 380;  
Best Local Similarity 71.4%; Pred. No. 32; Mismatches 2; Indels 0; Gaps 0;  
Matches 5; Conservative 2;

QY 1 YSSNLHS 7  
DB 70 YSSNLHS 76

Db 48 YAANLHS 54  
RESULT 10  
US-11-096-568A-21861  
Sequence 21861, Application US/11096568A  
Publication No. US20060048240A1  
GENERAL INFORMATION:  
APPLICANT: Alexandrov, Nickolai et al.  
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides  
FILE REFERENCE: 2750-1592PUS2  
CURRENT APPLICATION NUMBER: US/11/096,568A  
CURRENT FILING DATE: 2005-04-01  
NUMBER OF SEQ ID NOS: 34471  
SEQ ID NO 21861  
LENGTH: 256  
TYPE: PRT  
ORGANISM: Zea mays subsp. mays  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)..(256)  
OTHER INFORMATION: Ceres Seq. ID no. 12406578  
US-11-096-568A-21861

Query Match 81.1%; Score 30; DB 7; Length 256;  
Best Local Similarity 83.3%; Pred. No. 35; Mismatches 1; Indels 0; Gaps 0;  
Matches 5; Conservative 1;

QY 1 YSSNLH 6  
DB 46 YTSNLH 51

RESULT 11  
US-11-096-568A-21860  
Sequence 21860, Application US/11096568A  
Publication No. US20060048240A1  
GENERAL INFORMATION:  
APPLICANT: Alexandrov, Nickolai et al.  
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides  
FILE REFERENCE: 2750-1592PUS2  
CURRENT APPLICATION NUMBER: US/11/096,568A  
CURRENT FILING DATE: 2005-04-01  
NUMBER OF SEQ ID NOS: 34471  
SEQ ID NO 21860  
LENGTH: 323  
TYPE: PRT  
ORGANISM: Zea mays subsp. mays  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)..(323)  
OTHER INFORMATION: Ceres Seq. ID no. 12406577  
US-11-096-568A-21860

Query Match 81.1%; Score 30; DB 7; Length 323;  
Best Local Similarity 83.3%; Pred. No. 45; Mismatches 1; Indels 0; Gaps 0;  
Matches 5; Conservative 1;

QY 1 YSSNLH 6  
DB 113 YTSNLH 118

RESULT 12  
US-11-096-568A-11620  
Sequence 11620, Application US/11096568A  
Publication No. US20060048240A1  
GENERAL INFORMATION:  
APPLICANT: Alexandrov, Nickolai et al.  
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides  
US-11-096-568A-11620

; FILE REFERENCE: 2750-1592PUS2  
; CURRENT APPLICATION NUMBER: US/11/096,568A  
; CURRENT FILING DATE: 2005-04-01  
; NUMBER OF SEQ ID NOS: 34471  
; SEQ ID NO 11620  
; LENGTH: 468  
; TYPE: PRT  
; ORGANISM: Triticum aestivum  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)..(468)  
; OTHER INFORMATION: Ceres Seq. ID no. 13655855  
US-11-096-568A-11620

Query Match 81.1%; Score 30; DB 7; Length 468;  
Best Local Similarity 83.3%; Pred. No. 66;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLH 6  
|:||||  
Db 256 YTSNLH 261

RESULT 13  
US-11-096-568A-21859  
; Sequence 21859, Application US/11096568A  
; Publication No. US20060048240A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexandrov, Nikolai et al.  
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides  
; FILE REFERENCE: 2750-1592PUS2  
; CURRENT APPLICATION NUMBER: US/11/096,568A  
; CURRENT FILING DATE: 2005-04-01  
; NUMBER OF SEQ ID NOS: 34471  
; SEQ ID NO 21859  
; LENGTH: 470  
; TYPE: PRT  
; ORGANISM: Zea mays subsp. mays  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)..(470)  
; OTHER INFORMATION: Ceres Seq. ID no. 12406576  
US-11-096-568A-21859

Query Match 81.1%; Score 30; DB 7; Length 470;  
Best Local Similarity 83.3%; Pred. No. 66;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLH 6  
|:||||  
Db 260 YTSNLH 265

RESULT 14  
US-11-096-568A-11619  
; Sequence 11619, Application US/11096568A  
; Publication No. US20060048240A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexandrov, Nikolai et al.  
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides  
; FILE REFERENCE: 2750-1592PUS2  
; CURRENT APPLICATION NUMBER: US/11/096,568A  
; CURRENT FILING DATE: 2005-04-01  
; NUMBER OF SEQ ID NOS: 34471  
; SEQ ID NO 11619  
; LENGTH: 471  
; TYPE: PRT  
; ORGANISM: Triticum aestivum  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)..(471)

; OTHER INFORMATION: Ceres Seq. ID no. 13655854  
US-11-096-568A-11619

Query Match 81.1%; Score 30; DB 7; Length 471;  
Best Local Similarity 83.3%; Pred. No. 66;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLH 6  
|:||||  
Db 259 YTSNLH 264

RESULT 15  
US-11-096-568A-11618  
; Sequence 11618, Application US/11096568A  
; Publication No. US20060048240A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexandrov, Nikolai et al.  
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides  
; FILE REFERENCE: 2750-1592PUS2  
; CURRENT APPLICATION NUMBER: US/11/096,568A  
; CURRENT FILING DATE: 2005-04-01  
; NUMBER OF SEQ ID NOS: 34471  
; SEQ ID NO 11618  
; LENGTH: 502  
; TYPE: PRT  
; ORGANISM: Triticum aestivum  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)..(502)  
; OTHER INFORMATION: Ceres Seq. ID no. 13655853  
US-11-096-568A-11618

Query Match 81.1%; Score 30; DB 7; Length 502;  
Best Local Similarity 83.3%; Pred. No. 71;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLH 6  
|:||||  
Db 290 YTSNLH 295

RESULT 16  
US-11-122-396-5  
; Sequence 5, Application US/11122396  
; Publication No. US20060057698A1  
; GENERAL INFORMATION:  
; APPLICANT: Sherman, David  
; APPLICANT: Magarvey, Nathan  
; APPLICANT: Beck, Zachary Q  
; TITLE OF INVENTION: Nucleic Acids and Polypeptides Involved  
; TITLE OF INVENTION: in the Production of Cryptophycin  
; FILE REFERENCE: 09531/145001  
; CURRENT APPLICATION NUMBER: US/11/122,396  
; CURRENT FILING DATE: 2005-05-05  
; PRIOR APPLICATION NUMBER: 60/568,334  
; PRIOR FILING DATE: 2004-05-05  
; NUMBER OF SEQ ID NOS: 41  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5  
; LENGTH: 1943  
; TYPE: PRT  
; ORGANISM: Nostoc species  
; FEATURE:  
; NAME/KEY: VARIANT  
; LOCATION: 792-796 1402  
; OTHER INFORMATION: Xaa = Unknown  
US-11-122-396-5

Query Match 81.1%; Score 30; DB 7; Length 1943;  
Best Local Similarity 71.4%; Pred. No. 3e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLHS 7  
DB 1883 YSSNFHT 1889

RESULT 17  
US-11-195-095-14  
; Sequence 14, Application US/11195095  
; Publication No. US20060040323A1  
; GENERAL INFORMATION:  
; APPLICANT: Arepally, Gowthami  
; APPLICANT: Kiesel, Walter  
; APPLICANT: Kamei, Keiko  
; TITLE OF INVENTION: Kamei, Shintaro  
; TITLE OF INVENTION: Compositions and Methods Useful for the Diagnosis and Treatment of  
; TITLE OF INVENTION: Heparin Induced Thrombocytopenia/Thrombosis  
; FILE REFERENCE: 10312-2U1  
; CURRENT APPLICATION NUMBER: US/11/195,095  
; CURRENT FILING DATE: 2005-08-02  
; PRIOR APPLICATION NUMBER: US/09/615,872  
; PRIOR FILING DATE: 2000-07-13  
; PRIOR APPLICATION NUMBER: US 60/143,536  
; PRIOR FILING DATE: 1998-07-13  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 14  
; LENGTH: 99  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-11-195-095-14

Query Match 78.4%; Score 29; DB 7; Length 99;  
Best Local Similarity 71.4%; Pred. No. 21;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLHS 7  
DB 42 YTSSLHS 48

RESULT 18  
US-10-667-295-45  
; Sequence 45, Application US/10667295  
; Publication No. US20050257293A1  
; GENERAL INFORMATION:  
; APPLICANT: Mascia, Peter  
; TITLE OF INVENTION: BIOLOGICAL CONTAINMENT SYSTEM  
; FILE REFERENCE: 11696-047001  
; CURRENT APPLICATION NUMBER: US/10/667,295  
; CURRENT FILING DATE: 2003-09-17  
; PRIOR APPLICATION NUMBER: US 60/411,823  
; PRIOR FILING DATE: 2002-09-17  
; NUMBER OF SEQ ID NOS: 263  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 45  
; LENGTH: 138  
; TYPE: PRT  
; ORGANISM: Brassica napus  
; FEATURE:  
; NAME/KEY: VARIANT  
; LOCATION: (1)...(138)  
; OTHER INFORMATION: Ceres Seq. ID no. 6425498  
US-10-667-295-45

Query Match 78.4%; Score 29; DB 6; Length 138;  
Best Local Similarity 71.4%; Pred. No. 30;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLHS 7  
DB 20 YNSSLHS 26

RESULT 19  
US-11-172-740-2478  
; Sequence 2478, Application US/11172740  
; Publication No. US20060057724A1  
; GENERAL INFORMATION:  
; APPLICANT: Mascia, Peter  
; APPLICANT: ALEXANDROV, Nikolai  
; APPLICANT: BROVER, Vyacheslav  
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AND POLYPEPTIDES ENCODED THEREBY USEFUL FOR  
; TITLE OF INVENTION: PLANT CHARACTERISTICS AND PHENOTYPES  
; FILE REFERENCE: 2750-1602PUS2  
; CURRENT APPLICATION NUMBER: US/11/172,740  
; CURRENT FILING DATE: 2005-06-30  
; PRIOR APPLICATION NUMBER: 60/583,621  
; PRIOR FILING DATE: 2004-06-30  
; PRIOR APPLICATION NUMBER: 60/584,829  
; PRIOR FILING DATE: 2004-06-30  
; PRIOR APPLICATION NUMBER: 60/584,800  
; PRIOR FILING DATE: 2004-06-30  
; NUMBER OF SEQ ID NOS: 2523  
; SEQ ID NO 2478  
; LENGTH: 138  
; TYPE: PRT  
; ORGANISM: Brassica napus  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(138)  
; OTHER INFORMATION: Ceres CLONE ID no. 1126651  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION:  
; OTHER INFORMATION: Utility: Useful for making smaller plants  
US-11-172-740-2478

Query Match 78.4%; Score 29; DB 7; Length 138;  
Best Local Similarity 71.4%; Pred. No. 30;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLHS 7  
DB 20 YNSSLHS 26

RESULT 20  
US-11-180-044-14  
; Sequence 14, Application US/11180044  
; Publication No. US20060035303A1  
; GENERAL INFORMATION:  
; APPLICANT: Davis, Roger J.  
; APPLICANT: Flavell, Richard A.  
; APPLICANT: Rakic, Pasko  
; APPLICANT: Whitmarsh, Alan  
; APPLICANT: Kuan, Chia-Yi  
; APPLICANT: Yang, Di  
; TITLE OF INVENTION: JNK3 MODULATORS AND METHODS OF USE  
; NUMBER OF SEQUENCES: 24  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson P.C.  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows 95  
; SOFTWARE: FastSeq for Windows Version 2.0b  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/11/180,044  
; FILING DATE: 12-JULY-2005  
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/09/165,522  
; FILING DATE: 02-Oct-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/060,995  
; FILING DATE: 03-Oct-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Fasse, J. Peter  
; REGISTRATION NUMBER: 32,983  
; REFERENCE/DOCKET NUMBER: 10363/005001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617/542-5070  
; TELEFAX: 617/542-8906  
; TELEX: 200154  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 334 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; FRAGMENT TYPE: internal  
; US-11-180-044-14

Query Match 78.4%; Score 29; DB 7; Length 334;  
Best Local Similarity 71.4%; Pred. No. 75;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLHS 7  
|||:||||  
Db 159 YSASLHS 165

RESULT 21  
US-11-096-568A-20218  
; Sequence 20218, Application US/11096568A  
; Publication No. US20060048240A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexandrov, Nikolai et al.  
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides  
; FILE REFERENCE: 2750-1592PUS2  
; CURRENT APPLICATION NUMBER: US/11/096,568A  
; CURRENT FILING DATE: 2005-04-01  
; NUMBER OF SEQ ID NOS: 34471  
; SEQ ID NO 20218  
; LENGTH: 376  
; TYPE: PRT  
; ORGANISM: Zea mays subsp. mays  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)..(376)  
; OTHER INFORMATION: Ceres Seq. ID no. 12379655  
US-11-096-568A-20218

Query Match 78.4%; Score 29; DB 7; Length 376;  
Best Local Similarity 71.4%; Pred. No. 85;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLHS 7  
|||:||||  
Db 122 YSSSLHA 128

RESULT 22  
US-11-096-568A-29662  
; Sequence 29662, Application US/11096568A  
; Publication No. US20060048240A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexandrov, Nikolai et al.  
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides  
; FILE REFERENCE: 2750-1592PUS2  
; CURRENT APPLICATION NUMBER: US/11/096,568A  
; CURRENT FILING DATE: 2005-04-01

; NUMBER OF SEQ ID NOS: 34471  
; SEQ ID NO 29662  
; LENGTH: 392  
; TYPE: PRT  
; ORGANISM: Arabidopsis thaliana  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)..(392)  
; OTHER INFORMATION: Ceres Seq. ID no. 4920894  
US-11-096-568A-29662

Query Match 78.4%; Score 29; DB 7; Length 392;  
Best Local Similarity 71.4%; Pred. No. 89;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSNLHS 7  
|||:||||  
Db 42 YSSNAHA 48

RESULT 23  
US-11-096-568A-29661  
; Sequence 29661, Application US/11096568A  
; Publication No. US20060048240A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexandrov, Nikolai et al.  
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides  
; FILE REFERENCE: 2750-1592PUS2  
; CURRENT APPLICATION NUMBER: US/11/096,568A  
; CURRENT FILING DATE: 2005-04-01  
; NUMBER OF SEQ ID NOS: 34471  
; SEQ ID NO 29661  
; LENGTH: 409  
; TYPE: PRT  
; ORGANISM: Arabidopsis thaliana  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)..(409)  
; OTHER INFORMATION: Ceres Seq. ID no. 4920893  
US-11-096-568A-29661

Query Match 78.4%; Score 29; DB 7; Length 409;  
Best Local Similarity 71.4%; Pred. No. 93;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSNLHS 7  
|||:||||  
Db 59 YSSNAHA 65

RESULT 24  
US-10-793-626-1386  
; Sequence 1386, Application US/10793626  
; Publication No. US20050255478A1  
; GENERAL INFORMATION:  
; APPLICANT: KIMMERLY, WILLIAM JOHN  
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS  
; FILE REFERENCE: PU3480US  
; CURRENT APPLICATION NUMBER: US/10/793,626  
; CURRENT FILING DATE: 2004-03-04  
; PRIOR APPLICATION NUMBER: 60/164,258  
; PRIOR FILING DATE: 1999-11-09  
; NUMBER OF SEQ ID NOS: 4472  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1386  
; LENGTH: 496  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: amino acid sequence  
US-10-793-626-1386

```
Query Match      78.4%; Score 29; DB 6; Length 496;
Best Local Similarity 83.3%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 YSNNLH 6
Db      274 YDSNLH 279

RESULT 25
US-11-096-568A-29660
; Sequence 29660, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 29660
; LENGTH: 510
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(510)
; OTHER INFORMATION: Ceres Seq. ID no. 4920892
US-11-096-568A-29660

Query Match      78.4%; Score 29; DB 7; Length 510;
Best Local Similarity 71.4%; Pred. No. 1.2e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 YSNNLH 7
Db      160 YSSNAH 166

RESULT 26
US-11-210-316-2
; Sequence 2, Application US/11210316
; Publication No. US20050282278A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Stephen M.
; APPLICANT: Hitz, William D.
; APPLICANT: Kinney, Anthony J.
; TITLE OF INVENTION: Plant Sugar Transport Proteins
; FILE REFERENCE: BB1163USDIV
; CURRENT APPLICATION NUMBER: US/11/210,316
; CURRENT FILING DATE: 2005-08-24
; PRIOR APPLICATION NUMBER: US/10/051,902
; PRIOR FILING DATE: 2002-01-17
; PRIOR APPLICATION NUMBER: 60/083,044
; PRIOR FILING DATE: 1998-04-24
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 2
; LENGTH: 747
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (129)
; OTHER INFORMATION: Xaa = any amino acid
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (133)..(134)
; OTHER INFORMATION: Xaa = any amino acid
; FEATURE:
; NAME/KEY: UNSURE
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; LOCATION: (144)
; OTHER INFORMATION: Xaa = any amino acid
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (178)
; OTHER INFORMATION: Xaa = any amino acid
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (207)
; OTHER INFORMATION: Xaa = any amino acid
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (218)
; OTHER INFORMATION: Xaa = any amino acid
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (220)
; OTHER INFORMATION: Xaa = any amino acid
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (236)
; OTHER INFORMATION: Xaa = any amino acid
US-11-210-316-2

Query Match      78.4%; Score 29; DB 7; Length 747;
Best Local Similarity 71.4%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 YSNNLH 7
Db      368 YEDNLH 374

RESULT 27
US-10-999-866-56
; Sequence 56, Application US/10999866
; Publication No. US20050266004A1
; GENERAL INFORMATION:
; APPLICANT: GILES-KOMAR, Jill; SCALLON, Bernard J.; CAI, Ann
; TITLE OF INVENTION: ANTI-HUMAN LYMPHOTOXIN ALPHA ANTIBODIES, COMPOSITIONS, METHODS AN
; FILE REFERENCE: CEN5042NP
; CURRENT APPLICATION NUMBER: US/10/999,866
; CURRENT FILING DATE: 2004-11-30
; PRIOR APPLICATION NUMBER: 60/527,794
; PRIOR FILING DATE: 2003-12-08
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 56
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(7)
; OTHER INFORMATION: LC CDR2
US-10-999-866-56

Query Match      75.7%; Score 28; DB 6; Length 7;
Best Local Similarity 71.4%; Pred. No. 1.4e+05;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 YSNNLH 7
Db      1 YTSRLH 7

RESULT 28
US-11-009-939-39
; Sequence 39, Application US/11009939
; Publication No. US20050265998A1
; GENERAL INFORMATION:
; APPLICANT: Elson, Greg Christopher Andrew
; TITLE OF INVENTION: Neutralizing Antibodies and Methods of Use Thereof
```

```
; FILE REFERENCE: 23135-402
; CURRENT APPLICATION NUMBER: US/11/009,939
; CURRENT FILING DATE: 2005-12-10
; PRIOR APPLICATION NUMBER: 60/528,811
; PRIOR FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 60/528,812
; PRIOR FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 60/528,962
; PRIOR FILING DATE: 2003-12-10
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 39
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-009-939-39
```

```
Query Match 75.7%; Score 28; DB 7; Length 7;
Best Local Similarity 71.4%; Pred. No. 1.4e+05;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 YSSNLHS 7
Db 1 YTSKLHS 7
```

```
RESULT 29
US-11-004-399-1409
; Sequence 1409, Application US/11004399
; Publication No. US20060053516A1
; GENERAL INFORMATION:
; APPLICANT: Chye, Mee Lee
; APPLICANT: Li, Hong Ye
; APPLICANT: Ramalingam, Sathiskumar
; APPLICANT: Poon, Leo Lit Man
; APPLICANT: Peiris, Joseph Sriyal Malik
; TITLE OF INVENTION: Genetically Modified Plants Comprising SARS-Cov Viral Nucleotide
; FILE REFERENCE: Sequences and Methods of Use Thereof for Immunization Against SA
; FILE REFERENCE: 2587/73166/RDK
; CURRENT APPLICATION NUMBER: US/11/004,399
; CURRENT FILING DATE: 2004-12-03
; PRIOR APPLICATION NUMBER: US 60/527,637
; PRIOR FILING DATE: 2003-12-03
; NUMBER OF SEQ ID NOS: 4043
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1409
; LENGTH: 10
; TYPE: PRT
; ORGANISM: SARS-Cov Virus
US-11-004-399-1409
```

```
Query Match 75.7%; Score 28; DB 7; Length 10;
Best Local Similarity 57.1%; Pred. No. 3;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 YSSNLHS 7
Db 4 YGSNNHT 10
```

```
RESULT 30
US-11-004-399-2238
; Sequence 2238, Application US/11004399
; Publication No. US20060053516A1
; GENERAL INFORMATION:
; APPLICANT: Chye, Mee Lee
; APPLICANT: Li, Hong Ye
; APPLICANT: Ramalingam, Sathiskumar
; APPLICANT: Poon, Leo Lit Man
; APPLICANT: Peiris, Joseph Sriyal Malik
; TITLE OF INVENTION: Genetically Modified Plants Comprising SARS-Cov Viral Nucleotide
; FILE REFERENCE: Sequences and Methods of Use Thereof for Immunization Against SA
; FILE REFERENCE: 2587/73166/RDK
```

```
; CURRENT APPLICATION NUMBER: US/11/004,399
; CURRENT FILING DATE: 2004-12-03
; PRIOR APPLICATION NUMBER: US 60/527,637
; PRIOR FILING DATE: 2003-12-03
; NUMBER OF SEQ ID NOS: 4043
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2238
; LENGTH: 52
; TYPE: PRT
; ORGANISM: SARS-Cov Virus
US-11-004-399-2238
```

```
Query Match 75.7%; Score 28; DB 7; Length 52;
Best Local Similarity 57.1%; Pred. No. 17;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 YSSNLHS 7
Db 43 YGSNIHA 49
```

```
RESULT 31
US-10-999-866-43
; Sequence 43, Application US/10999866
; Publication No. US2005026004A1
; GENERAL INFORMATION:
; APPLICANT: GILES-KOMAR, Jill; SCALLON, Bernard J.; CAI, Ann
; TITLE OF INVENTION: ANTI-HUMAN LYMPHOTOXIN ALPHA ANTIBODIES, COMPOSITIONS, METHODS A
; FILE REFERENCE: CEN5042NP
; CURRENT APPLICATION NUMBER: US/10/999,866
; CURRENT FILING DATE: 2004-11-30
; PRIOR APPLICATION NUMBER: 2004-11-30
; PRIOR FILING DATE: 2003-12-08
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 43
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)-(107)
; OTHER INFORMATION: LC variable region
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)-(23)
; OTHER INFORMATION: Framework 1
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (24)-(34)
; OTHER INFORMATION: CDR1
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (35)-(50)
; OTHER INFORMATION: Framework 2
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (51)-(56)
; OTHER INFORMATION: CDR2
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (57)-(89)
; OTHER INFORMATION: Framework 3
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (90)-(97)
; OTHER INFORMATION: CDR3
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (98)-(107)
; OTHER INFORMATION: Jk2
US-10-999-866-43
```

Query Match 75.7%; Score 28; DB 6; Length 107;  
 Best Local Similarity 71.4%; Pred. No. 37;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSNLHS 7  
 | : | | |  
 DB 50 YTSRLHS 56

RESULT 32  
 US-10-946-836A-10  
 ; Sequence 10, Application US/10946836A  
 ; Publication No. US20060009382A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Tegenero AG  
 ; APPLICANT: Hanke, Thomas  
 ; APPLICANT: Lin, Chia-Huey  
 ; TITLE OF INVENTION: USE OF A CD28 BINDING PHARMACEUTICAL SUBSTANCE FOR MAKING A  
 ; FILE REFERENCE: 7003/25, TEG/US/0407  
 ; CURRENT APPLICATION NUMBER: US/10/946,836A  
 ; CURRENT FILING DATE: 2004-09-22  
 ; PRIOR APPLICATION NUMBER: DE 103 45 008.4  
 ; PRIOR FILING DATE: 2003-09-22  
 ; PRIOR APPLICATION NUMBER: DE 103 49 371.9  
 ; PRIOR FILING DATE: 2003-10-20  
 ; NUMBER OF SEQ ID NOS: 19  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 10  
 ; LENGTH: 107  
 ; TYPE: PRT  
 ; ORGANISM: Artificial  
 ; FEATURE:  
 ; OTHER INFORMATION: monoclonal antibody 9D7 partial sequence  
 US-10-946-836A-10

Query Match 75.7%; Score 28; DB 6; Length 107;  
 Best Local Similarity 71.4%; Pred. No. 37;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSNLHS 7  
 | : | | |  
 DB 50 YTSRLHS 56

RESULT 33  
 US-10-988-207-10  
 ; Sequence 10, Application US/10988207  
 ; Publication No. US20060008457A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Tegenero AG  
 ; APPLICANT: Hanke, Thomas  
 ; TITLE OF INVENTION: USE OF AN EFFECTIVE SUBSTANCE BINDING TO CD28 FOR PRODUCING A  
 ; FILE REFERENCE: TEG/US/0409  
 ; CURRENT APPLICATION NUMBER: US/10/988,207  
 ; CURRENT FILING DATE: 2004-11-12  
 ; PRIOR APPLICATION NUMBER: DE 103 52 900.4  
 ; PRIOR FILING DATE: 2003-11-11  
 ; NUMBER OF SEQ ID NOS: 28  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 10  
 ; LENGTH: 107  
 ; TYPE: PRT  
 ; ORGANISM: Artificial  
 ; FEATURE:  
 ; OTHER INFORMATION: mab 5.11A partial sequence  
 US-10-988-207-10

Query Match 75.7%; Score 28; DB 6; Length 107;  
 Best Local Similarity 71.4%; Pred. No. 37;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSNLHS 7  
 | : | | |  
 DB 50 YTSRLHS 56

RESULT 34  
 US-11-183-205-51  
 ; Sequence 51, Application US/11183205  
 ; Publication No. US20060030521A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Neose Technologies, Inc.  
 ; APPLICANT: Defrees, Shawn  
 ; APPLICANT: Zopf, David  
 ; APPLICANT: Bayer, Robert  
 ; APPLICANT: Bower, Caryn  
 ; APPLICANT: Hakes, David  
 ; APPLICANT: Chen, Xi  
 ; TITLE OF INVENTION: REMODELING AND GLYCOCONJUGATION OF PEPTIDES  
 ; FILE REFERENCE: 040853-01-5052-US01  
 ; CURRENT APPLICATION NUMBER: US/11/183,205  
 ; CURRENT FILING DATE: 2005-07-15  
 ; PRIOR APPLICATION NUMBER: US 11/183,205  
 ; PRIOR FILING DATE: 2005-07-15  
 ; PRIOR APPLICATION NUMBER: US 60/334,233  
 ; PRIOR FILING DATE: 2001-11-28  
 ; PRIOR APPLICATION NUMBER: US 60/334,301  
 ; PRIOR FILING DATE: 2001-11-28  
 ; PRIOR APPLICATION NUMBER: US 60/387,292  
 ; PRIOR FILING DATE: 2002-06-07  
 ; PRIOR APPLICATION NUMBER: US 60/391,777  
 ; PRIOR FILING DATE: 2002-06-25  
 ; PRIOR APPLICATION NUMBER: US 60/396,594  
 ; PRIOR FILING DATE: 2002-07-17  
 ; PRIOR APPLICATION NUMBER: US 60/404,249  
 ; PRIOR FILING DATE: 2002-08-16  
 ; PRIOR APPLICATION NUMBER: US 60/407,527  
 ; PRIOR FILING DATE: 2002-08-28  
 ; PRIOR APPLICATION NUMBER: PCT/US2002/032263  
 ; PRIOR FILING DATE: 2002-10-09  
 ; PRIOR APPLICATION NUMBER: US 10/287,994  
 ; PRIOR FILING DATE: 2002-11-05  
 ; NUMBER OF SEQ ID NOS: 62  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 51  
 ; LENGTH: 107  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-11-183-205-51

Query Match 75.7%; Score 28; DB 7; Length 107;  
 Best Local Similarity 71.4%; Pred. No. 37;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSNLHS 7  
 | : | | |  
 DB 50 YTSRLHS 56

RESULT 35  
 US-11-183-205-52  
 ; Sequence 52, Application US/11183205  
 ; Publication No. US20060030521A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Neose Technologies, Inc.  
 ; APPLICANT: Defrees, Shawn  
 ; APPLICANT: Zopf, David  
 ; APPLICANT: Bayer, Robert  
 ; APPLICANT: Bower, Caryn  
 ; APPLICANT: Hakes, David  
 ; APPLICANT: Chen, Xi  
 ; TITLE OF INVENTION: REMODELING AND GLYCOCONJUGATION OF PEPTIDES  
 ; FILE REFERENCE: 040853-01-5052-US01  
 ; CURRENT APPLICATION NUMBER: US/11/183,205



; CURRENT FILING DATE: 2005-07-15  
; PRIOR APPLICATION NUMBER: US 11/183,205  
; PRIOR FILING DATE: 2005-07-15  
; PRIOR APPLICATION NUMBER: US 60/334,233  
; PRIOR FILING DATE: 2001-11-28  
; PRIOR APPLICATION NUMBER: US 60/334,301  
; PRIOR FILING DATE: 2001-11-28  
; PRIOR APPLICATION NUMBER: US 60/387,292  
; PRIOR FILING DATE: 2002-06-07  
; PRIOR APPLICATION NUMBER: US 60/391,777  
; PRIOR FILING DATE: 2002-06-25  
; PRIOR APPLICATION NUMBER: US 60/396,594  
; PRIOR FILING DATE: 2002-07-17  
; PRIOR APPLICATION NUMBER: US 60/404,249  
; PRIOR FILING DATE: 2002-08-16  
; PRIOR APPLICATION NUMBER: US 60/407,527  
; PRIOR FILING DATE: 2002-08-28  
; PRIOR APPLICATION NUMBER: PCT/US2002/032263  
; PRIOR FILING DATE: 2002-10-09  
; PRIOR APPLICATION NUMBER: US 10/287,994  
; PRIOR FILING DATE: 2002-11-05  
; NUMBER OF SEQ ID NOS: 62  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 52  
; LENGTH: 107  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-11-183-205-52

Query Match 75.7%; Score 28; DB 7; Length 107;  
Best Local Similarity 71.4%; Pred. No. 37;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSNLHS 7  
|:| |||  
Db 50 YTSKLHS 56

RESULT 36  
US-11-009-939-37  
; Sequence 37, Application US/11009939  
; Publication No. US20050265998A1  
; GENERAL INFORMATION:  
; APPLICANT: Elson, Greg Christopher Andrew  
; TITLE OF INVENTION: Neutralizing Antibodies and Methods of Use Thereof  
; FILE REFERENCE: 23135-402  
; CURRENT APPLICATION NUMBER: US/11/009,939  
; CURRENT FILING DATE: 2005-12-10  
; PRIOR APPLICATION NUMBER: 60/528,811  
; PRIOR FILING DATE: 2003-12-10  
; PRIOR APPLICATION NUMBER: 60/528,812  
; PRIOR FILING DATE: 2003-12-10  
; PRIOR APPLICATION NUMBER: 60/528,962  
; PRIOR FILING DATE: 2003-12-10  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 37  
; LENGTH: 108  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-11-009-939-37

Query Match 75.7%; Score 28; DB 7; Length 108;  
Best Local Similarity 71.4%; Pred. No. 37;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSNLHS 7  
|:| |||  
Db 50 YTSKLHS 56

RESULT 37  
US-11-096-074-52

; Sequence 52, Application US/11096074  
; Publication No. US20050260193A1  
; GENERAL INFORMATION:  
; APPLICANT: LIEBERBURG, IVAN  
; TITLE OF INVENTION: STEROID SPARING AGENTS AND METHODS OF USING SAME  
; FILE REFERENCE: 034008-112  
; CURRENT APPLICATION NUMBER: US/11/096,074  
; CURRENT FILING DATE: 2005-04-01  
; PRIOR APPLICATION NUMBER: 60/558,120  
; PRIOR FILING DATE: 2004-04-01  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: PatentIn Ver. 3.3  
; SEQ ID NO 52  
; LENGTH: 109  
; TYPE: PRT  
; ORGANISM: Mus sp.  
US-11-096-074-52

Query Match 75.7%; Score 28; DB 7; Length 109;  
Best Local Similarity 71.4%; Pred. No. 37;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSNLHS 7  
|:| |||  
Db 51 YASRLHS 57

RESULT 38  
US-11-095-822-52  
; Sequence 52, Application US/11095822  
; Publication No. US20060004019A1  
; GENERAL INFORMATION:  
; APPLICANT: LIEBERBURG, IVAN  
; TITLE OF INVENTION: STEROID SPARING AGENTS AND METHODS OF USING SAME  
; FILE REFERENCE: 002010-872  
; CURRENT APPLICATION NUMBER: US/11/095,822  
; CURRENT FILING DATE: 2005-04-01  
; PRIOR APPLICATION NUMBER: 60/558,121  
; PRIOR FILING DATE: 2004-04-01  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: PatentIn Ver. 3.3  
; SEQ ID NO 52  
; LENGTH: 109  
; TYPE: PRT  
; ORGANISM: Mus sp.  
US-11-095-822-52

Query Match 75.7%; Score 28; DB 7; Length 109;  
Best Local Similarity 71.4%; Pred. No. 37;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSNLHS 7  
|:| |||  
Db 51 YASRLHS 57

RESULT 39  
US-11-089-872-5  
; Sequence 5, Application US/11089872  
; Publication No. US20050260212A1  
; GENERAL INFORMATION:  
; APPLICANT: Zhang, Yongke  
; APPLICANT: Ramakrishnan, Vanitha  
; APPLICANT: Law, Debbie  
; TITLE OF INVENTION: ANTI-LFL2 ANTIBODIES FOR THE DIAGNOSIS, PROGNOSIS AND TREATMENT  
; TITLE OF INVENTION: OF CANCER  
; FILE REFERENCE: 05882.0223.NFUS02  
; CURRENT APPLICATION NUMBER: US/11/089,872  
; CURRENT FILING DATE: 2005-03-25  
; PRIOR APPLICATION NUMBER: 60/557,440  
; PRIOR FILING DATE: 2004-03-26  
; PRIOR APPLICATION NUMBER: 60/638,708  
; PRIOR FILING DATE: 2004-12-22

; NUMBER OF SEQ ID NOS: 15  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 5  
 ; LENGTH: 127  
 ; TYPE: PRT  
 ; ORGANISM: Mus musculus  
 US-11-089-872-5

Query Match 75.7%; Score 28; DB 7; Length 127;  
 Best Local Similarity 71.4%; Pred. No. 44;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSNLHS 7  
 Db 69 YTSRLHS 75

RESULT 40  
 US-11-025-712-11  
 ; Sequence 11, Application US/11025712  
 ; Publication No. US20050255108A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bednar, Martin M.  
 ; Thomas, G. Roger  
 ; Gross, Cordell E.  
 ; TITLE OF INVENTION: ANTI-CD18 ANTIBODIES IN STROKE  
 ; NUMBER OF SEQUENCES: 15  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Genentech, Inc.  
 ; STREET: 1 DNA Way  
 ; CITY: South San Francisco  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 94080

; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Winpatin (Genentech)  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/11/025,712  
 ; FILING DATE: 28-Dec-2004  
 ; CLASSIFICATION: <Unknown>  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US/10/404,286  
 ; FILING DATE: 31-Mar-2003  
 ; APPLICATION NUMBER: 09/811384  
 ; FILING DATE: 20-DEC-2000  
 ; APPLICATION NUMBER: 09/251652  
 ; FILING DATE: 17-FEB-2000  
 ; APPLICATION NUMBER: 08/788800  
 ; FILING DATE: 22-JAN-1997  
 ; APPLICATION NUMBER: 60/093038  
 ; FILING DATE: 23-JAN-1996  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Evans, David W.  
 ; REGISTRATION NUMBER: NONE  
 ; REFERENCE/DOCKET NUMBER: P1729C2  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 650/225-1739  
 ; TELEFAX: 650/952-9881

; INFORMATION FOR SEQ ID NO: 11:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 214 amino acids  
 ; TYPE: Amino Acid  
 ; TOPOLOGY: Linear  
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 11:  
 US-11-025-712-11

Query Match 75.7%; Score 28; DB 7; Length 214;  
 Best Local Similarity 71.4%; Pred. No. 77;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSNLHS 7  
 Db 50 YTSILHS 56  
 RESULT 41  
 US-11-173-564-1  
 ; Sequence 1, Application US/11173564  
 ; Publication No. US20050271654A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Rinderknecht, Ernst H.  
 ; APPLICANT: Zapata, Gerardo A.  
 ; TITLE OF INVENTION: ANTIBODY PURIFICATION  
 ; NUMBER OF SEQUENCES: 2  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Genentech, Inc.  
 ; STREET: 460 Point San Bruno Blvd  
 ; CITY: South San Francisco  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 94080  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: patin (Genentech)  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/11/173,564  
 ; FILING DATE: 01-JUL-2005  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/811,757  
 ; FILING DATE: 06-MAR-1997  
 ; CLASSIFICATION:  
 ; APPLICATION NUMBER: 08/425,763  
 ; FILING DATE: 20-APR-1995  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Lee, Wendy M.  
 ; REGISTRATION NUMBER: 00,000  
 ; REFERENCE/DOCKET NUMBER: 941  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 415/225-1994  
 ; TELEFAX: 415/952-9881  
 ; TELEX: 910/371-7168  
 ; INFORMATION FOR SEQ ID NO: 1:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 214 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 US-11-173-564-1

Query Match 75.7%; Score 28; DB 7; Length 214;  
 Best Local Similarity 71.4%; Pred. No. 77;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSNLHS 7  
 Db 50 YTSILHS 56

RESULT 42  
 US-11-183-205-55  
 ; Sequence 55, Application US/11183205  
 ; Publication No. US20060030521A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Neose Technologies, Inc.  
 ; APPLICANT: DePree, Shawn  
 ; APPLICANT: Zopf, David  
 ; APPLICANT: Bayer, Robert  
 ; APPLICANT: Hakes, Caryn  
 ; APPLICANT: Hakes, David  
 ; APPLICANT: Chen, Xi  
 ; TITLE OF INVENTION: REMODELING AND GLYCOCONJUGATION OF PEPTIDES

```

; FILE REFERENCE: 040853-01-5052-US01
; CURRENT APPLICATION NUMBER: US/11/183,205
; CURRENT FILING DATE: 2005-07-15
; PRIOR APPLICATION NUMBER: US 11/183,205
; PRIOR FILING DATE: 2005-07-15
; PRIOR APPLICATION NUMBER: US 60/334,233
; PRIOR FILING DATE: 2001-11-28
; PRIOR APPLICATION NUMBER: US 60/334,301
; PRIOR FILING DATE: 2001-11-28
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: PCT/US2002/032263
; PRIOR FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US 10/287,994
; PRIOR FILING DATE: 2002-11-05
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 55
; LENGTH: 214
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-183-205-55

```

```

Query Match 75.7%; Score 28; DB 7; Length 214;
Best Local Similarity 71.4%; Pred. No. 77;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 1 YSSNLHS 7
|.||||
Db 50 YSTSLHS 56

```

```

RESULT 43
US-11-087-099-7721
; Sequence 7721, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 7721
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Pseudomonas fluorescens PfO-1
US-11-087-099-7721

```

```

Query Match 75.7%; Score 28; DB 7; Length 228;
Best Local Similarity 83.3%; Pred. No. 82;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 1 YSSNLH 6
|||
Db 57 YSSNTH 62

```

```

RESULT 44
US-11-096-568A-23186
; Sequence 23186, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides

```

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; TITLE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 23186
; LENGTH: 315
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(315)
; OTHER INFORMATION: Ceres Seq. ID no. 12411562
US-11-096-568A-23186

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Query Match 75.7%; Score 28; DB 7; Length 315;
Best Local Similarity 71.4%; Pred. No. 1.2e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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QY 1 YSSNLHS 7
:|||||
Db 240 WSSNFHS 246

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RESULT 45
US-11-098-686-10170
; Sequence 10170, Application US/11098686
; Publication No. US20060024696A1
; GENERAL INFORMATION:
; APPLICANT: Kapur, Vivek and Gebhart, Connie J.
; TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES
; TITLE OF INVENTION: FROM LAWSONIA INTRACELLULARIS AND METHODS OF USING
; FILE REFERENCE: 09531-128001
; CURRENT APPLICATION NUMBER: US/11/098,686
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: PCT/US03/31318
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: US 60/416,395
; PRIOR FILING DATE: 2002-10-04
; NUMBER OF SEQ ID NOS: 11433
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10170
; LENGTH: 537
; TYPE: PRT
; ORGANISM: Lawsonia intracellularis
US-11-098-686-10170

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Query Match 75.7%; Score 28; DB 7; Length 537;
Best Local Similarity 83.3%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 YSSNLH 6
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Db 268 YSHNLH 273

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RESULT 46
US-11-096-568A-27962
; Sequence 27962, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 27962
; LENGTH: 562
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:

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; NAME/KEY: misc feature
; LOCATION: (1)..(562)
; OTHER INFORMATION: Ceres Seq. ID no. 2149395
US-11-096-568A-27962

Query Match      75.7%; Score 28; DB 7; Length 562;
Best Local Similarity 85.7%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSNLHS 7
Db 22 YSSNLKS 28

RESULT 47
US-11-096-568A-27961
; Sequence 27961, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 27961
; LENGTH: 570
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(570)
; OTHER INFORMATION: Ceres Seq. ID no. 2149394
US-11-096-568A-27961

Query Match      75.7%; Score 28; DB 7; Length 570;
Best Local Similarity 85.7%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSSNLHS 7
Db 30 YSSNLKS 36

RESULT 48
US-11-167-636-16
; Sequence 16, Application US/11167636
; Publication No. US20060024347A1
; GENERAL INFORMATION:
; APPLICANT: Biosurface Engineering Technologies, Inc.
; APPLICANT: Zamora, Paul O.
; APPLICANT: Campion, Sarah
; TITLE OF INVENTION: Bioactive Peptide Coatings
; FILE REFERENCE: 30817-1008-Util
; CURRENT APPLICATION NUMBER: US/11/167,636
; CURRENT FILING DATE: 2005-06-27
; PRIOR APPLICATION NUMBER: US 11/055,428
; PRIOR FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: US 60/543,616
; PRIOR FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: US 60/583,566
; PRIOR FILING DATE: 2004-06-28
; PRIOR APPLICATION NUMBER: US 60/655,570
; PRIOR FILING DATE: 2005-02-24
; PRIOR APPLICATION NUMBER: US 60/656,174
; PRIOR FILING DATE: 2005-02-25
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 16
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Artificial
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; FEATURE:
; OTHER INFORMATION: synthetic FGF-9 analog
US-11-167-636-16

Query Match      73.0%; Score 27; DB 7; Length 21;
Best Local Similarity 83.3%; Pred. No. 11;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLH 6
Db 1 YSSNLY 6

RESULT 49
US-11-096-568A-30950
; Sequence 30950, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 30950
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(76)
; OTHER INFORMATION: Ceres Seq. ID no. 4981196
US-11-096-568A-30950

Query Match      73.0%; Score 27; DB 7; Length 76;
Best Local Similarity 71.4%; Pred. No. 42;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSSNLHS 7
Db 65 HSSSLHS 71

RESULT 50
US-10-485-788A-809
; Sequence 809, Application US/10485788A
; Publication No. US20050282743A1
; GENERAL INFORMATION:
; APPLICANT: Lu, Peter S.
; APPLICANT: Rabinowitz, Joshua D.
; APPLICANT: Schweizer, Johannes
; APPLICANT: Carrick, Deanna Marie
; APPLICANT: Arbor Vita Corporation
; TITLE OF INVENTION: Molecular Interactions in Cells
; FILE REFERENCE: 20054-003320US
; CURRENT APPLICATION NUMBER: US/10/485,788A
; CURRENT FILING DATE: 2004-02-03
; PRIOR APPLICATION NUMBER: US 60/309,841
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 60/360,061
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: WO PCT/US02/24655
; PRIOR FILING DATE: 2002-08-02
; NUMBER OF SEQ ID NOS: 841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 809
; LENGTH: 84
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-485-788A-809

Query Match      73.0%; Score 27; DB 6; Length 84;
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Best Local Similarity 71.4%; Pred. No. 46;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YSSNLHS 7  
|  
|  
|  
|  
Db 11 YGFNLHS 17

Search completed: April 6, 2006, 09:22:44  
Job time : 16.1186 secs

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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 6, 2006, 08:54:46 ; Search time 66.8136 Seconds  
(without alignments)  
59.186 Million cell updates/sec

Title: US-10-089-500-8

Perfect score: 56

Sequence: 1 HQYSKLPWT 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database : A\_Geneseq\_21.\*

1: Geneseq1980s.\*  
2: Geneseq1990s.\*  
3: Geneseq2000s.\*  
4: Geneseq2001s.\*  
5: Geneseq2002s.\*  
6: Geneseq2003as.\*  
7: Geneseq2003bs.\*  
8: Geneseq2004s.\*  
9: Geneseq2005s.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	56	100.0	9	AAB81984	Aab81984 Gangliosid
2	56	100.0	9	ABU11009	Abu11009 Modified
3	56	100.0	9	ADZ57815	Adz57815 Gangliosid
4	56	100.0	108	AAB81988	Aab81988 Gangliosid
5	56	100.0	108	AAB81986	Aab81986 Gangliosid
6	56	100.0	108	AAB81990	Aab81990 Gangliosid
7	56	100.0	108	ABU11011	Abu11011 Modified
8	56	100.0	108	ABU11013	Abu11013 Modified
9	56	100.0	108	ADZ57819	Adz57819 Gangliosid
10	56	100.0	108	ADZ57822	Adz57822 Gangliosid
11	56	100.0	108	ADZ57823	Adz57823 Gangliosid
12	56	100.0	108	ADZ57817	Adz57817 Gangliosid
13	56	100.0	108	ADZ57820	Adz57820 Gangliosid
14	56	100.0	128	AAR33257	Aar33257 Rat immun
15	56	100.0	128	AAR53340	Aar53340 KM641 H C
16	56	100.0	128	AAV28368	Aay28368 pKM641 LA
17	56	100.0	128	AAB01628	Aab01628 Murine im
18	56	100.0	128	AAB81994	Aab81994 Gangliosid
19	56	100.0	128	AAB81995	Aab81995 Gangliosid
20	56	100.0	128	AAB81997	Aab81997 Gangliosid
21	56	100.0	128	AAB81978	Aab81978 Gangliosid
22	56	100.0	128	AAB81996	Aab81996 Gangliosid
23	56	100.0	128	AAB81999	Aab81999 Gangliosid
24	56	100.0	128	AAB81993	Aab81993 Gangliosid

25	56	100.0	128	4	AAB81992	Aab81992 Gangliosid
26	56	100.0	128	4	AAB81998	Aab81998 Gangliosid
27	56	100.0	128	6	ABU11003	Abu11003 Modified
28	48	85.7	107	9	AEC20796	Aec20796 M-CSF epe
29	48	85.7	107	9	ADY85024	Ady85024 Monoclonal
30	48	85.7	126	2	AAR12237	Aar12237 Mouse Mab
31	48	85.7	127	2	AAR12359	Aar12359 Light (ka
32	48	85.7	214	9	AEC20774	Aec20774 M-CSF epe
33	44	78.6	109	6	ADA89188	Ada89188 Human ant
34	43	76.8	9	9	AEA17144	Aea17144 Human TNF
35	43	76.8	109	9	AEA17138	Aea17138 Human TNF
36	43	76.8	215	5	ABP43158	Abp43158 Human ova
37	42	75.0	107	8	ADO07305	Ado07305 Human pro
38	42	75.0	107	8	ADO07307	Ado07307 Human pro
39	41	73.2	9	9	AEA44051	Aea44051 Anti-TPO
40	41	73.2	106	9	ABE12544	Aeb12544 Antibody
41	41	73.2	106	9	ABE12558	Aeb12558 Humanized
42	41	73.2	108	9	AEA89805	Aea89805 Antibody
43	41	73.2	108	9	AEA44098	Aea44098 Anti-TPO
44	41	73.2	113	4	ABA848936	Aba848936 Anti-TrkA
45	41	73.2	255	8	ADS14282	Adsl4282 Murine pr
46	41	73.2	295	4	AAB48934	Aab48934 Anti-TrkA
47	41	73.2	519	8	ADS14288	Adsl4288 Murine pr
48	40	71.4	8	8	ADR69579	Adr69579 Novel hyb
49	40	71.4	8	8	ADU08271	Adu08271 Heat shoc
50	40	71.4	9	3	AAB06354	Aab06354 Randomise
51	40	71.4	9	3	AAB06352	Aab06352 Randomise
52	40	71.4	107	2	AAR30770	Aar30770 Consensus
53	40	71.4	107	4	AAB62087	Aab62087 Human V1
54	40	71.4	107	4	AAB60400	Aab60400 Consensus
55	40	71.4	107	4	AAB61585	Aab61585 Human var
56	40	71.4	107	8	ADE71454	Ade71454 Human ant
57	40	71.4	107	8	ADJ88008	Adj88008 Human var
58	40	71.4	107	8	ADN12054	Adn12054 Variable
59	40	71.4	107	8	ADP43328	Adp43328 Human mon
60	40	71.4	107	9	ADW21305	Adw21305 Human kap
61	40	71.4	108	2	AAW04177	Aaw04177 Variant v
62	40	71.4	108	2	AAW00834	Aaw00834 Variable
63	40	71.4	108	2	AAW16620	Aaw16620 Anti-huma
64	40	71.4	108	2	AAW70622	Aaw70622 Human con
65	40	71.4	108	3	AAW82345	Aaw82345 Human con
66	40	71.4	108	4	AAE12062	Aae12062 Human ant
67	40	71.4	108	5	ABP61191	Abp61191 Human ant
68	40	71.4	108	8	ADG38991	Adg38991 Human con
69	40	71.4	108	8	ADR03366	Adr03366 Human sub
70	40	71.4	108	8	ADP79572	Adp79572 Human kap
71	40	71.4	109	5	AAU74544	Aau74544 Human sub
72	40	71.4	109	9	AEA38745	Aea38745 Human VL
73	40	71.4	110	5	AAE28149	Aae28149 Human con
74	40	71.4	111	9	ADV21490	Adv21490 Human ant
75	40	71.4	111	9	ADZ83509	Adz83509 CCR5 ligh
76	40	71.4	125	6	ABG71755	Abg71755 Variable
77	40	71.4	125	9	ADY58503	Ady58503 Consensus
78	40	71.4	126	2	AAV17492	Aav17492 Consensus
79	40	71.4	126	2	AAV08702	Aav08702 Human lig
80	40	71.4	126	2	AAV08703	Aav08703 Human lig
81	40	71.4	126	2	AAV08701	Aav08701 Human con
82	40	71.4	126	3	AAV83645	Aav83645 Conserved
83	40	71.4	126	5	ABB04943	Abb04943 Human CD2
84	40	71.4	126	5	ABU10768	Abu10768 Amino aci
85	40	71.4	126	6	ABG71656	Abg71656 Consensus
86	40	71.4	126	6	ABG71769	Abg71769 Variable
87	40	71.4	126	7	ADD00054	Add00054 Human con
88	40	71.4	128	5	ABU10774	Abu10774 Light cha
89	40	71.4	129	6	ABG71751	Abg71751 Antibody
90	40	71.4	132	5	AAU10775	Aau10775 Light cha
91	40	71.4	133	6	ABG71752	Abg71752 Antibody
92	40	71.4	153	6	AEA17763	Aea17763 Hybridoma
93	40	71.4	154	6	ABO04851	Ab004851 Human epi
94	40	71.4	154	9	AEA17778	Aea17778 Hybridoma
95	40	71.4	157	6	ABO04855	Ab004855 Human epi
96	40	71.4	157	9	AEA17779	Aea17779 Hybridoma
97	40	71.4	159	9	AEA17767	Aea17767 Hybridoma

98	40	71.4	491	9	ADV21543	Mature fo	171	39	69.6	113	2	AAR92993	Monoclonal
99	40	71.4	492	9	ADZ83586	CD3 speci	172	39	69.6	113	2	AAR92995	Humanisee
100	40	71.4	492	9	ADZ83594	CD3 speci	173	39	69.6	214	7	ADC26157	Anti-VEGF
101	40	71.4	492	9	ADZ83590	CD3 speci	174	39	69.6	214	7	ADC26154	Parent an
102	40	71.4	492	9	ADZ83588	CD3 speci	175	39	69.6	214	7	ADC26156	Anti-VEGF
103	40	71.4	492	9	ADZ83584	CD3 speci	176	39	69.6	237	2	AAW70703	Protein e
104	40	71.4	492	9	ADZ83592	CD3 speci	177	39	69.6	237	5	ABP81107	Anti-VEGF
105	40	71.4	497	9	ADV21541	Mature fo	178	39	69.6	237	5	ABP51952	Plasmid p
106	39	69.6	9	2	AAW70616	Anti-VEGF	179	39	69.6	237	8	ADO14128	Plasmid p
107	39	69.6	9	3	AAW70633	Randomise	180	39	69.6	237	8	ADO14131	Plasmid p
108	39	69.6	9	5	ABP61185	Humanised	181	39	69.6	237	8	ADO90703	Anti-VEGF
109	39	69.6	103	7	ADF09995	Antibody	182	39	69.6	237	8	ADO90701	Anti-VEGF
110	39	69.6	103	7	ADF10059	VEGF anti	183	39	69.6	237	8	ADO90705	Anti-VEGF
111	39	69.6	107	2	AAW68804	Variable	184	39	69.6	237	8	ADO90709	Anti-VEGF
112	39	69.6	107	2	AAW68805	Variable	185	39	69.6	237	8	ADO90723	Anti-VEGF
113	39	69.6	107	2	AAW70623	Humanised	186	39	69.6	237	8	ADO90721	Anti-VEGF
114	39	69.6	107	2	AAW70625	Humanised	187	39	69.6	237	8	ADO90707	Anti-VEGF
115	39	69.6	107	5	ABP61192	Humanised	188	39	69.6	258	8	ADO61167	Nostoc sp
116	39	69.6	107	5	ABP61194	Humanised	189	39	69.6	258	8	ADO61084	Nostoc sp
117	39	69.6	107	6	ABR40159	Humanised	190	39	69.6	258	8	ADP74100	Nostoc sp
118	39	69.6	107	8	ADG64762	CI mouse	191	39	69.6	258	8	ADQ38253	Nostoc sp
119	39	69.6	107	9	AEA40449	Anti-VEGF	192	39	69.6	258	8	ADR03868	Nostoc sp
120	39	69.6	107	9	AEA40445	Anti-VEGF	193	39	69.6	258	8	ADR03948	Nostoc ke
121	39	69.6	107	9	AEA40440	Anti-VEGF	194	39	69.6	258	9	ADY52414	Novel ket
122	39	69.6	107	9	AEA40443	Anti-VEGF	195	39	69.6	258	9	ADY51347	Nostoc sp
123	39	69.6	107	9	AEA40450	Anti-VEGF	196	39	69.6	263	2	AAR15055	Qm212 ein
124	39	69.6	107	9	AEA40452	Anti-VEGF	197	39	69.6	351	4	ABP61119	Drosophila
125	39	69.6	107	9	AEA40447	Anti-VEGF	198	39	69.6	650	5	ABP61241	Phase-dis
126	39	69.6	107	9	AEA40446	Anti-VEGF	199	39	69.6	650	6	ABR62591	Anti-CD7
127	39	69.6	107	9	AEA40439	Anti-VEGF	200	39	69.6	651	6	ABR62590	Anti-CD7
128	39	69.6	107	9	AEA40444	Anti-VEGF	201	38	67.9	9	AEA40655	Anti-VEGF	
129	39	69.6	107	9	AEA40442	Anti-VEGF	202	38	67.9	107	5	ABP79887	Anti-MN a
130	39	69.6	107	9	AEA40451	Anti-VEGF	203	38	67.9	107	5	ABP82005	G250 ligh
131	39	69.6	107	9	AEA40448	Anti-VEGF	204	38	67.9	107	9	AEA40462	Anti-VEGF
132	39	69.6	107	9	AEA40722	Anti-VEGF	205	38	67.9	107	9	AEA40467	Anti-VEGF
133	39	69.6	107	9	AEA40441	Anti-VEGF	206	38	67.9	116	4	ABP67070	Murine G2
134	39	69.6	108	2	AAW70620	Anti-VEGF	207	38	67.9	133	7	ADC24968	Murine G2
135	39	69.6	108	2	AAW70618	Anti-VEGF	208	38	67.9	133	7	ADK51723	Murine G2
136	39	69.6	108	2	AAW70696	Anti-VEGF	209	38	67.9	352	5	AAU87031	Adenoviru
137	39	69.6	108	5	ABP61189	Murine an	210	38	67.9	358	6	ABM70568	Photorhab
138	39	69.6	108	5	ABP61265	Humanised	211	38	67.9	389	3	AAV32465	Schizochy
139	39	69.6	108	5	ABP61187	Humanised	212	38	67.9	465	5	AAU87033	Adenoviru
140	39	69.6	108	8	ADG31770	V(L) doma	213	38	67.9	529	8	ADP44832	Human but
141	39	69.6	108	8	ADG31782	V(L) doma	214	38	67.9	530	9	AEA60644	Human but
142	39	69.6	108	8	ADG31768	V(L) doma	215	38	67.9	565	5	AAU87034	Adenoviru
143	39	69.6	108	8	ADG31893	V(L) proc	216	38	67.9	566	8	ADH13709	Human ENZ
144	39	69.6	108	9	ADX80647	Humanized	217	38	67.9	573	9	AEA60535	Human but
145	39	69.6	110	2	AAW70673	Anti-VEGF	218	38	67.9	573	9	AEA60495	Human but
146	39	69.6	110	2	AAW70685	Anti-VEGF	219	38	67.9	574	5	AAE25235	Human but
147	39	69.6	110	2	AAW70681	Anti-VEGF	220	38	67.9	574	5	AAO18934	Human but
148	39	69.6	110	2	AAW70683	Anti-VEGF	221	38	67.9	574	5	AAO18977	Human but
149	39	69.6	110	2	AAW70677	Anti-VEGF	222	38	67.9	574	5	AAO18957	Human but
150	39	69.6	110	2	AAW70667	Anti-VEGF	223	38	67.9	574	5	AAO18968	Human but
151	39	69.6	110	2	AAW70675	Anti-VEGF	224	38	67.9	574	5	AAO18899	Human but
152	39	69.6	110	2	AAW70679	Anti-VEGF	225	38	67.9	574	5	AAO18900	Human but
153	39	69.6	110	3	AAW05897	Humanised	226	38	67.9	574	5	AAO18949	Human but
154	39	69.6	110	3	AAW05898	Humanised	227	38	67.9	574	5	AAO18956	Human but
155	39	69.6	110	3	AAW13378	Anti-VEGF	228	38	67.9	574	5	AAO18926	Human but
156	39	69.6	110	3	AAW13380	Anti-VEGF	229	38	67.9	574	5	AAO18939	Human but
157	39	69.6	110	3	AAW13379	Anti-VEGF	230	38	67.9	574	5	AAO18943	Human but
158	39	69.6	110	3	AAW13386	Anti-VEGF	231	38	67.9	574	5	AAO18963	Human but
159	39	69.6	110	3	AAW13387	Anti-VEGF	232	38	67.9	574	5	AAO18981	Human but
160	39	69.6	110	3	AAW13377	Anti-VEGF	233	38	67.9	574	5	AAO18901	Human but
161	39	69.6	110	3	AAW13388	Anti-VEGF	234	38	67.9	574	5	AAO18927	Human but
162	39	69.6	110	3	AAW13376	F(ab)-12	235	38	67.9	574	5	AAO18932	Human but
163	39	69.6	110	5	ABP61242	Humanised	236	38	67.9	574	5	AAO18940	Human but
164	39	69.6	110	5	ABP61250	Humanised	237	38	67.9	574	5	AAO18942	Human but
165	39	69.6	110	5	ABP61256	Humanised	238	38	67.9	574	5	AAO18950	Human but
166	39	69.6	110	5	ABP61252	Humanised	239	38	67.9	574	5	AAO18951	Human but
167	39	69.6	110	5	ABP61254	Humanised	240	38	67.9	574	5	AAO18959	Human but
168	39	69.6	110	5	ABP61244	Humanised	241	38	67.9	574	5	AAO18960	Human but
169	39	69.6	110	5	ABP61246	Humanised	242	38	67.9	574	5	AAO18975	Human but
170	39	69.6	110	5	ABP61248	Humanised	243	38	67.9	574	5	AAO18982	Human but



244	38	67.9	574	5	AAO18952	Aao18952	Human	but	317	38	67.9	574	8	ADP44763	Adp44763	Human	but
245	38	67.9	574	5	AAO18972	Aao18972	Human	but	318	38	67.9	574	8	ADP44765	Adp44765	Human	but
246	38	67.9	574	5	AAO18974	Aao18974	Human	but	319	38	67.9	574	8	ADP44767	Adp44767	Human	but
247	38	67.9	574	5	AAO18953	Aao18953	Human	but	320	38	67.9	574	8	ADP44772	Adp44772	Human	but
248	38	67.9	574	5	AAO18958	Aao18958	Human	but	321	38	67.9	574	8	ADP44775	Adp44775	Human	but
249	38	67.9	574	5	AAO18970	Aao18970	Human	but	322	38	67.9	574	8	ADP44797	Adp44797	Human	but
250	38	67.9	574	5	AAO18971	Aao18971	Human	but	323	38	67.9	574	8	ADP44817	Adp44817	Human	but
251	38	67.9	574	5	AAO18903	Aao18903	Horse	but	324	38	67.9	574	8	ADP44741	Adp44741	Human	but
252	38	67.9	574	5	AAO18930	Aao18930	Human	but	325	38	67.9	574	8	ADP44748	Adp44748	Human	but
253	38	67.9	574	5	AAO18944	Aao18944	Human	but	326	38	67.9	574	8	ADP44807	Adp44807	Human	but
254	38	67.9	574	5	AAO18978	Aao18978	Human	but	327	38	67.9	574	8	ADP44827	Adp44827	Human	but
255	38	67.9	574	5	AAO18983	Aao18983	Human	but	328	38	67.9	574	8	ADP44745	Adp44745	Human	but
256	38	67.9	574	5	AAO18929	Aao18929	Human	but	329	38	67.9	574	8	ADP44752	Adp44752	Human	but
257	38	67.9	574	5	AAO18933	Aao18933	Human	but	330	38	67.9	574	8	ADP44776	Adp44776	Human	but
258	38	67.9	574	5	AAO18938	Aao18938	Human	but	331	38	67.9	574	8	ADP44799	Adp44799	Human	but
259	38	67.9	574	5	AAO18979	Aao18979	Human	but	332	38	67.9	574	8	ADP44813	Adp44813	Human	but
260	38	67.9	574	5	AAO18980	Aao18980	Human	but	333	38	67.9	574	8	ADP44824	Adp44824	Human	but
261	38	67.9	574	5	AAO18945	Aao18945	Human	but	334	38	67.9	574	8	ADP44826	Adp44826	Human	but
262	38	67.9	574	5	AAO18967	Aao18967	Human	but	335	38	67.9	574	8	ADP44829	Adp44829	Human	but
263	38	67.9	574	5	AAO18902	Aao18902	Human	but	336	38	67.9	574	8	ADP44740	Adp44740	Human	but
264	38	67.9	574	5	AAO18935	Aao18935	Human	but	337	38	67.9	574	8	ADP44751	Adp44751	Human	but
265	38	67.9	574	5	AAO18947	Aao18947	Human	but	338	38	67.9	574	8	ADP44768	Adp44768	Human	but
266	38	67.9	574	5	AAO18965	Aao18965	Human	but	339	38	67.9	574	8	ADP44781	Adp44781	Human	but
267	38	67.9	574	5	AAO18937	Aao18937	Human	but	340	38	67.9	574	8	ADP44739	Adp44739	Human	but
268	38	67.9	574	5	AAO18948	Aao18948	Human	but	341	38	67.9	574	8	ADP44746	Adp44746	Human	but
269	38	67.9	574	5	AAO18954	Aao18954	Human	but	342	38	67.9	574	8	ADP44759	Adp44759	Human	but
270	38	67.9	574	5	AAO18955	Aao18955	Human	but	343	38	67.9	574	8	ADP44771	Adp44771	Human	but
271	38	67.9	574	5	AAO18936	Aao18936	Human	but	344	38	67.9	574	8	ADP44810	Adp44810	Human	but
272	38	67.9	574	5	AAO18941	Aao18941	Human	but	345	38	67.9	574	8	ADP44814	Adp44814	Human	but
273	38	67.9	574	5	AAO18961	Aao18961	Human	but	346	38	67.9	574	8	ADP44831	Adp44831	Human	but
274	38	67.9	574	5	AAO18964	Aao18964	Human	but	347	38	67.9	574	8	ADP44754	Adp44754	Human	but
275	38	67.9	574	5	AAO18969	Aao18969	Human	but	348	38	67.9	574	8	ADP44758	Adp44758	Human	but
276	38	67.9	574	5	AAO18931	Aao18931	Human	but	349	38	67.9	574	8	ADP44821	Adp44821	Human	but
277	38	67.9	574	5	AAO18946	Aao18946	Human	but	350	38	67.9	574	8	ADP44639	Adp44639	Human	but
278	38	67.9	574	5	AAO18962	Aao18962	Human	but	351	38	67.9	574	8	ADP44743	Adp44743	Human	but
279	38	67.9	574	5	AAO18973	Aao18973	Human	but	352	38	67.9	574	8	ADP44749	Adp44749	Human	but
280	38	67.9	574	5	AAO18976	Aao18976	Human	but	353	38	67.9	574	8	ADP44795	Adp44795	Human	but
281	38	67.9	574	5	AAO18928	Aao18928	Human	but	354	38	67.9	574	8	ADP44822	Adp44822	Human	but
282	38	67.9	574	5	AAO18966	Aao18966	Human	but	355	38	67.9	574	8	ADP44833	Adp44833	Human	but
283	38	67.9	574	5	AAO18898	Aao18898	Human	but	356	38	67.9	574	8	ADP44744	Adp44744	Human	but
284	38	67.9	574	6	ABR62391	Abw62391	Human	but	357	38	67.9	574	8	ADP44774	Adp44774	Human	but
285	38	67.9	574	7	ABW00724	Abw00724	Human	but	358	38	67.9	574	8	ADP44816	Adp44816	Human	but
286	38	67.9	574	7	ABW00695	Abw00695	Human	but	359	38	67.9	574	8	ADP44761	Adp44761	Human	but
287	38	67.9	574	7	ABW00725	Abw00725	Human	but	360	38	67.9	574	8	ADP44777	Adp44777	Human	but
288	38	67.9	574	7	ABW00722	Abw00722	Human	but	361	38	67.9	574	8	ADP44782	Adp44782	Human	but
289	38	67.9	574	7	ABW00723	Abw00723	Human	but	362	38	67.9	574	8	ADP44823	Adp44823	Human	but
290	38	67.9	574	8	ADP44756	Adp44756	Human	but	363	38	67.9	574	8	ADP44738	Adp44738	Human	but
291	38	67.9	574	8	ADP44760	Adp44760	Human	but	364	38	67.9	574	8	ADP44801	Adp44801	Human	but
292	38	67.9	574	8	ADP44762	Adp44762	Human	but	365	38	67.9	574	8	ADP44820	Adp44820	Human	but
293	38	67.9	574	8	ADP44769	Adp44769	Human	but	366	38	67.9	574	8	ADP44785	Adp44785	Human	but
294	38	67.9	574	8	ADP44800	Adp44800	Human	but	367	38	67.9	574	8	ADP44798	Adp44798	Human	but
295	38	67.9	574	8	ADP44819	Adp44819	Human	but	368	38	67.9	574	8	ADP44803	Adp44803	Human	but
296	38	67.9	574	8	ADP44757	Adp44757	Human	but	369	38	67.9	574	8	ADP44815	Adp44815	Human	but
297	38	67.9	574	8	ADP44766	Adp44766	Human	but	370	38	67.9	574	8	ADP44818	Adp44818	Human	but
298	38	67.9	574	8	ADP44783	Adp44783	Human	but	371	38	67.9	574	8	ADP44753	Adp44753	Human	but
299	38	67.9	574	8	ADP44784	Adp44784	Human	but	372	38	67.9	574	8	ADP44780	Adp44780	Human	but
300	38	67.9	574	8	ADP44796	Adp44796	Human	but	373	38	67.9	574	8	ADP44805	Adp44805	Human	but
301	38	67.9	574	8	ADP44804	Adp44804	Human	but	374	38	67.9	574	8	ADP44806	Adp44806	Human	but
302	38	67.9	574	8	ADP44812	Adp44812	Human	but	375	38	67.9	574	8	ADP44809	Adp44809	Human	but
303	38	67.9	574	8	ADP44750	Adp44750	Human	but	376	38	67.9	574	8	ADP44807	Adp44807	Human	but
304	38	67.9	574	8	ADP44764	Adp44764	Human	but	377	38	67.9	574	8	ADP44803	Adp44803	Human	but
305	38	67.9	574	8	ADP44770	Adp44770	Human	but	378	38	67.9	574	8	ADP44805	Adp44805	Human	but
306	38	67.9	574	8	ADP44773	Adp44773	Human	but	379	38	67.9	574	8	ADP44809	Adp44809	Human	but
307	38	67.9	574	8	ADP44778	Adp44778	Human	but	380	38	67.9	574	8	ADP44805	Adp44805	Human	but
308	38	67.9	574	8	ADP44779	Adp44779	Human	but	381	38	67.9	574	8	ADP44809	Adp44809	Human	but
309	38	67.9	574	8	ADP44808	Adp44808	Human	but	382	38	67.9	574	8	ADP44805	Adp44805	Human	but
310	38	67.9	574	8	ADP44742	Adp44742	Human	but	383	38	67.9	574	8	ADP44805	Adp44805	Human	but
311	38	67.9	574	8	ADP44747	Adp44747	Human	but	384	38	67.9	574	8	ADP44805	Adp44805	Human	but
312	38	67.9	574	8	ADP44802	Adp44802	Human	but	385	38	67.9	574	8	ADP44805	Adp44805	Human	but
313	38	67.9	574	8	ADP44809	Adp44809	Human	but	386	38	67.9	574	8	ADP44805	Adp44805	Human	but
314	38	67.9	574	8	ADP44811	Adp44811	Human	but	387	38	67.9	574	8	ADP44805	Adp44805	Human	but
315	38	67.9	574	8	ADP44828	Adp44828	Human	but	388	38	67.9	574	8	ADP44805	Adp44805	Human	but
316	38	67.9	574	8	ADP44755	Adp44755	Human	but	389	38	67.9	574	8	ADP44805	Adp44805	Human	but

390	38	67.9	574	8	ADR01067	Adr01067 Human but	463	38	67.9	574	9	AEA60445	Aea60445 Human but
391	38	67.9	574	8	ADR01073	Adr01073 Human but	464	38	67.9	574	9	AEA60453	Aea60453 Human but
392	38	67.9	574	8	ADR01061	Adr01061 Human but	465	38	67.9	574	9	AEA60499	Aea60499 Human but
393	38	67.9	574	8	ADR01065	Adr01065 Human but	466	38	67.9	574	9	AEA60507	Aea60507 Human but
394	38	67.9	574	8	ADR01071	Adr01071 Human but	467	38	67.9	574	9	AEA60545	Aea60545 Human but
395	38	67.9	574	8	ADR01035	Adr01035 Human but	468	38	67.9	574	9	AEA60457	Aea60457 Human but
396	38	67.9	574	8	ADR01043	Adr01043 Butyrylch	469	38	67.9	574	9	AEA60467	Aea60467 Human but
397	38	67.9	574	8	ADR01037	Adr01037 Human but	470	38	67.9	574	9	AEA60501	Aea60501 Human but
398	38	67.9	574	8	ADR01049	Adr01049 Human but	471	38	67.9	574	9	AEA60567	Aea60567 Human but
399	38	67.9	574	8	ADR01069	Adr01069 Human but	472	38	67.9	574	9	AEA60469	Aea60469 Human but
400	38	67.9	574	8	ADR01078	Adr01078 Human but	473	38	67.9	574	9	AEA60579	Aea60579 Human but
401	38	67.9	574	9	AEA60543	Aea60543 Human but	474	38	67.9	574	9	AEA60475	Aea60475 Human but
402	38	67.9	574	9	AEA60589	Aea60589 Human but	475	38	67.9	574	9	AEA60541	Aea60541 Human but
403	38	67.9	574	9	AEA60493	Aea60493 Human but	476	38	67.9	574	9	AEA60569	Aea60569 Human but
404	38	67.9	574	9	AEA60515	Aea60515 Human but	477	38	67.9	574	9	AEA60577	Aea60577 Human but
405	38	67.9	574	9	AEA60547	Aea60547 Human but	478	38	67.9	574	9	AEA60595	Aea60595 Human but
406	38	67.9	574	9	AEA60573	Aea60573 Human but	479	38	67.9	574	9	AEA60505	Aea60505 Human but
407	38	67.9	574	9	AEA60607	Aea60607 Human but	480	38	67.9	574	9	AEA60539	Aea60539 Human but
408	38	67.9	574	9	AEA60633	Aea60633 Human but	481	38	67.9	574	9	AEA60581	Aea60581 Human but
409	38	67.9	574	9	AEA60479	Aea60479 Human but	482	38	67.9	574	9	AEA60587	Aea60587 Human but
410	38	67.9	574	9	AEA60511	Aea60511 Human but	483	38	67.9	574	9	AEA60609	Aea60609 Human but
411	38	67.9	574	9	AEA60571	Aea60571 Human but	484	38	67.9	602	2	AA37442 Full-leng	Aar37442 Full-leng
412	38	67.9	574	9	AEA60601	Aea60601 Human but	485	38	67.9	602	3	AA49486	Aay49486 Human but
413	38	67.9	574	9	AEA60605	Aea60605 Human but	486	38	67.9	602	3	AA49481	Aay49481 Human but
414	38	67.9	574	9	AEA60611	Aea60611 Human but	487	38	67.9	602	3	AA49481	Aay49481 Human but
415	38	67.9	574	9	AEA60617	Aea60617 Human but	488	38	67.9	602	3	AA49472	Aay49472 Human but
416	38	67.9	574	9	AEA60625	Aea60625 Human but	489	38	67.9	602	3	AA49474	Aay49474 Human but
417	38	67.9	574	9	AEA60635	Aea60635 Human but	490	38	67.9	602	3	AA49477	Aay49477 Human but
418	38	67.9	574	9	AEA60455	Aea60455 Human but	491	38	67.9	602	3	AA49480	Aay49480 Human but
419	38	67.9	574	9	AEA60487	Aea60487 Human but	492	38	67.9	602	3	AA49484	Aay49484 Human but
420	38	67.9	574	9	AEA60489	Aea60489 Human but	493	38	67.9	602	3	AA49485	Aay49485 Human but
421	38	67.9	574	9	AEA60449	Aea60449 Human but	494	38	67.9	602	3	AA49482	Aay49482 Human but
422	38	67.9	574	9	AEA60473	Aea60473 Human but	495	38	67.9	602	3	AA49476	Aay49476 Human but
423	38	67.9	574	9	AEA60517	Aea60517 Human but	496	38	67.9	602	3	AA49487	Aay49487 Human but
424	38	67.9	574	9	AEA60537	Aea60537 Human but	497	38	67.9	602	3	AA49479	Aay49479 Human but
425	38	67.9	574	9	AEA60603	Aea60603 Human but	498	38	67.9	602	3	AA49478	Aay49478 Human but
426	38	67.9	574	9	AEA60619	Aea60619 Human but	499	38	67.9	602	3	AA49483	Aay49483 Human but
427	38	67.9	574	9	AEA60523	Aea60523 Human but	500	38	67.9	602	3	AA49473	Aay49473 Human but
428	38	67.9	574	9	AEA60583	Aea60583 Human but	501	38	67.9	602	3	AA49488	Aay49488 Human but
429	38	67.9	574	9	AEA60599	Aea60599 Human but	502	38	67.9	602	3	AA49471	Aay49471 Human will
430	38	67.9	574	9	AEA60631	Aea60631 Human but	503	38	67.9	602	3	AA49475	Aay49475 Human but
431	38	67.9	574	9	AEA60451	Aea60451 Human but	504	38	67.9	602	3	AA49473	Aay49473 Human will
432	38	67.9	574	9	AEA60459	Aea60459 Human but	505	38	67.9	602	3	AA49474	Aay49474 Human but
433	38	67.9	574	9	AEA60481	Aea60481 Human but	506	38	67.9	602	5	AAO18897	Aeol18897 Human but
434	38	67.9	574	9	AEA60497	Aea60497 Human but	507	38	67.9	602	6	ABR62392	ABr62392 Human but
435	38	67.9	574	9	AEA60509	Aea60509 Human but	508	38	67.9	602	7	ADF90908	Adf90908 Human hep
436	38	67.9	574	9	AEA60519	Aea60519 Human but	509	38	67.9	602	7	AD287330	Ad287330 Human but
437	38	67.9	574	9	AEA60531	Aea60531 Human but	510	38	67.9	635	1	AAp60097 Sequence	Aap60097 Sequence
438	38	67.9	574	9	AEA60585	Aea60585 Human but	511	38	67.9	635	2	AAr41509 Full-leng	Aar41509 Full-leng
439	38	67.9	574	9	AEA60597	Aea60597 Human but	512	38	67.9	765	8	ADp44643	Adp44643 Human ant
440	38	67.9	574	9	AEA60621	Aea60621 Human but	513	38	67.9	765	9	AEA60643	Aea60643 Human ant
441	38	67.9	574	9	AEA60629	Aea60629 Human but	514	38	67.9	782	8	ADp44637	Adp44637 Murine an
442	38	67.9	574	9	AEA60471	Aea60471 Human but	515	38	67.9	782	9	AEA60463	Aea60463 Mouse ant
443	38	67.9	574	9	AEA60491	Aea60491 Human but	516	37	66.1	9	2	AAW70695	Aaw70695 Anti-VEGF
444	38	67.9	574	9	AEA60513	Aea60513 Human but	517	37	66.1	9	3	AABo6351	Aab06351 Randomlee
445	38	67.9	574	9	AEA60533	Aea60533 Human but	518	37	66.1	9	5	ABp61264	Abp61264 Anti-VEGF
446	38	67.9	574	9	AEA60465	Aea60465 Human but	519	37	66.1	9	7	ADp94242	Adp94242 Mouse HUI
447	38	67.9	574	9	AEA60485	Aea60485 Human but	520	37	66.1	9	8	ADo60481	Ado60481 Mouse ant
448	38	67.9	574	9	AEA60485	Aea60485 Human but	521	37	66.1	9	9	AEA40653	Aea40653 Anti-VEGF
449	38	67.9	574	9	AEA60527	Aea60527 Human but	522	37	66.1	9	9	ABE24633	Aeb24633 Humanized
450	38	67.9	574	9	AEA60593	Aea60593 Human but	523	37	66.1	58	4	AAm95612	Aam95612 Human rep
451	38	67.9	574	9	AEA60447	Aea60447 Human but	524	37	66.1	58	4	AAm95612	Aam95612 Human rep
452	38	67.9	574	9	AEA60477	Aea60477 Human but	525	37	66.1	94	4	AAO10270	Aao10270 Human pol
453	38	67.9	574	9	AEA60483	Aea60483 Human but	526	37	66.1	107	9	AEA40454	Aea40454 Anti-VEGF
454	38	67.9	574	9	AEA60503	Aea60503 Human but	527	37	66.1	108	8	ADo60445	Ado60445 Humanised
455	38	67.9	574	9	AEA60529	Aea60529 Human but	528	37	66.1	108	8	ADo60443	Ado60443 Mouse ant
456	38	67.9	574	9	AEA60521	Aea60521 Human but	529	37	66.1	108	9	ABE24597	Aeb24597 Humanized
457	38	67.9	574	9	AEA60575	Aea60575 Human but	530	37	66.1	108	9	ABE24597	Aeb24597 Murine MA
458	38	67.9	574	9	AEA60591	Aea60591 Human but	531	37	66.1	108	9	ABE24642	Aeb24642 Humanized
459	38	67.9	574	9	AEA60613	Aea60613 Human but	532	37	66.1	112	4	AAE00697	Aae00697 Human hum
460	38	67.9	574	9	AEA60615	Aea60615 Human but	533	37	66.1	122	5	ADK35007	Adk35007 Novel hum
461	38	67.9	574	9	AEA60623	Aea60623 Human but	534	37	66.1	128	6	ABb82797	Abb82797 Antibody
462	38	67.9	574	9	AEA60639	Aea60639 Human but	535	37	66.1	213	4	ABg26815	Abg26815 Novel hum

536	37	66.1	214	3	Aau78253	Mouse agg	609	35	62.5	233	2	AAR22755	Reshaped
537	37	66.1	309	4	AAB70841	SNV-env 1	610	35	62.5	241	4	AAB82912	Human imm
538	37	66.1	821	7	ADD43916	Chlamydia	611	35	62.5	253	9	ADY52916	Nostoc pu
539	37	66.1	821	9	AEA19208	Chlamydia	612	35	62.5	254	8	ADY52971	Nostoc pu
540	37	66.1	856	2	AAY37408	Protein i	613	35	62.5	291	8	ADN06993	Human BFG
541	37	66.1	1149	7	ABM90357	Rice abio	614	35	62.5	318	6	ABU38309	Protein e
542	37	66.1	1498	7	ABW77084	Rat sulph	615	35	62.5	343	7	ABO80459	Pseudomon
543	37	66.1	1498	2	AAR77085	Hamster s	616	35	62.5	346	5	ABB92632	Herbicida
544	37	66.1	1582	2	AAR77088	Hamster s	617	35	62.5	396	5	ABP39701	Staphyloc
545	37	66.1	1582	2	AAR77087	Rat sulph	618	35	62.5	435	5	ADY29954	Human CGI
546	36	64.3	100	3	ABD23346	Drosophil	619	35	62.5	440	8	ADS07495	Staphyloc
547	36	64.3	114	8	ADX91095	Plant ful	620	35	62.5	469	4	AU51944	Propionib
548	36	64.3	121	8	ADO66608	Novel hum	621	35	62.5	469	6	ABM48463	Propionib
549	36	64.3	140	2	AAR13845	Fusaric a	622	35	62.5	480	8	ADN26378	Bacterial
550	36	64.3	173	8	ADK52430	Human ant	623	35	62.5	493	5	ABP73490	Candida a
551	36	64.3	193	4	AAG84949	Shrimp wh	624	35	62.5	530	8	ADY07673	Plant ful
552	36	64.3	193	8	ADX90439	Plant ful	625	35	62.5	533	5	AAE25072	Murine CI
553	36	64.3	220	4	ABG04607	Novel hum	626	35	62.5	535	8	ADN99732	Novel hum
554	36	64.3	239	6	ABU07879	Venezuela	627	35	62.5	535	8	ADP23947	PRO poly
555	36	64.3	240	6	ABU07882	Venezuela	628	35	62.5	542	8	ADY10824	Plant ful
556	36	64.3	240	6	ABU07880	Venezuela	629	35	62.5	574	5	AAO18905	Rat butyr
557	36	64.3	240	6	ABU07883	Venezuela	630	35	62.5	574	8	ADR01081	Horse but
558	36	64.3	240	6	ABU07881	Venezuela	631	35	62.5	585	2	AAV29953	Human CGI
559	36	64.3	240	8	ADR59119	Anti-K88/	632	35	62.5	585	6	ABR58055	Human bee
560	36	64.3	296	8	ADS20752	SBP tagge	633	35	62.5	607	8	ADN47292	Thermococ
561	36	64.3	393	8	ADX76325	Plant ful	634	35	62.5	638	4	ABG13913	Novel hum
562	36	64.3	438	6	ABU32283	Protein e	635	35	62.5	639	7	ADI21608	Novel hum
563	36	64.3	460	6	ABM67944	Photorhab	636	35	62.5	644	7	ABM85671	Human pro
564	36	64.3	500	7	ADM26228	Hyperther	637	35	62.5	644	8	ABM82374	Tumour-as
565	36	64.3	518	5	ABB91462	Herbicida	638	35	62.5	644	9	ADY17181	PRO poly
566	36	64.3	525	9	ADY64624	S. mansoni	639	35	62.5	710	5	AAE27069	Mouse TCR
567	36	64.3	588	8	ADN23849	Bacterial	640	35	62.5	728	7	ABO73441	Pseudomon
568	36	64.3	622	4	ABB60638	Drosophil	641	35	62.5	738	7	ABO78545	Pseudomon
569	36	64.3	1030	3	ABB23339	Drosophil	642	35	62.5	766	7	ADI21131	Novel hum
570	36	64.3	1030	3	AAU07472	Drosophil	643	35	62.5	784	6	ABP71687	Lactococc
571	35	62.5	9	4	ADY26806	Synthetic	644	35	62.5	825	8	ADF43080	Bacillus
572	35	62.5	9	9	ADY26806	Human ant	645	35	62.5	831	8	ADI81606	Human van
573	35	62.5	9	9	ADY26812	Human ant	646	35	62.5	956	8	ADN17523	Bacterial
574	35	62.5	9	9	AEA40650	Anti-VEGF	647	35	62.5	989	4	AAU00860	Human bon
575	35	62.5	9	9	AEA40652	Anti-VEGF	648	35	62.5	1934	7	ADE95604	Human NOV
576	35	62.5	30	2	AAV29956	Human CGI	649	35	62.5	4243	8	ADR40115	Human PKH
577	35	62.5	52	4	ABB16009	Human ner	650	35	62.5	4243	8	ADR39911	Human PKH
578	35	62.5	78	6	ABR62710	Human imm	651	35	62.5	5183	6	AAE14793	Human mic
579	35	62.5	78	8	ADP20976	Human sec	652	35	62.5	5183	8	ADO44006	Amino aci
580	35	62.5	78	8	ADW00878	Human int	653	35	62.5	5183	9	ADX06154	Cyclin-de
581	35	62.5	78	8	ADW00878	Amino aci	654	34.5	61.6	109	4	ABE62756	Human HIV
582	35	62.5	83	5	ABP32817	Human ORF	655	34.5	61.6	111	4	ABB15395	Human ner
583	35	62.5	83	8	ADR40104	Human PKH	656	34.5	61.6	213	7	ADM05446	Human pro
584	35	62.5	94	4	AAW94427	Human rep	657	34.5	61.6	625	4	AAW41689	Human pol
585	35	62.5	94	4	ABB10765	Human ova	658	34.5	61.6	662	4	AAW39903	Human tra
586	35	62.5	107	9	ADY26773	Anti-NGF-	659	34.5	61.6	662	5	ABB80684	Human pol
587	35	62.5	107	9	AEA40460	Anti-VEGF	660	34.5	61.6	662	8	ADL26987	Protein o
588	35	62.5	107	9	AEA40463	Anti-VEGF	661	34	60.7	9	AEA45081	Apolipop	
589	35	62.5	107	9	AEA40470	Anti-VEGF	662	34	60.7	9	AEA40648	Anti-VEGF	
590	35	62.5	107	9	AEA40456	Anti-VEGF	663	34	60.7	49	4	ABG27473	Novel hum
591	35	62.5	107	9	AEA40456	Anti-VEGF	664	34	60.7	53	9	ABE86422	Mature mo
592	35	62.5	107	9	AEA40466	Anti-VEGF	665	34	60.7	74	4	AAW89436	Human imm
593	35	62.5	107	9	AEA40472	Anti-VEGF	666	34	60.7	107	2	AAW38614	Low-risk
594	35	62.5	107	9	AEA40455	Anti-VEGF	667	34	60.7	107	2	AAW41283	Moderate-
595	35	62.5	107	9	AEA40459	Anti-VEGF	668	34	60.7	107	2	AAW77302	Variable
596	35	62.5	107	9	AEA40464	Anti-VEGF	669	34	60.7	107	2	AAW58478	Humanised
597	35	62.5	107	9	AEA40469	Anti-VEGF	670	34	60.7	107	2	AAW58515	Protein S
598	35	62.5	108	4	AAU07490	Synthetic	671	34	60.7	107	2	AAW58505	H65 prote
599	35	62.5	108	9	ADY26775	Anti-NGF-	672	34	60.7	107	2	AAW22428	TM27 anti
600	35	62.5	109	4	ABE62050	Mouse mon	673	34	60.7	107	7	ADP03916	Murine-ex
601	35	62.5	109	6	ABP72768	Anti-full	674	34	60.7	107	7	ADP03913	Murine-ex
602	35	62.5	118	2	AAW06253	Variable	675	34	60.7	107	8	ADI01168	Murine mo
603	35	62.5	128	2	AAR22753	Rat CD4 a	676	34	60.7	107	8	ADI01228	Murine mo
604	35	62.5	139	4	AAU30002	Novel hum	677	34	60.7	107	8	ADI01167	Murine mo
605	35	62.5	161	5	ABP07310	Human ORF	678	34	60.7	107	9	AEA40453	Anti-VEGF
606	35	62.5	224	4	AAB75043	TRO005 Hu	679	34	60.7	108	2	AAW21292	Murine VL
607	35	62.5	225	7	ADC25901	Human met	680	34	60.7	108	2	AAW21310	Light cha
608	35	62.5	225	8	ADR59028	Human met	681	34	60.7	108	8	ADN41877	Humanised

682	34	60.7	108	9	AEA45109	Aea45109	Apollipop	755	34	60.7	574	5	AAO18904	Aaol18904	Cat butyr
683	34	60.7	108	9	AEb11698	Aeb11698	Anti-Pseu	756	34	60.7	574	8	ADR01082	Adr01082	Cat butyr
684	34	60.7	109	2	AAW18271	Aaw18271	Prp 37 11	757	34	60.7	583	6	ABU39613	Abu39613	Protein e
685	34	60.7	109	2	AAW85910	Aaw85910	Prp 37 11	758	34	60.7	583	6	ABU39613	Abu39613	Protein e
686	34	60.7	109	4	AAg65862	Aag65862	Anti-Prp	759	34	60.7	589	3	AAg52481	Aag52481	Arabidops
687	34	60.7	109	5	ABP51796	Abp51796	Anti-prio	760	34	60.7	653	2	AAW69845	Aaw69845	Amino aci
688	34	60.7	109	6	ABU58877	Abu58877	Anti-prio	761	34	60.7	658	3	AAg52480	Aag52480	Arabidops
689	34	60.7	109	8	ADJ10235	Adj10235	Murine an	762	34	60.7	721	4	ABE62213	AbE62213	Drosophil
690	34	60.7	109	9	ABE92150	Abe92150	Murine pr	763	34	60.7	764	3	AAg45801	Aag45801	Arabidops
691	34	60.7	128	2	AAr06252	Aar06252	Variable	764	34	60.7	879	3	AAg45800	Aag45800	Arabidops
692	34	60.7	128	2	AAr41686	Aar41686	128.1 VL	765	34	60.7	940	6	ABE99489	AbE99489	Amino aci
693	34	60.7	129	2	AAr30880	Aar30880	pXOM2. 3/	766	34	60.7	975	3	AAg45799	Aag45799	Arabidops
694	34	60.7	129	2	AAr65018	Aar65018	93KA9 ant	767	34	60.7	1154	4	ABE62830	AbE62830	Drosophil
695	34	60.7	146	1	AAp30251	Aap30251	Sequence	768	34	60.7	8147	8	AQ91698	Aq91698	Polyketid
696	34	60.7	147	9	ADY94497	Ady94497	Human/mou	769	34	60.7	8147	8	ABE86865	AbE86865	Streptomy
697	34	60.7	166	8	ADL89675	Adl89675	Human mod	770	34	60.7	8147	8	ABE86662	AbE86662	Streptomy
698	34	60.7	169	8	ADQ67120	Adq67120	Novel hum	771	33.5	59.8	555	6	ABU39997	Abu39997	Protein e
699	34	60.7	214	8	ADN41870	Adn41870	Amino aci	772	33.5	59.8	781	5	ABP73604	AbP73604	Candida a
700	34	60.7	229	9	ADY52422	Ady52422	Novel ket	773	33.5	59.8	1068	6	ABU39393	Abu39393	Protein e
701	34	60.7	229	9	ADY51355	Ady51355	Nodularia	774	33	58.9	9	4	ABE67495	AbE67495	Human lig
702	34	60.7	233	9	ADY51414	Ady51414	Nodularia	775	33	58.9	9	6	ABE38069	AbE38069	Human 17G
703	34	60.7	234	4	ABE65699	Abe65699	Novel pro	776	33	58.9	9	7	ADD40557	AdD40557	3E1/4G11
704	34	60.7	234	4	ADI29308	Adi29308	Mouse MAR	777	33	58.9	9	9	ADW04581	AdW04581	PAPP-A im
705	34	60.7	238	8	ADQ67593	Adq67593	Novel hum	778	33	58.9	9	9	ADZ45512	AdZ45512	Murine fa
706	34	60.7	253	9	ADY52914	Ady52914	Nostoc pu	779	33	58.9	9	9	ADZ45528	AdZ45528	Murine fa
707	34	60.7	254	9	ADY52966	Ady52966	Nostoc pu	780	33	58.9	9	9	AEA46199	Aea46199	Apollipop
708	34	60.7	257	6	ABU07877	Abu07877	Anti-Vene	781	33	58.9	9	9	ABE70885	AbE70885	Toll-like
709	34	60.7	260	9	ADY52912	Ady52912	Nodularia	782	33	58.9	15	4	AAb45752	Aab45752	Human zal
710	34	60.7	260	9	ADY52908	Ady52908	Nodularia	783	33	58.9	15	4	AAb45765	Aab45765	Murine za
711	34	60.7	260	9	ADY52910	Ady52910	Nodularia	784	33	58.9	15	8	ADG42416	AdG42416	Human zal
712	34	60.7	260	9	ADY52906	Ady52906	N. spumig	785	33	58.9	15	8	ADG42434	AdG42434	Mouse zal
713	34	60.7	262	8	ADP74108	Adp74108	Nostoc pu	786	33	58.9	27	2	AAW40007	Aaw40007	Peptide e
714	34	60.7	262	8	ADP74102	Adp74102	Nostoc pu	787	33	58.9	28	2	ADW44429	AdW44429	Human ant
715	34	60.7	262	8	ADP74106	Adp74106	Nostoc pu	788	33	58.9	33	9	ADR68571	AdR68571	Human EPO
716	34	60.7	262	8	ADQ38319	Adq38319	Nostoc pu	789	33	58.9	33	9	ADY62193	AdY62193	SARS viru
717	34	60.7	262	8	ADQ94520	Adq94520	Nostoc sp	790	33	58.9	47	4	AAb45774	Aab45774	Human zal
718	34	60.7	262	8	ADRO3870	Adr03870	Nostoc pu	791	33	58.9	47	8	ADG42443	AdG42443	Human zal
719	34	60.7	262	8	ADRO3950	Adr03950	Nostoc pu	792	33	58.9	53	9	ABE86416	Abe86416	Mature mo
720	34	60.7	262	9	ADY52430	Ady52430	Novel ket	793	33	58.9	54	9	ADY64632	AdY64632	S. mansoni
721	34	60.7	262	9	ADY52424	Ady52424	Novel ket	794	33	58.9	57	4	AAb45771	Aab45771	Human zal
722	34	60.7	262	9	ADY52432	Ady52432	Novel ket	795	33	58.9	57	8	ADG42440	AdG42440	Human zal
723	34	60.7	262	9	ADY51357	Ady51357	Nostoc pu	796	33	58.9	61	3	AAQ00399	Aaq00399	Human sec
724	34	60.7	264	7	ABO68169	AbO68169	Pseudomon	797	33	58.9	62	3	AAy64772	Aay64772	Human 5'
725	34	60.7	264	9	ADY52976	Ady52976	Nodularia	798	33	58.9	62	8	ADU72336	AdU72336	Signal pe
726	34	60.7	264	9	ADY52974	Ady52974	Nodularia	799	33	58.9	62	8	ADU72332	AdU72332	Human inc
727	34	60.7	284	6	ADA34692	Ada34692	Acinetoba	800	33	58.9	64	5	ABJ03733	AbJ03733	Human ova
728	34	60.7	310	3	AAE52074	Aae52074	Gene 10 h	801	33	58.9	74	8	AAb45770	Aab45770	Human zal
729	34	60.7	310	5	ABBS7285	Abbs7285	Mouse isc	802	33	58.9	74	8	ADG42439	AdG42439	Human zal
730	34	60.7	310	8	ADG38784	Adg38784	Mouse mat	803	33	58.9	74	8	ADS10742	AdS10742	Human the
731	34	60.7	334	8	ADS26480	Ads26480	Bacterial	804	33	58.9	76	2	AAW27742	Aaw27742	Staphyloc
732	34	60.7	334	9	ADZ75742	Adz75742	Xanthomon	805	33	58.9	87	9	AEA20313	Aea20313	Novel hum
733	34	60.7	339	8	ADS26852	Ads26852	Bacterial	806	33	58.9	89	8	ADU69719	AdU69719	S agalact
734	34	60.7	339	8	ADS27225	Ads27225	Protein e	807	33	58.9	99	4	ABG26480	AbG26480	Novel hum
735	34	60.7	345	8	ADP12553	Adp12553	Protein e	808	33	58.9	103	9	ADY33941	AdY33941	Anti-Tie
736	34	60.7	381	4	ABBS5942	Abbs5942	Drosophil	809	33	58.9	105	2	AAW80970	Aaw80970	Kappa lig
737	34	60.7	426	2	AAW36003	Aaw36003	Human Fch	810	33	58.9	105	6	ABO04833	AbO04833	Human epi
738	34	60.7	426	2	AAW80584	Aaw80584	Signal tr	811	33	58.9	105	6	AEA17747	Aea17747	Hybridoma
739	34	60.7	426	2	AAW96813	Aaw96813	A murine	812	33	58.9	107	7	ADP03909	AdP03909	Murine-ex
740	34	60.7	426	2	AAW96814	Aaw96814	A human S	813	33	58.9	107	7	ADP03914	AdP03914	Murine-ex
741	34	60.7	426	2	AAy26344	Aay26344	Human Sma	814	33	58.9	107	9	ABZ45509	AbZ45509	Murine fa
742	34	60.7	426	4	AAy45014	Aay45014	Protein e	815	33	58.9	107	9	ABE70882	AbE70882	Toll-like
743	34	60.7	426	4	AAE51288	Aae51288	Human Sma	816	33	58.9	108	4	AAE62770	Aae62770	Human HTV
744	34	60.7	426	6	AAO29768	Aao29768	Human Sma	817	33	58.9	108	4	AAE93666	Aae93666	Human ant
745	34	60.7	426	6	AAO29769	Aao29769	Mouse Sma	818	33	58.9	108	6	AAE38059	Aae38059	Human 17G
746	34	60.7	426	6	AAO29770	Aao29770	Rat Smad-	819	33	58.9	108	6	ABO27473	AbO27473	Novel hum
747	34	60.7	426	8	ADP23766	Adp23766	PRO polyd	820	33	58.9	108	7	ABE78583	AbE78583	Rat F997+
748	34	60.7	426	8	ADR96772	Adr96772	Human SVA	821	33	58.9	108	8	ADQ16703	AdQ16703	Modified
749	34	60.7	426	9	ADX05600	Adx05600	Cyclin-de	822	33	58.9	108	8	ADS84382	AdS84382	Human and
750	34	60.7	429	8	ADN22371	Adn22371	Bacterial	823	33	58.9	108	8	ADR68524	AdR68524	Anti-EPO-
751	34	60.7	474	7	ADF72892	Adf72892	Protein r	824	33	58.9	108	9	ADV44439	AdV44439	pAX116 va
752	34	60.7	485	3	AAE52482	Aae52482	Arabidops	825	33	58.9	108	9	ABE12911	AbE12911	Antibody
753	34	60.7	547	8	ADS43535	Ads43535	Bacterial	826	33	58.9	109	8	ADP46971	AdP46971	Murine 11
754	34	60.7	551	2	AAy29955	Aay29955	Mouse CGI	827	33	58.9	109	8	ADP46972	AdP46972	Murine 11

828	33	58.9	110	5	AAUB37804	Aau83804 MS-GPC-6	901	33	58.9	342	4	ABB56381	Abb56381 Non-endog
829	33	58.9	110	5	ABBS7562	Abbs7562 HLA-DR-sp	902	33	58.9	342	5	ABB77918	Abb77918 Amino aci
830	33	58.9	110	9	ADRB6132	Adw86132 Novel cyc	903	33	58.9	342	5	ABB77904	Abb77904 Amino aci
831	33	58.9	112	9	ADV44477	Adv44477 Anti-teta	904	33	58.9	342	6	ABRS8632	AbR58632 Human can
832	33	58.9	112	9	ADY70834	Ady70834 MS-GPC-6	905	33	58.9	342	6	ABP81943	Abp81943 Human pla
833	33	58.9	117	9	ADW04977	Adw04977 PAPP-A im	906	33	58.9	342	7	ADC33526	Adc33526 Rat VTR 1
834	33	58.9	120	5	ABBB89764	Abb89764 Human pol	907	33	58.9	342	7	ADf63109	Adf63109 Human apo
835	33	58.9	120	7	ADDA0551	Ad40551 3EL/4G11	908	33	58.9	342	8	ADO29612	Ado29612 Human GPC
836	33	58.9	126	5	ADK34653	Adk34653 Novel hum	909	33	58.9	342	9	ADX57714	Adx57714 Rheumatol
837	33	58.9	126	5	ADV91477	Adv91477 Human Gas	910	33	58.9	343	3	AGX31719	Aeg31719 Arabidops
838	33	58.9	127	4	AAAB45768	Aab45768 Human Zal	911	33	58.9	346	2	AAW13841	Aaw13841 Phase res
839	33	58.9	127	8	ADG42437	Adg42437 Human Zal	912	33	58.9	346	2	AAW13842	Aaw13842 Phase res
840	33	58.9	130	2	AAEB12948	Aeb12948 Chimeric	913	33	58.9	346	3	AAE16708	Aeg16708 Arabidops
841	33	58.9	130	9	AAEB12948	Aeb12948 Chimeric	914	33	58.9	346	3	AAE16708	Aeg16708 Arabidops
842	33	58.9	131	6	ABJ36926	Abj36926 Anti-CD40	915	33	58.9	352	2	AAE35315	Aea35315 Tetraodon
843	33	58.9	131	6	ABJ36928	Abj36928 Anti-CD40	916	33	58.9	358	2	AAE35315	Aea35315 Tetraodon
844	33	58.9	132	6	ADSI10741	Adsi10741 Human the	917	33	58.9	360	8	ADK90633	Adk90633 Clawed fr
845	33	58.9	135	5	ADK34663	Adk34663 Novel hum	918	33	58.9	373	3	AGX31718	Aeg31718 Arabidops
846	33	58.9	136	4	AAO11523	Aao11523 Human pol	919	33	58.9	375	3	AAV70952	Aav70952 Arabidops
847	33	58.9	137	4	ABGO1697	Abg01697 Novel hum	920	33	58.9	375	3	AAV70952	Aav70952 Arabidops
848	33	58.9	137	7	ADP60257	Adp60257 Human con	921	33	58.9	375	7	ADJ30496	Adj30496 Plant yle
849	33	58.9	137	8	ADSI2000	Adsi2000 Human the	922	33	58.9	375	8	ADI43881	Adi43881 Plant tra
850	33	58.9	137	8	ADSI1999	Adsi1999 Human the	923	33	58.9	376	3	AAE16707	Aeg16707 Arabidops
851	33	58.9	141	4	AAU64529	Aau64529 Propionib	924	33	58.9	388	8	ADG44090	Adg44090 Bacterial
852	33	58.9	141	6	ABM61048	Abm61048 Propionib	925	33	58.9	398	8	ADT59440	Adt59440 Plant pol
853	33	58.9	141	8	ADX95466	Adx95466 Plant ful	926	33	58.9	399	7	ABO74843	Abm74843 Pseudomon
854	33	58.9	145	4	AAAB45748	Aab45748 Human Zal	927	33	58.9	416	6	ABM67786	Abm67786 Photorhab
855	33	58.9	147	8	ADG42412	Adg42412 Mature hu	928	33	58.9	452	4	ABG16485	Abg16485 Novel hum
856	33	58.9	147	2	AAV34312	Aav34312 IGM antib	929	33	58.9	452	4	ABG12981	Abg12981 Novel hum
857	33	58.9	150	2	AAW62790	Aaw62790 Amino aci	930	33	58.9	456	8	ADR86000	Adr86000 Aspergill
858	33	58.9	159	7	ADC87786	Adc87786 Ribosomal	931	33	58.9	462	4	ABG18819	Abg18819 Novel hum
859	33	58.9	159	8	ADX52302	Adx52302 Human ant	932	33	58.9	486	7	ABM74223	Abm74223 DNA clone
860	33	58.9	160	8	ADY05215	Ady05215 Plant ful	933	33	58.9	499	7	ABO75102	Abm75102 Pseudomon
861	33	58.9	165	6	ABM69860	Abm69860 Photorhab	934	33	58.9	501	5	ABP74015	Abp74015 Candida a
862	33	58.9	170	4	AAAB45747	Aab45747 Human Zal	935	33	58.9	536	7	ADJ68221	Adj68221 Human hea
863	33	58.9	170	8	ADG42411	Adg42411 Human Zal	936	33	58.9	536	7	ADJ68221	Adj68221 Human hea
864	33	58.9	173	4	AAAB45759	Aab45759 Murine za	937	33	58.9	544	8	ADX74160	Adx74160 Plant ful
865	33	58.9	173	8	ADG42425	Adg42425 Mature mo	938	33	58.9	553	3	AAE53424	Aae53424 Human col
866	33	58.9	176	4	AAAB45761	Aab45761 Murine va	939	33	58.9	553	3	AAE53424	Aae53424 Human col
867	33	58.9	176	8	ADG42428	Adg42428 Mature mo	940	33	58.9	553	6	ABU04266	Abu04266 Human exp
868	33	58.9	187	4	ABBS7901	Abbs7901 Drosophil	941	33	58.9	553	6	ABU04268	Abu04268 Human exp
869	33	58.9	197	8	AAW93957	Aaw93957 Human pol	942	33	58.9	559	6	ABU00839	Abu00839 S. pneumo
870	33	58.9	197	8	ADL32127	Adl32127 Human pro	943	33	58.9	559	6	ABP81329	Abp81329 Streptoco
871	33	58.9	198	4	AAAB45758	Aab45758 Murine za	944	33	58.9	559	8	ADM92099	Adm92099 S. pneumon
872	33	58.9	198	8	ADG42424	Adg42424 Mouse Zal	945	33	58.9	559	8	ADN21954	Adn21954 Bacterial
873	33	58.9	201	4	AAAB45760	Aab45760 Murine va	946	33	58.9	567	8	ADN24711	Adn24711 Bacterial
874	33	58.9	201	8	ADG42427	Adg42427 Mouse var	947	33	58.9	579	8	ADN20597	Adn20597 Bacterial
875	33	58.9	209	7	ABO69571	Abm69571 Pseudomon	948	33	58.9	597	2	AAW52821	Aaw52821 Human PRC
876	33	58.9	215	8	ADQ16702	Adq16702 Modified	949	33	58.9	618	2	AAW52827	Aaw52827 Human chr
877	33	58.9	215	9	ADV44438	Adv44438 pAX116 va	950	33	58.9	700	2	AAW52822	Aaw52822 Human Non
878	33	58.9	215	9	ABE12910	Aeb12910 Antibody	951	33	58.9	827	8	ADX97213	Adx97213 Plant ful
879	33	58.9	239	9	ADV44458	Adv44458 Anti-teta	952	33	58.9	834	2	AAW52820	Aaw52820 Human PRC
880	33	58.9	239	9	ABE12929	Aeb12929 Antibody	953	33	58.9	877	3	AAE15996	Aae15996 E. coli p
881	33	58.9	241	5	ABP45876	Abp45876 Human Bly	954	33	58.9	972	4	ABG15949	Abg15949 Novel hum
882	33	58.9	241	7	ADG96703	Adg96703 Single ch	955	33	58.9	972	4	ABG15949	Abg15949 Novel hum
883	33	58.9	244	7	ADP58846	Adp58846 Human pol	956	33	58.9	1067	6	ABU04263	Abu04263 Human exp
884	33	58.9	248	7	ADM26586	Adm26586 Hyperther	957	33	58.9	1073	2	AAE52722	Aae52722 Alpha 6A
885	33	58.9	254	8	ADL05047	Adl05047 M. catarr	958	33	58.9	1073	2	AAE52722	Aae52722 Alpha 6A
886	33	58.9	256	9	ADY52918	Ady52918 Gloeobact	959	33	58.9	1073	4	AAE68088	Aae68088 Amino aci
887	33	58.9	256	9	ADY52980	Ady52980 Gloeobact	960	33	58.9	1073	5	AAE14706	Aae14706 Human alp
888	33	58.9	264	8	ABM82967	Abm82967 Human dia	961	33	58.9	1073	6	ABU04272	Abu04272 Human exp
889	33	58.9	264	9	ABM91274	Abm91274 M. xanthu	962	33	58.9	1073	6	ABU04271	Abu04271 Human exp
890	33	58.9	279	9	ABM97153	Abm97153 M. xanthu	963	33	58.9	1073	6	ABU04269	Abu04269 Human exp
891	33	58.9	326	2	AAAR48718	Aar48718 G-protein	964	33	58.9	1073	6	ABU04265	Abu04265 Human exp
892	33	58.9	326	2	AAW02690	Aaw02690 G-protein	965	33	58.9	1073	6	ABU04265	Abu04265 Human exp
893	33	58.9	327	9	ADY57297	Ady57297 Human G-p	966	33	58.9	1073	7	ADU50087	Adu50087 Human alp
894	33	58.9	334	6	ABU38457	Abu38457 Protein e	967	33	58.9	1073	7	ADU50087	Adu50087 Human alp
895	33	58.9	341	5	AAW50842	Aaw50842 Mouse phe	968	33	58.9	1073	8	ADJ32521	Adj32521 Human alp
896	33	58.9	341	8	ADQ29613	Adq29613 Mouse GPC	969	33	58.9	1073	8	ADJ64242	Adj64242 Human alp
897	33	58.9	342	2	AAAR25835	Aar25835 Human pla	970	33	58.9	1073	8	ADJ64235	Adj64235 Human alp
898	33	58.9	342	2	AAAR25834	Aar25834 Guinea pi	971	33	58.9	1073	8	ADM99593	Adm99593 Human int
899	33	58.9	342	2	AAW12243	Aaw12243 Guinea pi	972	33	58.9	1073	8	ADP54273	Adp54273 Human PRO
900	33	58.9	342	2	AAV49550	Aav49550 Human pla	973	33	58.9	1073	8	ADP23243	Adp23243 PRO polyp

974 33 58.9 1073 8 ADU06328 Novel bro  
 975 33 58.9 1073 9 ADY25777 MRAC ITGA  
 976 33 58.9 1073 9 ADY19465 PRO polyp  
 977 33 58.9 1073 9 ADY14616 PRO polyp  
 978 33 58.9 1073 9 ADY247341 Human int  
 979 33 58.9 1073 9 AEA23993 Human PRO  
 980 33 58.9 1073 9 AEB78069 Human int  
 981 33 58.9 1091 2 AAR28822 Alpha 6B  
 982 33 58.9 1091 6 ABU04270 Human exp  
 983 33 58.9 1130 8 ABU04273 Human exp  
 984 33 58.9 1130 8 ADK40839 Human CD4  
 985 33 58.9 1130 9 ADY27732 Human tra  
 986 33 58.9 1313 4 AAB94745 Human pro  
 987 33 58.9 1364 7 ADL33355 Human tra  
 988 33 58.9 1406 3 AAB42916 Human ORF  
 989 33 58.9 1406 7 ADL15041 Human KIA  
 990 33 58.9 1406 8 ADQ19821 Human sof  
 991 33 58.9 1410 8 ADH22564 Human tra  
 992 33 58.9 1413 7 ADC33239 Human nov  
 993 33 58.9 1510 6 ADA05866 Human NOV  
 994 33 58.9 1510 8 ADH63029 Human NOV  
 995 33 58.9 1543 8 ADJ27180 Human TRI  
 996 33 58.9 1580 2 AAW57412 Homo sapi  
 997 33 58.9 1581 5 ABP52115 Homo sapi  
 998 33 58.9 1581 6 ADA05864 Human NOV  
 999 33 58.9 1581 8 ADH63027 Human NOV  
 1000 33 58.9 1581 9 ADX08064 Cyclin-de

# ALIGNMENTS

RESULT 1  
 AAB81984  
 ID AAB81984 standard; peptide; 9 AA.  
 XX  
 AC AAB81984;  
 XX  
 DT 03-JUL-2001 (first entry)  
 XX  
 DE Ganglioside GD3 specific antibody related peptide SEQ ID NO: 8.  
 XX  
 KW Ganglioside; GD3; complementarity determining region; CDR; antibody;  
 KW cancer.  
 XX  
 OS Mus musculus.  
 XX  
 PN WO200123432-A1.  
 XX  
 PD 05-APR-2001.  
 XX  
 PF 29-SEP-2000; 2000WO-JP006774.  
 XX  
 PR 30-SEP-1999; 99JP-00278291.  
 PR 06-APR-2000; 2000JP-00105086.  
 XX  
 PA (KYOW ) KYOWA HAKKO KOGYO KK.  
 XX  
 PI Hanai N, Shitara K, Nakamura K, Niwa R;  
 XX  
 DR WPI; 2001-266143/27.  
 XX  
 PT New human type complementation-determining region-transplanted antibody  
 PT and derivatives against ganglioside GD3, useful in diagnosis and therapy  
 PT of e.g. tumors, with low antigenicity, little side effects but potent  
 PT activity in cancer.  
 XX  
 PS Claim 4; Page 142; 183pp; Japanese.  
 XX  
 CC The present invention describes a monoclonal antibody which can react  
 CC specifically with ganglioside GD3. The antibody and its derivatives are  
 CC useful in the diagnosis and therapy of tumors, particularly cancer  
 CC diagnosis. The present sequence is a protein used in the exemplification

CC of the invention  
 XX Sequence 9 AA;  
 SQ  
 Query Match 100.0%; Score 56; DB 4; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 HOYSKLPWT 9  
 DB 1 HOYSKLPWT 9  
 RESULT 2  
 ABU11009  
 ID ABU11009 standard; peptide; 9 AA.  
 XX  
 AC ABU11009;  
 XX  
 DT 04-FEB-2003 (first entry)  
 XX  
 DE Modified ganglioside GD3 antibody associated peptide #6.  
 XX  
 KW Ganglioside GD3; anti-ganglioside GD3 antibody; tumour; melanoma.  
 XX  
 OS Mus musculus.  
 XX  
 PN WO200278739-A1.  
 XX  
 PD 10-OCT-2002.  
 XX  
 PF 29-MAR-2002; 2002WO-JP003170.  
 XX  
 PR 29-MAR-2001; 2001JP-00097483.  
 XX  
 PA (KYOW ) KYOWA HAKKO KOGYO KK.  
 XX  
 PI Shitara K, Niwa R, Kanazawa J, Asada M;  
 XX  
 DR WPI; 2003-067410/06.  
 XX  
 PT Drugs containing genetically-modified antibody against ganglioside GD3,  
 PT its fragment, immunocompetent cell activators or/and antitumor agents in  
 PT combination, applicable in treating malignant tumor like melanoma.  
 XX  
 PS Claim 6; Page 99; 121pp; Japanese.  
 XX  
 CC The invention describes drugs contain a genetically-modified antibody  
 CC against ganglioside GD3 or its fragment and at least 1 of a substance  
 CC capable of activating immunocompetent cells and a substance having an  
 CC antitumor activity in combination. The drugs can be used to treat tumour  
 CC like melanoma and can provide a treatment with enhanced therapeutic  
 CC effect and little side-reactions, particularly to relieve problems of  
 CC side-effects during the conventional single administration. This sequence  
 CC represents a peptide associated with the anti- ganglioside GD3 antibody  
 XX  
 SQ Sequence 9 AA;  
 Query Match 100.0%; Score 56; DB 6; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 HOYSKLPWT 9  
 DB 1 HOYSKLPWT 9  
 RESULT 3  
 ADZ57815  
 ID ADZ57815 standard; peptide; 9 AA.  
 XX  
 AC ADZ57815;  
 XX

DT 30-JUN-2005 (first entry)  
 DE Ganglioside GD3 binding antibody associated CDR3 SEQ ID NO 19.  
 XX  
 KW cytostatic; antibody engineering; cancer; neoplasm; ganglioside; GD3;  
 KW pharmaceutical.  
 XX  
 OS Mus musculus.  
 XX  
 PN WO200503577-A1.  
 XX  
 PD 21-APR-2005.  
 XX  
 XX 08-OCT-2004; 2004WO-JP015314.  
 PF  
 XX 08-OCT-2003; 2003JP-00350161.  
 PR  
 XX (KYOW ) KYOWA HAKKO KOGYO KK.  
 PA  
 PI Iida S, Satoh M, Urakubo M, Wakitani M, Uchida K, Niwa R;  
 PI Shitara K;  
 XX  
 XX WPI; 2005-346195/35.  
 DR  
 XX Antibody composition for treating ganglioside GD3 associated disease e.g.  
 PT cancer, comprises genetically modified antibody molecule, which  
 PT specifically binds to ganglioside GD3 and has N-glycoside-binding sugar  
 PT chain in its Fc domain.  
 XX  
 XX Claim 9; SEQ ID NO 19; 124pp; Japanese.  
 PS  
 XX The invention describes an antibody composition (I), comprising a  
 CC genetically modified antibody molecule which specifically binds to  
 CC ganglioside GD3 and has an N-glycoside-binding complex sugar chain in its  
 CC Fc domain, where the N-glycoside-binding complex sugar chain is a sugar  
 CC chain having no fucose attached to N-acetylglucosamine at the reducing  
 CC end of the sugar chain. Also described are: a transformant (II) capable  
 CC of producing (I), obtained by introducing DNA that encodes the antibody  
 CC molecule which specifically binds with ganglioside GD3, to a host cell;  
 CC producing (I), involving cultivating (I) in a culture medium, such that  
 CC C1 (sic) is produced and accumulated in the culture, extracting and  
 CC purifying C1 from the culture medium; a pharmaceutical (III) containing  
 CC C1 as an active ingredient; and a therapeutic agent (A1) for ganglioside  
 CC GD3 associated disease, comprising C1 as an active ingredient. (I) is  
 CC useful for treating GD3 associated disease, which involves administering  
 CC (I), where the GD3 associated diseases is cancer. (A1) is also useful for  
 CC treating GD3 associated disease. (II) is useful for producing (I). (I) is  
 CC useful for manufacturing a therapeutic agent for GD3 associated disease.  
 CC This sequence represents a ganglioside GD3 binding antibody associated  
 CC peptide.  
 XX  
 SQ Sequence 9 AA;  
 Query Match 100.0%; Score 56; DB 9; Length 9;  
 Best Local Similarity 100.0%; Pred. NO. 2e+06;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 HOYSKLPWT 9  
 DB 1 HOYSKLPWT 9  
 RESULT 4  
 AAB81988  
 ID AAB81988 standard; protein; 108 AA.  
 XX  
 AC AAB81988;  
 XX  
 DT 03-JUL-2001 (first entry)  
 DE Ganglioside GD3 specific antibody related protein SEQ ID NO: 54.  
 XX  
 KW Ganglioside; GD3; complementarity determining region; CDR; antibody;

KW cancer.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200123432-A1.  
 XX  
 PD 05-APR-2001.  
 XX  
 XX 29-SEP-2000; 2000WO-JP006774.  
 PF  
 XX 30-SEP-1999; 99JP-00278291.  
 PR  
 PR 06-APR-2000; 2000JP-00105088.  
 XX  
 XX (KYOW ) KYOWA HAKKO KOGYO KK.  
 PA  
 XX Hanai N, Shitara K, Nakamura K, Niwa R;  
 PI WPI; 2001-266143/27.  
 DR  
 XX New human type complementation-determining region-transplanted antibody  
 PT and derivatives against ganglioside GD3, useful in diagnosis and therapy  
 PT of e.g. tumors, with low antigenicity, little side effects but potent  
 PT activity in cancer.  
 XX  
 XX Claim 22; Page 172-173; 183pp; Japanese.  
 PS  
 XX The present invention describes a monoclonal antibody which can react  
 CC specifically with ganglioside GD3. The antibody and its derivatives are  
 CC useful in the diagnosis and therapy of tumors, particularly cancer  
 CC diagnosis. The present sequence is a protein used in the exemplification  
 CC of the invention  
 XX  
 SQ Sequence 108 AA;  
 Query Match 100.0%; Score 56; DB 4; Length 108;  
 Best Local Similarity 100.0%; Pred. No. 0.052;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 HOYSKLPWT 9  
 DB 89 HOYSKLPWT 97  
 RESULT 5  
 AAB81986  
 ID AAB81986 standard; protein; 108 AA.  
 XX  
 AC AAB81986;  
 XX  
 DT 03-JUL-2001 (first entry)  
 DE Ganglioside GD3 specific antibody related protein SEQ ID NO: 10.  
 XX  
 KW Ganglioside; GD3; complementarity determining region; CDR; antibody;  
 KW cancer.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200123432-A1.  
 XX  
 PD 05-APR-2001.  
 XX  
 XX 29-SEP-2000; 2000WO-JP006774.  
 PF  
 XX 30-SEP-1999; 99JP-00278291.  
 PR  
 PR 06-APR-2000; 2000JP-00105088.  
 XX  
 XX (KYOW ) KYOWA HAKKO KOGYO KK.  
 PA  
 XX Hanai N, Shitara K, Nakamura K, Niwa R;  
 PI WPI; 2001-266143/27.  
 DR  
 XX



PT New human type complementation-determining region-transplanted antibody  
 PT and derivatives against ganglioside GD3; useful in diagnosis and therapy  
 PT of e.g. tumors, with low antigenicity, little side effects but potent  
 PT activity in cancer.

XX  
 XX  
 XX Example 1; Page 143-144; 183pp; Japanese.

CC The present invention describes a monoclonal antibody which can react  
 CC specifically with ganglioside GD3. The antibody and its derivatives are  
 CC useful in the diagnosis and therapy of tumors, particularly cancer  
 CC diagnosis. The present sequence is a protein used in the exemplification  
 CC of the invention

XX  
 XX Sequence 108 AA;

Query Match 100.0%; Score 56; DB 4; Length 108;  
 Best Local Similarity 100.0%; Pred. No. 0.052;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HOYSKLPWT 9  
 |||||  
 DB 89 HOYSKLPWT 97

## RESULT 6

AAB81990  
 ID AAB81990 standard; protein; 108 AA.

XX  
 AC AAB81990;

XX 03-JUL-2001 (first entry)

XX Ganglioside GD3 specific antibody related protein SEQ ID NO: 56.

DE Ganglioside; GD3; complementarity determining region; CDR; antibody;  
 KW cancer.

XX  
 OS Mus musculus.

XX WO200123432-A1.

XX 05-APR-2001.

XX 29-SEP-2000; 2000WO-JP006774.

XX 30-SEP-1999; 99JP-00278291.

PR 06-APR-2000; 2000JP-00105088.

XX (KYOW ) KYOWA HAKKO KOGYO KK.

XX Hanai N, Shitara K, Nakamura K, Niwa R;

XX WPI; 2001-266143/27.

XX New human type complementation-determining region-transplanted antibody  
 PT and derivatives against ganglioside GD3; useful in diagnosis and therapy  
 PT of e.g. tumors, with low antigenicity, little side effects but potent  
 PT activity in cancer.

XX Claim 11; Page 174-175; 183pp; Japanese.

XX The present invention describes a monoclonal antibody which can react  
 CC specifically with ganglioside GD3. The antibody and its derivatives are  
 CC useful in the diagnosis and therapy of tumors, particularly cancer  
 CC diagnosis. The present sequence is a protein used in the exemplification  
 CC of the invention

XX Sequence 108 AA;

Query Match 100.0%; Score 56; DB 4; Length 108;  
 Best Local Similarity 100.0%; Pred. No. 0.052;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HOYSKLPWT 9  
 |||||  
 DB 89 HOYSKLPWT 97

## RESULT 7

ABU11011

ID ABU11011 standard; protein; 108 AA.

XX  
 AC ABU11011;

XX 04-FEB-2003 (first entry)

XX Modified ganglioside GD3 antibody associated protein #4.

XX Ganglioside GD3; anti-ganglioside GD3 antibody; tumour; melanoma.

XX Synthetic.

XX WO200278739-A1.

XX 10-OCT-2002.

XX 29-MAR-2002; 2002WO-JP003170.

XX 29-MAR-2001; 2001JP-00097483.

XX (KYOW ) KYOWA HAKKO KOGYO KK.

XX Shitara K, Niwa R, Kanazawa J, Asada M;

XX WPI; 2003-067410/06.

XX Drugs containing genetically-modified antibody against ganglioside GD3,  
 PT its fragment, immunocompetent cell activators or/and antitumor agents in  
 PT combination, applicable in treating malignant tumor like melanoma.

XX Claim 8; Page 100; 121pp; Japanese.

XX The invention describes drugs contain a genetically-modified antibody  
 CC against ganglioside GD3 or its fragment and at least 1 of a substance  
 CC capable of activating immunocompetent cells and a substance having an  
 CC antitumor activity in combination. The drugs can be used to treat tumour  
 CC like melanoma and can provide a treatment with enhanced therapeutic  
 CC effect and little side-reactions, particularly to relieve problems of  
 CC side-effects during the conventional single administration. This sequence  
 CC represents a protein associated with the anti- ganglioside GD3 antibody

XX Sequence 108 AA;

Query Match 100.0%; Score 56; DB 6; Length 108;

Best Local Similarity 100.0%; Pred. No. 0.052;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HOYSKLPWT 9  
 |||||  
 DB 89 HOYSKLPWT 97

## RESULT 8

ABU11013

ID ABU11013 standard; protein; 108 AA.

XX  
 AC ABU11013;

XX 04-FEB-2003 (first entry)

XX Modified ganglioside GD3 antibody associated protein #6.

XX Ganglioside GD3; anti-ganglioside GD3 antibody; tumour; melanoma.

XX Mus musculus.



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PN WO200278739-A1.
XX
XX
XX
XX 29-MAR-2002; 2002WO-JP003170.
XX
XX 29-MAR-2003; 2001JP-00097483.
XX
XX (KYOW ) KYOWA HAKKO KOGYO KK.
XX
XX Shitara K, Niwa R, Kanazawa J, Asada M;
XX WPI; 2003-067410/06.
XX
XX Drugs containing genetically-modified antibody against ganglioside GD3,
XX its fragment, immunocompetent cell activators or/and antitumor agents in
XX combination, applicable in treating malignant tumor like melanoma.
XX
XX Claim 7; Page 113; 121pp; Japanese.
XX
XX The invention describes drugs contain a genetically-modified antibody
XX against ganglioside GD3 or its fragment and at least 1 of a substance
XX capable of activating immunocompetent cells and a substance having an
XX antitumor activity in combination. The drugs can be used to treat tumour
XX like melanoma and can provide a treatment with enhanced therapeutic
XX effect and little side-reactions, particularly to relieve problems of
XX side-effects during the conventional single administration. This sequence
XX represents a protein associated with the anti- ganglioside GD3 antibody
XX
XX Sequence 108 AA;

Query Match 100.0%; Score 56; DB 6; Length 108;
Best Local Similarity 100.0%; Pred. NO. 0.052;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HOYSKLPWT 9
DB 89 HOYSKLPWT 97

RESULT 9
ADZ57819
ID ADZ57819 standard; protein; 108 AA.
XX
XX ADZ57819;
XX
XX 30-JUN-2005 (first entry)
XX
XX Ganglioside GD3 binding antibody associated protein SEQ ID NO 23.
XX
XX cytostatic; antibody engineering; cancer; neoplasm; ganglioside; GD3;
XX pharmaceutical.
XX
XX Synthetic.
XX
XX WO2005035577-A1.
XX
XX 21-APR-2005.
XX
XX 08-OCT-2004; 2004WO-JP015314.
XX
XX 08-OCT-2003; 2003JP-00350161.
XX
XX (KYOW ) KYOWA HAKKO KOGYO KK.
XX
XX Iida S, Satoh M, Urakubo M, Wakitani M, Uchida K, Niwa R;
XX Shitara K;
XX
XX WPI; 2005-346195/35.
XX
XX Antibody composition for treating ganglioside GD3 associated disease e.g.
XX cancer, comprises genetically modified antibody molecule, which
XX specifically binds to ganglioside GD3 and has N-glycoside-binding sugar
XX chain in its Fc domain.

chain in its Fc domain.
PT
XX Claim 20; SEQ ID NO 23; 124pp; Japanese.
XX
XX The invention describes an antibody composition (I), comprising a
XX genetically modified antibody molecule which specifically binds to
XX ganglioside GD3 and has an N-glycoside-binding complex sugar chain in its
XX Fc domain, where the N-glycoside-binding complex sugar chain is a sugar
XX chain having no fucose attached to N-acetylglucosamine at the reducing
XX end of the sugar chain. Also described are: a transformant (II) capable
XX of producing (I), obtained by introducing DNA that encodes the antibody
XX molecule which specifically binds with ganglioside GD3, to a host cell;
XX producing (I), involving cultivating (I) in a culture medium, such that
XX Cl (sic) is produced and accumulated in the culture, extracting and
XX purifying Cl from the culture medium; a pharmaceutical (III) containing
XX Cl as an active ingredient; and a therapeutic agent (A1) for ganglioside
XX GD3 associated disease, comprising Cl as an active ingredient. (I) is
XX useful for treating GD3 associated disease, which involves administering
XX (I), where the GD3 associated disease is cancer. (A1) is also useful for
XX treating GD3 associated disease. (II) is useful for producing (I). (I) is
XX useful for manufacturing a therapeutic agent for GD3 associated disease.
XX This sequence represents a ganglioside GD3 binding antibody associated
XX protein.
XX
XX Sequence 108 AA;

Query Match 100.0%; Score 56; DB 9; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.052;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HOYSKLPWT 9
DB 89 HOYSKLPWT 97

RESULT 10
ADZ57822
ID ADZ57822 standard; protein; 108 AA.
XX
XX ADZ57822;
XX
XX 30-JUN-2005 (first entry)
XX
XX Ganglioside GD3 binding antibody associated protein SEQ ID NO 26.
XX
XX cytostatic; antibody engineering; cancer; neoplasm; ganglioside; GD3;
XX pharmaceutical.
XX
XX Synthetic.
XX
XX WO2005035577-A1.
XX
XX 21-APR-2005.
XX
XX 08-OCT-2004; 2004WO-JP015314.
XX
XX 08-OCT-2003; 2003JP-00350161.
XX
XX (KYOW ) KYOWA HAKKO KOGYO KK.
XX
XX Iida S, Satoh M, Urakubo M, Wakitani M, Uchida K, Niwa R;
XX Shitara K;
XX
XX WPI; 2005-346195/35.
XX
XX Antibody composition for treating ganglioside GD3 associated disease e.g.
XX cancer, comprises genetically modified antibody molecule, which
XX specifically binds to ganglioside GD3 and has N-glycoside-binding sugar
XX chain in its Fc domain.

Claim 25; SEQ ID NO 26; 124pp; Japanese.
XX
XX The invention describes an antibody composition (I), comprising a

```

CC genetically modified antibody molecule which specifically binds to  
 CC ganglioside GD3 and has an N-glycoside-binding complex sugar chain in its  
 CC Fc domain, where the N-glycoside-binding complex sugar chain is a sugar  
 CC chain having no fucose attached to N-acetylglucosamine at the reducing  
 CC end of the sugar chain. Also described are: a transformant (II) capable  
 CC of producing (I), obtained by introducing DNA that encodes the antibody  
 CC molecule which specifically binds with ganglioside GD3, to a host cell;  
 CC producing (I), involving cultivating (I) in a culture medium, such that  
 CC C1 (sic) is produced and accumulated in the culture, extracting and  
 CC purifying C1 from the culture medium; a pharmaceutical (III) containing  
 CC C1 as an active ingredient; and a therapeutic agent (A1) for ganglioside  
 CC GD3 associated disease, comprising C1 as an active ingredient. (I) is  
 CC useful for treating GD3 associated disease, which involves administering  
 CC (I), where the GD3 associated disease is cancer; (A1) is also useful for  
 CC treating GD3 associated disease. (II) is useful for producing (I). (I) is  
 CC useful for manufacturing a therapeutic agent for GD3 associated disease.  
 CC This sequence represents a ganglioside GD3 binding antibody associated  
 CC protein.

XX Sequence 108 AA;

Query Match 100.0%; Score 56; DB 9; Length 108;  
 Best Local Similarity 100.0%; Pred. No. 0.052;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HQYSKLPWT 9  
 DB 89 HQYSKLPWT 97  
 |||||

RESULT 11

ID ADZ57823 standard; protein; 108 AA.

AC ADZ57823;

DT 30-JUN-2005 (first entry)

DE Ganglioside GD3 binding antibody associated protein SEQ ID NO 27.

KW cytostatic; antibody engineering; cancer; neoplasm; ganglioside; GD3;  
 KW pharmaceutical.

XX Synthetic.

OS WO2005035577-A1.

PN 21-APR-2005.

PD 08-OCT-2004; 2004WO-JP015314.

PF 08-OCT-2003; 2003JP-00350161.

PR (KYOW ) KYOWA HAKKO KOGYO KK.

PI Iida S, Satoh M, Urakubo M, Wakitani M, Uchida K, Niwa R;  
 PI Shitara K;

XX WPI; 2005-346195/35.

XX Antibody composition for treating ganglioside GD3 associated disease e.g.  
 PT cancer, comprises genetically modified antibody molecule, which  
 PT specifically binds to ganglioside GD3 and has N-glycoside-binding sugar  
 PT chain in its Fc domain.

XX Claim 25; SEQ ID NO 27; 124pp; Japanese.

XX The invention describes an antibody composition (I), comprising a  
 CC genetically modified antibody molecule which specifically binds to  
 CC ganglioside GD3 and has an N-glycoside-binding complex sugar chain in its  
 CC Fc domain, where the N-glycoside-binding complex sugar chain is a sugar  
 CC chain having no fucose attached to N-acetylglucosamine at the reducing  
 CC end of the sugar chain. Also described are: a transformant (II) capable

CC of producing (I), obtained by introducing DNA that encodes the antibody  
 CC molecule which specifically binds with ganglioside GD3, to a host cell;  
 CC producing (I), involving cultivating (I) in a culture medium, such that  
 CC C1 (sic) is produced and accumulated in the culture, extracting and  
 CC purifying C1 from the culture medium; a pharmaceutical (III) containing  
 CC C1 as an active ingredient; and a therapeutic agent (A1) for ganglioside  
 CC GD3 associated disease, comprising C1 as an active ingredient. (I) is  
 CC useful for treating GD3 associated disease, which involves administering  
 CC (I), where the GD3 associated disease is cancer. (A1) is also useful for  
 CC treating GD3 associated disease. (II) is useful for producing (I). (I) is  
 CC useful for manufacturing a therapeutic agent for GD3 associated disease.  
 CC This sequence represents a ganglioside GD3 binding antibody associated  
 CC protein.

XX Sequence 108 AA;

Query Match 100.0%; Score 56; DB 9; Length 108;  
 Best Local Similarity 100.0%; Pred. No. 0.052;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HQYSKLPWT 9  
 DB 89 HQYSKLPWT 97  
 |||||

RESULT 12

ID ADZ57817 standard; protein; 108 AA.

AC ADZ57817;

DT 30-JUN-2005 (first entry)

DE Ganglioside GD3 binding antibody associated protein SEQ ID NO 21.

KW cytostatic; antibody engineering; cancer; neoplasm; ganglioside; GD3;  
 KW pharmaceutical.

OS Mus musculus.

PN WO2005035577-A1.

PD 21-APR-2005.

PF 08-OCT-2004; 2004WO-JP015314.

PR 08-OCT-2003; 2003JP-00350161.

XX (KYOW ) KYOWA HAKKO KOGYO KK.

PI Iida S, Satoh M, Urakubo M, Wakitani M, Uchida K, Niwa R;  
 PI Shitara K;

XX WPI; 2005-346195/35.

XX Antibody composition for treating ganglioside GD3 associated disease e.g.  
 PT cancer, comprises genetically modified antibody molecule, which  
 PT specifically binds to ganglioside GD3 and has N-glycoside-binding sugar  
 PT chain in its Fc domain.

XX Claim 14; SEQ ID NO 21; 124pp; Japanese.

XX The invention describes an antibody composition (I), comprising a  
 CC genetically modified antibody molecule which specifically binds to  
 CC ganglioside GD3 and has an N-glycoside-binding complex sugar chain in its  
 CC Fc domain, where the N-glycoside-binding complex sugar chain is a sugar  
 CC chain having no fucose attached to N-acetylglucosamine at the reducing  
 CC end of the sugar chain. Also described are: a transformant (II) capable  
 CC of producing (I), obtained by introducing DNA that encodes the antibody  
 CC molecule which specifically binds with ganglioside GD3, to a host cell;  
 CC producing (I), involving cultivating (I) in a culture medium, such that  
 CC C1 (sic) is produced and accumulated in the culture, extracting and  
 CC purifying C1 from the culture medium; a pharmaceutical (III) containing

CC C1 as an active ingredient; and a therapeutic agent (A1) for ganglioside  
 CC GD3 associated disease, comprising C1 as an active ingredient. (I) is  
 CC useful for treating GD3 associated diseases, which involves administering  
 CC (I), where the GD3 associated diseases is cancer. (A1) is also useful for  
 CC treating GD3 associated disease. (II) is useful for producing (I). (I) is  
 CC useful for manufacturing a therapeutic agent for GD3 associated disease.  
 CC This sequence represents a ganglioside GD3 binding antibody associated  
 CC protein.

XX Sequence 108 AA;

Query Match 100.0%; Score 56; DB 9; Length 108;  
 Best Local Similarity 100.0%; Pred. No. 0.052;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HOYSKLPWT 9  
 DB 89 HOYSKLPWT 97

## RESULT 13

ADZ57820  
 ID ADZ57820 standard; protein; 108 AA.

XX  
 AC ADZ57820;

DT 30-JUN-2005 (first entry)

DE Ganglioside GD3 binding antibody associated protein SEQ ID NO 24.

XX cytosolic; antibody engineering; cancer; neoplasm; ganglioside; GD3;  
 KW pharmaceutical.

XX Synthetic.

PN WO2005035577-A1.

XX 21-APR-2005.

XX 08-OCT-2004; 2004WO-JP015314.

XX 08-OCT-2003; 2003JP-00350161.

PA (KYOW ) KYOWA HAKKO KOGYO KK.

PI Tida S, Satoh M, Urakubo M, Wakitani M, Uchida K, Niwa R;  
 PI Shitara K;

DR WPI; 2005-346195/35.

XX Antibody composition for treating ganglioside GD3 associated disease e.g.  
 PT cancer, comprises genetically modified antibody molecule, which  
 PT specifically binds to ganglioside GD3 and has N-glycoside-binding sugar  
 PT chain in its FC domain.

PS Claim 21; SEQ ID NO 24; 124pp; Japanese.

XX The invention describes an antibody composition (I), comprising a  
 CC genetically modified antibody molecule which specifically binds to  
 CC ganglioside GD3 and has an N-glycoside-binding complex sugar chain in its  
 CC FC domain, where the N-glycoside-binding complex sugar chain is a sugar  
 CC chain having no fucose attached to N-acetylglucosamine at the reducing  
 CC end of the sugar chain. Also described are: a transformant (II) capable  
 CC of producing (I), obtained by introducing DNA that encodes the antibody  
 CC molecule which specifically binds with ganglioside GD3, to a host cell;  
 CC producing (I), involving cultivating (I) in a culture medium, such that  
 CC C1 (sic) is produced and accumulated in the culture, extracting and  
 CC purifying C1 from the culture medium; a pharmaceutical (III) containing  
 CC C1 as an active ingredient; and a therapeutic agent (A1) for ganglioside  
 CC GD3 associated disease, comprising C1 as an active ingredient. (I) is  
 CC useful for treating GD3 associated disease, which involves administering  
 CC (I), where the GD3 associated diseases is cancer. (A1) is also useful for  
 CC treating GD3 associated disease. (II) is useful for producing (I). (I) is

CC useful for manufacturing a therapeutic agent for GD3 associated disease.  
 CC This sequence represents a ganglioside GD3 binding antibody associated  
 CC protein.

XX Sequence 108 AA;

Query Match 100.0%; Score 56; DB 9; Length 108;  
 Best Local Similarity 100.0%; Pred. No. 0.052;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HOYSKLPWT 9  
 DB 89 HOYSKLPWT 97

## RESULT 14

AAR33257  
 ID AAR33257 standard; protein; 128 AA.

XX  
 AC AAR33257;

XX 25-MAR-2003 (revised)

DT 12-JUL-1993 (first entry)

DE Rat immunoglobulin L chain variable region of pKM641LA2.

XX Promoter; variable; region; rat; immunoglobulin; heavy; H; chain;  
 KW humanised; chimeric; antibody; expression vector.

XX Rattus rattus.

XX Key Location/Qualifiers  
 FT Peptide 1..20 /note= "Signal peptide"  
 FT Protein 21..128  
 FT /note= "Mature protein"

XX EP533199-A2.

XX 24-MAR-1993.

XX 18-SEP-1992; 92EP-00116026.

XX 18-SEP-1991; 91JP-00238375.

PA (KYOW ) KYOWA HAKKO KOGYO CO LTD.

PI Shitara K, Hanai N, Hasegawa M, Miyaji H, Kuwana Y;

DR WPI; 1993-095510/12.

DR N-PSDB; AAQ33258.

XX Humanised chimeric antibody prodn. against ganglioside GD3 - for treating  
 PT cancers, such as melanoma, neuroblastoma, etc.

PS Claim 6; Page 30-31; 63pp; English.

XX The sequences given in AAR33256-57 represent rat heavy and light chain  
 CC variable regions respectively. The DNA sequences encoding these proteins  
 CC were used in the construction of humanised chimeric antibody expression  
 CC vectors. In these humanised antibodies none of the amino acids of the non  
 CC -human animal Ab variable region have been changed. (Updated on 25-MAR-  
 CC 2003 to correct PN field.)

XX Sequence 128 AA;

Query Match 100.0%; Score 56; DB 2; Length 128;  
 Best Local Similarity 100.0%; Pred. No. 0.061;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HOYSKLPWT 9  
 DB 109 HOYSKLPWT 117

```
RESULT 15
AAR53340
ID AAR53340 standard; protein; 128 AA.
XX
AC AAR53340;
XX
DT 18-NOV-1994 (first entry)
XX
DE KM641 H chain variable region.
XX
KW Monoclonal antibody; Ab; ganglioside GM2; chimera; chimeric antibody;
KW expression vector; heavy; light; chain; hypervariable region; CDR;
KW constant region; hybridoma; Ig; immunoglobulin; promoter; enhancer.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT Peptide i..20
FT /label= sig_peptide
XX
PN AU9346181-A.
XX
PD 17-MAR-1994.
XX
PF 07-SEP-1993; 93AU-00046181.
XX
PR 07-SEP-1992; 92JP-00238452.
XX
PA (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI Nakamura K, Koike M, Shitara K, Hanai N, Kuwana Y, Hasegawa M;
XX
DR WPI; 1994-126857/16.
DR N-PSDB; AAQ45438.
XX
PT Humanised antibody specific for ganglioside GM2 - used for producing a
PT cytotoxic effect on cancers such as melanoma, neuroblastoma and glioma.
XX
PS Example 2; Page 115-116; 191pp; English.
XX
CC Example 2 describes the construction of the vector pChi641HA1 for
CC chimeric human antibody H chain expression. mRNA from mouse anti-GD3
CC monoclonal Ab KM641-producing cells was isolated and KM641 H and L chain
CC cDNAs isolated. The base sequences of the Ig variable regions in KM641 H
CC chain cDNA (pKM641HA3) and KM641 L chain cDNA (pKM641LA2) are given in
CC AAQ45438-39. A KM641-derived chimeric human Ab H chain expression vector
CC was constructed by joining the H chain variable region gene from
CC pKM641HA3 to a vector for chimeric human Ab H chain expression using the
CC synthetic DNAs given in AAQ63439 and AAQ63440
XX
SQ Sequence 128 AA;
Query Match 100.0%; Score 56; DB 2; Length 128;
Best Local Similarity 100.0%; Pred. No. 0.061;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HOYSKLPWT 9
DB 109 HQYSKLPWT 117
RESULT 16
AAY28368
ID AAY28368 standard; protein; 128 AA.
XX
AC AAY28368;
XX
DT 04-NOV-1999 (first entry)
XX
DE pKM641 LA2 immunoglobulin light chain.
XX
KW antibody; nucleotide; genomic; hypervariable region; chimeric;
KW light chain; amino acid.
XX
OS Mus sp.
XX
PN US5939532-A.
XX
PD 17-AUG-1999.
XX
PF 07-JUN-1995; 95US-00483528.
XX
PR 07-SEP-1993; 93US-00116778.
XX
PA (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI Nakamura K, Hanai N, Kuwana Y, Hasegawa M, Koike M, Shitara K;
XX
DR WPI; 1999-468416/39.
DR N-PSDB; AAX99481.
XX
FT Chimeric human antibody expression vectors.
XX
PS Example 1; Col 99; 188pp; English.
XX
CC This immunoglobulin region was isolated from pKM641LA2 A methionine
CC codon, presumably the initiation codon ARG, was found in the vicinity of
CC the 5' terminus and the sequence has a full length leader sequence. The
CC chimeric human antibodies are useful in the treatment of cancer,
CC especially that which is of neural ectodermal origin. In contrast to
CC prior art constructs based on mouse monoclonal antibodies, the chimeric
CC human antibodies do not cause anti-mouse immunoglobulin production. The
CC chimeric human antibodies have a prolonged half-life and a reduced
CC frequency of adverse effects when compared to mouse monoclonal antibodies
XX
SQ Sequence 128 AA;
Query Match 100.0%; Score 56; DB 2; Length 128;
Best Local Similarity 100.0%; Pred. No. 0.061;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HOYSKLPWT 9
DB 109 HQYSKLPWT 117
RESULT 17
AAB01628
ID AAB01628 standard; protein; 128 AA.
XX
AC AAB01628;
XX
DT 07-DEC-2000 (first entry)
XX
DE Murine immunoglobulin light chain variable region.
XX
KW Mouse; immunoglobulin; L chain; light chain; variable region; cancer;
KW humanised antibody.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FT Peptide i..20
FT /label= signal_peptide
FT Protein 21..128
FT /label= mature_immunoglobulin_light_chain_v_region
XX
PN EP1013761-A2.
XX
PD 28-JUN-2000.
XX
PF 18-SEP-1992; 99EP-00124345.
XX
PR 18-SEP-1991; 91JP-00238375.
```



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AAB81997
ID AAB81997 standard; protein; 128 AA.
XX
AC AAB81997;
XX
DT 03-JUL-2001 (first entry)
XX
DE Ganglioside GD3 specific antibody related protein #6.
XX
KW Ganglioside; GD3; complementarity determining region; CDR; antibody;
KW cancer.
XX
OS Synthetic.
XX
PN WO200123432-A1.
XX
PD 05-APR-2001.
XX
PF 29-SEP-2000; 2000WO-JP006774.
XX
PR 30-SEP-1999; 99JP-00278291.
PR 06-APR-2000; 2000JP-00105088.
XX
PA (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI Hanai N, Shitara K, Nakamura K, Niwa R;
XX
DR WPI; 2001-266143/27.
XX
N-PSDB; AAF86907.
XX
PT New human type complementation-determining region-transplanted antibody
PT and derivatives against ganglioside GD3; useful in diagnosis and therapy
PT of e.g. tumors, with low antigenicity, little side effects but potent
PT activity in cancer.
XX
PS Example 1; Page 161-162; 183pp; Japanese.
XX
CC The present invention describes a monoclonal antibody which can react
CC specifically with ganglioside GD3. The antibody and its derivatives are
CC useful in the diagnosis and therapy of tumours, particularly cancer
CC diagnosis. The present sequence is a protein used in the exemplification
CC of the invention
XX
SQ Sequence 128 AA;
XX
Query Match 100.0%; Score 56; DB 4; Length 128;
Best Local Similarity 100.0%; Pred. No. 0.061;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HOYSKLPWT 9
DB 109 HOYSKLPWT 117
XX
RESULT 21
AAB81978
ID AAB81978 standard; protein; 128 AA.
XX
AC AAB81978;
XX
DT 03-JUL-2001 (first entry)
XX
DE Ganglioside GD3 specific antibody related protein SEQ ID NO: 2.
XX
KW Ganglioside; GD3; complementarity determining region; CDR; antibody;
KW cancer.
XX
OS Mus musculus.
XX
PN WO200123432-A1.
XX
PD 05-APR-2001.
XX
Query Match 100.0%; Score 56; DB 4; Length 128;
Best Local Similarity 100.0%; Pred. No. 0.061;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HOYSKLPWT 9
DB 109 HOYSKLPWT 117
XX
RESULT 22
AAB81996
ID AAB81996 standard; protein; 128 AA.
XX
AC AAB81996;
XX
DT 03-JUL-2001 (first entry)
XX
DE Ganglioside GD3 specific antibody related protein #5.
XX
KW Ganglioside; GD3; complementarity determining region; CDR; antibody;
KW cancer.
XX
OS Synthetic.
XX
PN WO200123432-A1.
XX
PD 05-APR-2001.
XX
PF 29-SEP-2000; 2000WO-JP006774.
XX
PR 30-SEP-1999; 99JP-00278291.
PR 06-APR-2000; 2000JP-00105088.
XX
PA (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI Hanai N, Shitara K, Nakamura K, Niwa R;
XX
DR WPI; 2001-266143/27.
XX
N-PSDB; AAF86904.
XX
PT New human type complementation-determining region-transplanted antibody
PT and derivatives against ganglioside GD3; useful in diagnosis and therapy
PT of e.g. tumors, with low antigenicity, little side effects but potent
PT activity in cancer.
XX
PS Example 1; Page 159-160; 183pp; Japanese.
XX
```

CC The present invention describes a monoclonal antibody which can react  
CC specifically with ganglioside GD3. The antibody and its derivatives are  
CC useful in the diagnosis and therapy of tumours, particularly cancer  
CC diagnosis. The present sequence is a protein used in the exemplification  
CC of the invention  
XX  
SQ Sequence 128 AA;

Query Match 100.0%; Score 56; DB 4; Length 128;  
Best Local Similarity 100.0%; Pred. No. 0.061;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HOYSKLPWT 9  
DB 109 HOYSKLPWT 117

## RESULT 23

AAB81999  
ID AAB81999 standard; protein; 128 AA.

XX  
AC AAB81999;

XX  
DT 03-JUL-2001 (first entry)

XX  
DE Ganglioside GD3 specific antibody related protein #8.

XX  
KW Ganglioside; GD3; complementarity determining region; CDR; antibody;  
KW cancer.

XX  
OS Synthetic.

XX  
PN WO200123432-A1.

XX  
PD 05-APR-2001.

XX  
PF 29-SEP-2000; 2000WO-JP006774.

XX  
PR 30-SEP-1999; 99JP-00278291.

XX  
PR 06-APR-2000; 2000JP-00105088.

XX  
PA (KYOW ) KYOWA HAKKO KOGYO KK.

XX  
PI Hanai N, Shitara K, Nakamura K, Niwa R;

XX  
DR WPI; 2001-266143/27.

XX  
DR N-PSDB; AAF86913.

XX  
PT New human type complementation-determining region-transplanted antibody  
PT and derivatives against ganglioside GD3, useful in diagnosis and therapy  
PT of e.g. tumors, with low antigenicity, little side effects but potent  
PT activity in cancer.

XX  
PS Example 1; Page 166; 183pp; Japanese.

XX  
CC The present invention describes a monoclonal antibody which can react  
CC specifically with ganglioside GD3. The antibody and its derivatives are  
CC useful in the diagnosis and therapy of tumours, particularly cancer  
CC diagnosis. The present sequence is a protein used in the exemplification  
CC of the invention  
XX  
SQ Sequence 128 AA;

Query Match 100.0%; Score 56; DB 4; Length 128;  
Best Local Similarity 100.0%; Pred. No. 0.061;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HOYSKLPWT 9  
DB 109 HOYSKLPWT 117

## RESULT 24

AAB81999

ID AAB81999 standard; protein; 128 AA.

XX  
AC AAB81999;

XX  
DT 03-JUL-2001 (first entry)

XX  
DE Ganglioside GD3 specific antibody related protein #2.

XX  
KW Ganglioside; GD3; complementarity determining region; CDR; antibody;  
KW cancer.

XX  
OS Synthetic.

XX  
PN WO200123432-A1.

XX  
PD 05-APR-2001.

XX  
PF 29-SEP-2000; 2000WO-JP006774.

XX  
PR 30-SEP-1999; 99JP-00278291.

XX  
PR 06-APR-2000; 2000JP-00105088.

XX  
PA (KYOW ) KYOWA HAKKO KOGYO KK.

XX  
PI Hanai N, Shitara K, Nakamura K, Niwa R;

XX  
DR WPI; 2001-266143/27.

XX  
DR N-PSDB; AAF86895.

XX  
PT New human type complementation-determining region-transplanted antibody  
PT and derivatives against ganglioside GD3, useful in diagnosis and therapy  
PT of e.g. tumors, with low antigenicity, little side effects but potent  
PT activity in cancer.

XX  
PS Example 1; Page 153; 183pp; Japanese.

XX  
CC The present invention describes a monoclonal antibody which can react  
CC specifically with ganglioside GD3. The antibody and its derivatives are  
CC useful in the diagnosis and therapy of tumours, particularly cancer  
CC diagnosis. The present sequence is a protein used in the exemplification  
CC of the invention  
XX  
SQ Sequence 128 AA;

Query Match 100.0%; Score 56; DB 4; Length 128;  
Best Local Similarity 100.0%; Pred. No. 0.061;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HOYSKLPWT 9  
DB 109 HOYSKLPWT 117

## RESULT 25

AAB81999

ID AAB81999 standard; protein; 128 AA.

XX  
AC AAB81999;

XX  
DT 03-JUL-2001 (first entry)

XX  
DE Ganglioside GD3 specific antibody related protein #1.

XX  
KW Ganglioside; GD3; complementarity determining region; CDR; antibody;  
KW cancer.

XX  
OS Synthetic.

XX  
PN WO200123432-A1.

XX  
PD 05-APR-2001.

XX

```

PF 29-SEP-2000; 2000WO-JP006774.
XX
XX
PR 30-SEP-1999; 99JP-00278291.
PR 06-APR-2000; 2000JP-00105088.
XX
XX
XX (KYOW ) KYOWA HAKKO KOGYO KK.
XX
XX
PI Hanai N, Shitara K, Nakamura K, Niwa R;
XX
XX
DR WPI; 2001-266143/27.
DR N-PSDB; AAF86892.
XX
XX
PT New human type complementation-determining region-transplanted antibody
PT and derivatives against ganglioside GD3; useful in diagnosis and therapy
PT of e.g. tumors, with low antigenicity, little side effects but potent
PT activity in cancer.
XX
XX
PS Example 1; Page 150-151; 183pp; Japanese.
XX
XX
CC The present invention describes a monoclonal antibody which can react
CC specifically with ganglioside GD3. The antibody and its derivatives are
CC useful in the diagnosis and therapy of tumors, particularly cancer
CC diagnosis. The present sequence is a protein used in the exemplification
CC of the invention
XX
XX
SQ Sequence 128 AA;
Query Match 100.0%; Score 56; DB 4; Length 128;
Best Local Similarity 100.0%; Pred. No. 0.061;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HOYSKLPWT 9
DB 109 HOYSKLPWT 117

RESULT 27
ABU11003
ID ABU11003 standard; protein; 128 AA.
XX
XX ABU11003;
XX
XX 04-FEB-2003 (first entry)
XX
XX Modified ganglioside GD3 antibody associated protein #2.
XX
XX Ganglioside GD3; anti-ganglioside GD3 antibody; tumour; melanoma.
XX
XX Mus musculus.
XX
XX WO200278739-A1.
XX
XX 10-OCT-2002.
XX
XX 29-MAR-2002; 2002WO-JP003170.
XX
XX 29-MAR-2001; 2001JP-00097483.
XX
XX (KYOW ) KYOWA HAKKO KOGYO KK.
XX
XX Shitara K, Niwa R, Kanazawa J, Asada M;
XX
XX WPI; 2003-067410/06.
XX
XX Drugs containing genetically-modified antibody against ganglioside GD3,
XX its fragment, immunocompetent cell activators or/and antitumor agents in
XX combination, applicable in treating malignant tumor like melanoma.
XX
XX Example 3; Page 98; 121pp; Japanese.
XX
XX The invention describes drugs contain a genetically-modified antibody
XX against ganglioside GD3 or its fragment and at least 1 of a substance
XX capable of activating immunocompetent cells and a substance having an
XX antitumor activity in combination. The drugs can be used to treat tumour
XX like melanoma and can provide a treatment with enhanced therapeutic
XX effect and little side-reactions, particularly to relieve problems of
XX side-effects during the conventional single administration. This sequence
XX represents a protein associated with the anti- ganglioside GD3 antibody
XX
XX
SQ Sequence 128 AA;
Query Match 100.0%; Score 56; DB 6; Length 128;
Best Local Similarity 100.0%; Pred. No. 0.061;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HOYSKLPWT 9
DB 109 HOYSKLPWT 117

RESULT 28
AAB81998
ID AAB81998 standard; protein; 128 AA.
XX
XX
XX AAB81998;
XX
XX 03-JUL-2001 (first entry)
XX
XX Ganglioside GD3 specific antibody related protein #7.
XX
XX Ganglioside; GD3; complementarity determining region; CDR; antibody;
XX cancer.
XX
XX Synthetic.
XX
XX WO200123432-A1.
XX
XX 05-APR-2001.
XX
XX 29-SEP-2000; 2000WO-JP006774.
XX
XX 30-SEP-1999; 99JP-00278291.
PR 06-APR-2000; 2000JP-00105088.
XX
XX (KYOW ) KYOWA HAKKO KOGYO KK.
XX
XX
XX
PI Hanai N, Shitara K, Nakamura K, Niwa R;
XX
XX
XX WPI; 2001-266143/27.
DR N-PSDB; AAF86912.
XX
XX
PT New human type complementation-determining region-transplanted antibody
PT and derivatives against ganglioside GD3; useful in diagnosis and therapy
PT of e.g. tumors, with low antigenicity, little side effects but potent
PT activity in cancer.
XX
XX
XX Example 3; Page 164-165; 183pp; Japanese.

```



AEC20796  
 ID AEC20796 standard; peptide; 9 AA.  
 XX AC AEC20796;  
 XX DT 20-OCT-2005 (first entry)  
 XX DE M-CSF specific murine antibody MC-1 light chain CDR3.  
 XX endocrine-gen.; antiarthritic; antibacterial; antiinflammatory;  
 KW antirheumatic; antithyroid; bone metastases; calcium antagonist; cancer;  
 KW cardiovascular-gen.; degeneration; eating-disorders-gen.;  
 KW endocrine disease; endocrine-gen.; endocrine-gen.; gastrointestinal-gen.;  
 KW genetic disorder; light chain; hepatotropic; hypercalcemia;  
 KW immune disorder; immunotherapy; inflammation; monoclonal antibody;  
 KW mouth disease; musculoskeletal disease; neoplasm; nephrotropic;  
 KW osteopathic; osteoporosis; osteoporosis; pagets disease;  
 KW periodontal disease; pharmaceutical; rheumatoid arthritis; MC-1.  
 XX OS Mus musculus.  
 XX WO2005068503-A2.  
 XX PD 28-JUL-2005.  
 XX PF 06-JAN-2005; 2005WO-US000546.  
 XX PR 07-JAN-2004; 2004US-0535181P.  
 XX PR 02-JUN-2004; 2004US-0576417P.  
 XX PA (CHIR ) CHIRON CORP.  
 XX PA (XOMA ) XOMA TECHNOLOGY LTD.  
 XX PI Liu C, Zimmerman DL, Harrowe GM, Kothe K, Kavanaugh WM, Long L;  
 PI Calderon-Cacia M, Horwitz AH;  
 XX WPI; 2005-597707/61.  
 XX Novel non-murine antibody that competes with monoclonal antibody RX1 for  
 PT binding to macrophage colony stimulating factor, useful for treating  
 PT hypogonadism, hypercalcemia, rickets, scurvy, homocystinuria, cancer,  
 PT osteoporosis.  
 XX Claim 21; SEQ ID NO 35; 269pp; English.  
 XX The invention describes a non-murine antibody (I) that competes with  
 CC monoclonal antibody RX1 for binding to macrophage colony stimulating  
 CC factor (M-CSF) by more than 75%, where the monoclonal antibody RX1 has  
 CC the heavy chain and light chain amino acid sequences having a fully  
 CC defined 447 amino acids (SEQ ID No. 2) and 214 amino acids (SEQ ID No. 4)  
 CC sequences given in the specification, respectively. (I) is useful for  
 CC preventing a subject afflicted with a disease that causes or contributes  
 CC to osteolysis, where the antibody effectively reduces the severity of  
 CC bone loss associated with the disease. The disease is chosen from  
 CC metabolic bone diseases associated with relatively increased osteoclast  
 CC activity, including endocrinopathies, hypercalcemia, deficiency states,  
 CC chronic diseases, and hereditary diseases, cancer, osteoporosis,  
 CC osteopetrosis, inflammation of bone associated with arthritis and  
 CC rheumatoid arthritis, periodontal disease, fibrous dysplasia, and/or  
 CC Paget's disease. (I) is useful for preventing or treating metastatic  
 CC cancer. Antibodies of the invention are useful for preventing or reducing  
 CC bone loss; osteolysis; metastatic cancer to bone and cancer. (I) is  
 CC useful for manufacturing a medicament for preventing or reducing bone  
 CC loss in a patient exhibiting osteolysis, manufacturing a medicament for  
 CC treating a patient afflicted with a disease that causes or contributes to  
 CC osteolysis, and metastatic cancer to bone in a patient suffering from  
 CC metastatic cancer, for manufacturing a medicament for treating a patient  
 CC having cancer. (I) in synergistic combination, is useful for preparing a  
 CC medicament for treating a patient exhibiting osteolysis. This is the  
 CC amino acid sequence of macrophage colony stimulating factor (M-CSF)  
 CC specific murine antibody MC-1 light chain CDR3.  
 XX Sequence 9 AA;

Query Match 85.7%; Score 48; DB 9; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 QYSKLPWT 9  
 DB 2 QYSKLPWT 9  
 RESULT 29  
 ADY85024  
 ID ADY85024 standard; protein; 107 AA.  
 XX AC ADY85024;  
 XX DT 02-JUN-2005 (first entry)  
 XX DE Monoclonal antibody 2E11 HMGB1 V kappa domain.  
 XX High mobility group box; HMGB1; monoclonal antibody; antibody therapy;  
 KW sepsis; antibacterial immunosuppressive; graft rejection; arthritis;  
 KW antiarthritic; asthma; antiasthmatic; lupus erythematosus;  
 KW antiinflammatory; inflammation; dermatological;  
 KW respiratory distress syndrome; respiratory-gen.; psoriasis;  
 KW antipsoriatic; chronic obstructive pulmonary disease; pancreatitis;  
 KW peritonitis; burns; vulvular; ischemia; vasotropic; Behcets disease;  
 KW gastrointestinal-gen.; multiple sclerosis neuroprotective; cachexia;  
 KW anabolic; infection; musculoskeletal disease; immune disorder;  
 KW light chain variable region.  
 XX OS Mus sp.  
 XX FH Key  
 XX FT Region  
 XX FT /label= CDR1  
 XX FT Region  
 XX FT /label= CDR2  
 XX FT Region  
 XX FT /label= CDR3  
 XX WO2005026209-A2.  
 XX PD 24-MAR-2005.  
 XX PF 10-SEP-2004; 2004WO-US029527.  
 XX PR 11-SEP-2003; 2003US-0502568P.  
 XX PA (CRIT-) CRITICAL THERAPEUTICS INC.  
 XX PI Newman W, Qin S, Okeefe T, Obar R;  
 XX WPI; 2005-233483/24.  
 XX DR N-PSDB; ADY85023.  
 XX New antibody or its antigen-binding fragment specific to a vertebrate  
 PT high mobility group box (HMGB) A box that inhibits release of a  
 PT proinflammatory cytokine from a cell treated with HMGB protein, useful  
 PT for treating, e.g. sepsis.  
 XX Example 4; SEQ ID NO 13; 123pp; English.  
 XX The invention provides antibodies, or their antigen-binding fragments,  
 CC that bind to a vertebrate high mobility group box (HMGB) polypeptide, to  
 CC methods of detecting and/or identifying an agent that binds to an HMGB  
 CC polypeptide, methods of treating a condition in a subject characterized  
 CC by activation of an inflammatory cytokine cascade, and methods of  
 CC detecting an HMGB polypeptide in a sample. The antibody for antigen-  
 CC binding fragment) binds to a vertebrate HMGB A box but does not  
 CC specifically bind to non-A box epitopes of HMGB, and inhibits release of  
 CC a proinflammatory cytokine from a vertebrate cell treated with an HMGB

CC protein. A method of treating a condition characterized by activation of  
 CC an inflammatory cytokine cascade comprises administering an antibody of  
 CC the invention, or its antigen-binding fragment. The condition is selected  
 CC from sepsis, allograft rejection, arthritis, asthma, lupus, adult  
 CC respiratory distress syndrome, chronic obstructive pulmonary disease,  
 CC psoriasis, pancreatitis, peritonitis, burns, ischemia, Behcet's disease,  
 CC graft versus host disease, inflammatory bowel disease, multiple sclerosis  
 CC and cachexia, especially sepsis, arthritis, or lupus. The present  
 CC sequence is the protein sequence of the light chain variable region  
 CC (Vkappa) of an anti-HMGB1 monoclonal antibody produced by claimed murine  
 CC hybridoma 2E11 HMGB1 (ATCC PTA-5431). This monoclonal antibody binds a  
 CC peptide corresponding to amino acid residues 151-168 of human HMGB1  
 CC ADY85012.  
 XX

SQ Sequence 107 AA;

Query Match 85.7%; Score 48; DB 9; Length 107;  
 Best Local Similarity 100.0%; Pred. No. 1.3;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QYSKLPWT 9  
 DB 90 QYSKLPWT 97  
 |||||

RESULT 30

AA12237  
 ID AAR12237 standard; protein; 126 AA.

AC AAR12237;  
 XX 25-MAR-2003 (revised)  
 DT 19-AUG-1991 (first entry)

XX Mouse MAb 1C11 L chain V region.  
 XX HIV-1; chimera.

XX Mus sp.

XX WO9107494-A.

XX 30-MAY-1991.

XX PF 13-NOV-1989; 89US-00433703.

XX PR 13-NOV-1989; 89US-00433703.

XX PA (XOMA ) XOMA CORP.

XX PA (GREC ) GREEN CROSS CORP.

XX PA (ZOMA-) ZOMA CORP.

XX PI Better MD, Horwitz AH, Ghoshdasti P, Robinson RR;

XX WPI: 1991-178106/24.

XX DR N-PSDB; AAQ12017.

XX New chimeric mouse human antibodies - used in treatment, diagnosis and  
 PT prophylaxis of HIV infections.

XX Disclosure; Fig 13; 108pp; English.

XX The mouse VL gene product may be used to produce chimeric mouse- human  
 CC Abs against HIV-1 comprising human Ig constant regions and murine  
 CC variable regions. These novel sequence are useful in treatment, diagnosis  
 CC and prophylaxis of HIV infections, and may be produced by a bacterial,  
 CC yeast or mammalian expression system. (Updated on 25-MAR-2003 to correct  
 CC PA field.) (Updated on 25-MAR-2003 to correct PI field.)  
 XX

SQ Sequence 126 AA;

Query Match 85.7%; Score 48; DB 2; Length 126;  
 Best Local Similarity 100.0%; Pred. No. 1.6;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 QYSKLPWT 9  
 DB 110 QYSKLPWT 117  
 |||||

RESULT 31

AA12359  
 ID AAR12359 standard; protein; 127 AA.

XX AC AAR12359;

XX 25-MAR-2003 (revised)

DT 15-AUG-1991 (first entry)

XX Light (kappa) chain variable region of murine 1C11 immunoglobulin.

XX Chimeric antibodies; immunoconjugates; HIV; AIDS.

XX Mus musculus.

XX WO9107493-A.

XX 30-MAY-1991.

XX PF 13-NOV-1989; 89US-00433730.

XX PR 13-NOV-1989; 89US-00433730.

XX PA (XOMA ) XOMA CORP.

XX PA (GREC ) GREEN CROSS CORP.

XX PI Better MD, Horwitz AH, Ghoshdasti P, Robinson R;

XX WPI: 1991-178105/24.

XX DR N-PSDB; AAQ12061.

XX New chimeric mouse-human antibodies - used to detect, kill and remove HIV  
 PT -1 antigen from sample.

XX Disclosure; Fig 13; 107pp; English.

XX This is the light (kappa) - chain variable (V) region of a mouse  
 CC monoclonal antibody (MAb), 1C11, and is specific for an HIV-1 viral  
 CC antigen. It is used in the construction of a chimeric MAb comprising  
 CC heavy and light chains having murine V regions and human C regions. The  
 CC chimeric MAbs are more effective than murine MAb 1C11 since they have an  
 CC increased compatibility in humans. The heavy and light chain V-regions  
 CC are joined by manipulating their respective joining (J) regions, to  
 CC generate restriction enzyme recognition sites. The chimeric MAbs can be  
 CC used as immunoconjugates, in association with e.g. toxins for HIV  
 CC treatment. They can also be used in diagnosis of HIV. See also AAQ12056-  
 CC 60 and AAQ12062-63. (Updated on 25-MAR-2003 to correct PA field.)  
 CC (Updated on 25-MAR-2003 to correct PI field.) (Updated on 25-MAR-2003 to  
 CC correct DR field.)  
 XX

SQ Sequence 127 AA;

Query Match 85.7%; Score 48; DB 2; Length 127;  
 Best Local Similarity 100.0%; Pred. No. 1.6;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QYSKLPWT 9

DB 110 QYSKLPWT 117

|||||

RESULT 32

AEC20774  
 ID AEC20774 standard; protein; 214 AA.

XX AC AEC20774;

XX DT 20-OCT-2005 (first entry)

XX DE M-CSF specific murine antibody MC-1 light chain SEQ ID NO 13.

XX KW endocrine-gen.; antiarthritic; antibacterial; antiinflammatory;

XX KW antirheumatic; antithyroid; bone metastases; calcium antagonist; cancer;

XX KW cardiovascular-gen.; degeneration; eating-disorders-gen.; gastrointestinal-gen.;

XX KW endocrine disease; endocrine-gen.; endocrine-gen.; hypercalcemia;

XX KW genetic disorder; light chain; hepatotropic; inflammation; monoclonal antibody;

XX KW immune disorder; immunotherapy; inflammation; monoclonal antibody;

XX KW mouth disease; musculoskeletal disease; neoplasm; nephrotropic;

XX KW osteopathic; osteoporosis; osteoporosis; pagets disease;

XX KW periodontal disease; pharmaceutical; rheumatoid arthritis; MC-1.

XX OS Mus musculus.

XX KW WO2005068503-A2.

XX PN 28-JUL-2005.

XX PF 06-JAN-2005; 2005WO-US000546.

XX PR 07-JAN-2004; 2004US-0535181P.

XX PR 02-JUN-2004; 2004US-057641P.

XX PA (CHIR ) CHIRON CORP.

XX PA (XOMA ) XOMA TECHNOLOGY LTD.

XX LIU C, Zimmerman DL, Harrowe GM, Koths K, Kavanaugh WM, Long L;

XX CALDERON-CACIA M, Horwitz AH;

XX WPI; 2005-597707/61.

XX Novel non-murine antibody that competes with monoclonal antibody RX1 for

XX binding to macrophage colony stimulating factor, useful for treating

XX hypogonadism, hypercalcemia, rickets, scurvy, homocystinuria, cancer,

XX osteoporosis.

XX Example 10; SEQ ID NO 13; 269pp; English.

XX The invention describes a non-murine antibody (I) that competes with

XX monoclonal antibody RX1 for binding to macrophage colony stimulating

XX factor (M-CSF) by more than 75%, where the monoclonal antibody RX1 has

XX the heavy chain and light chain amino acid sequences having a fully

XX defined 447 amino acids (SEQ ID No. 2) and 214 amino acids (SEQ ID No. 4)

XX sequences given in the specification, respectively. (I) is useful for

XX preventing a subject afflicted with a disease that causes or contributes

XX to osteolysis, where the antibody effectively reduces the severity of

XX bone loss associated with the disease. The disease is chosen from

XX metabolic bone diseases associated with relatively increased osteoclast

XX activity, including endocrinopathies, hypercalcemia, deficiency states,

XX chronic diseases, and hereditary diseases, cancer, osteoporosis,

XX osteopetrosis, inflammation of bone associated with arthritis and

XX rheumatoid arthritis, periodontal disease, fibrous dysplasia, and/or

XX Paget's disease. (I) is useful for preventing or treating metastatic

XX cancer. Antibodies of the invention are useful for preventing or reducing

XX bone loss; osteolysis; metastatic cancer to bone and cancer. (I) is

XX useful for manufacturing a medicament for preventing or reducing bone

XX loss in a patient exhibiting osteolysis, manufacturing a medicament for

XX treating a patient afflicted with a disease that causes or contributes to

XX osteolysis, and metastatic cancer to bone in a patient suffering from

XX metastatic cancer, for manufacturing a medicament for treating a patient

XX having cancer. (I) in synergistic combination, is useful for preparing a

XX medicament for treating a patient exhibiting osteolysis. This is the

XX amino acid sequence of macrophage colony stimulating factor (M-CSF)

XX specific murine antibody MC-1 light chain.

XX SQ Sequence 214 AA;

XX Query Match 85.7%; Score 48; DB 9; Length 214;

XX Best Local Similarity 100.0%; Pred. No. 2.7; 0; Indels 0; Gaps 0;

XX Matches 8; Conservative 0; Mismatches 0;

QY 2 QYSLKPWT 9

DB 90 QYSLKPWT 97

RESULT 33

ADA89188

ID ADA89188 standard; protein; 109 AA.

XX ADA89188;

XX 20-NOV-2003 (first entry)

XX Human antibody B22 light chain amino acid sequence SEQ ID NO:32.

XX immunoglobulin; Ig; heavy chain variable domain;

XX light chain variable domain; major histocompatibility complex; MHC;

XX gp100; MUC1; TAX; hTERT; cytostatic; gene therapy; cancerous disorder;

XX Cancer.

XX Synthetic.

XX Homo sapiens.

XX WO2003070752-A2.

XX 28-AUG-2003.

XX 20-FEB-2003; 2003WO-US005128.

XX 20-FEB-2002; 2002US-0358994P.

XX (DYAX-) DYAX CORP.

XX (TECR ) TECHNION RES & DEV FOUND LTD.

XX Hoogenboom HRJM, Reiter Y;

XX WPI; 2003-663847/62.

XX N-PSDB; ADA89187.

XX New protein comprising an immunoglobulin heavy chain variable (VH) domain

XX and an immunoglobulin light chain variable (VL) domain, useful for

XX preparing a composition for treating or preventing a cancerous disorder.

XX Disclosure; Fig 7A; 224pp; English.

XX The present invention describes a protein comprising an immunoglobulin

XX (Ig) heavy chain variable (VH) domain and an Ig light chain variable (VL)

XX domain. The protein binds a complex comprising a major histocompatibility

XX complex (MHC) and a peptide, does not substantially bind the MHC in the

XX absence of the bound peptide, and does not substantially bind the peptide

XX in the absence of the MHC. The peptide is a peptide fragment of gp100,

XX MUC1, TAX or hTERT. Also described: (1) a pharmaceutical composition

XX comprising the novel protein and a carrier; (2) a cytotoxic T cell

XX comprising one or more nucleic acids for expressing the Ig that binds a

XX complex having an MHC and a peptide, does not substantially bind the MHC

XX in the absence of the bound peptide, and does not substantially bind the

XX peptide in the absence of the MHC; (3) an isolated nucleic acid

XX comprising a first segment that encodes the Ig variable domain; (4) a

XX host cell comprising heterologous nucleic acid sequences that encodes the

XX novel protein; (5) a transgenic animal whose genome includes heterologous

XX nucleic acid sequences that encode the protein; (6) identifying the

XX protein that specifically binds the MHC-peptide complex; (7) expressing

XX an antigen-binding protein; (8) ablating or killing a target cell that

XX displays a peptide on a surface MHC molecule; (9) treating or preventing

XX a cancerous disorder in a subject; and (10) detecting an MHC-peptide

XX complex in a sample. A protein of the invention has cytostatic activity,

XX and can be used in gene therapy. The protein is useful for preparing a

XX composition for treating or preventing a cancerous disorder. The present

XX sequence represents the light chain of an antibody which binds to an MHC-

XX peptide complex where the peptide component in as peptide fragment of

XX gp100.

```
SQ Sequence 109 AA;
Query Match 78.6%; Score 44; DB 6; Length 109;
Best Local Similarity 77.8%; Pred. No. 6.9;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 HOYSKLPWT 9
    |||||
Db 90 HOYGFLPWT 98

RESULT 34
AEA17144
ID AEA17144 standard; peptide; 9 AA.
XX
XX
AC AEA17144;
XX
DT 28-JUL-2005 (first entry)
XX
DE Human TNF-alpha variable light chain antibody CDR3 peptide Seq 14.
XX
XX antibody; antibody production; tumor necrosis factor-alpha; cytokine;
KW rheumatoid arthritis; antiarthritic; antirheumatic; antiinflammatory.
XX
XX Homo sapiens.
OS
XX WO2005047329-A1.
FN
PD 26-MAY-2005.
XX
PF 16-NOV-2004; 2004WO-KR002964.
XX
PR 17-NOV-2003; 2003KR-00080950.
XX
PA (YUHA-) YUHAN CORP.
XX
PI Kang HI, Ko IY, Song MY, Kim CS, Park SK, Lee JS, Yoo TH;
PI Na KI;
XX
DR WPI; 2005-372349/38.
XX
PF 16-NOV-2004; 2004WO-KR002964.
XX
PR 17-NOV-2003; 2003KR-00080950.
XX
PA (YUHA-) YUHAN CORP.
XX
PI Kang HI, Ko IY, Song MY, Kim CS, Park SK, Lee JS, Yoo TH;
PI Na KI;
XX
DR WPI; 2005-372349/38.
XX
PF New antibody variable region of a monoclonal antibody specifically
PT binding to human tumor necrosis factor-alpha, useful as regulator for
PT controlling inflammatory cytokines in rheumatoid arthritis or for
PT treating rheumatoid arthritis.
XX
PS Claim 1; SEQ ID NO 14; 21pp; English.
XX
CC This invention relates to a novel antibody variable region of a
CC monoclonal antibody specifically binding to human tumor necrosis factor
CC (TNF)-alpha comprising at least one heavy chain variable region and a
CC light chain variable region. Specifically, it refers to a recombinant
CC vector pTK11-Hv comprising DNA encoding these heavy and light chain
CC variable regions, as well as a transformant Escherichia coli. The present
CC invention describes an antibody variable region of a monoclonal antibody
CC that specifically binds to human tumor necrosis factor-alpha, and is
CC useful as a direct or indirect regulator for controlling inflammatory
CC cytokines in rheumatoid arthritis. Accordingly, the pharmaceutical
CC compositions derived thereof are TNF-alpha modulators that exhibit
CC antiarthritic and antirheumatic activities and as such can be used for
CC treating rheumatoid arthritis. This peptide sequence is a complementarity
CC determining region of the human TNF-alpha light chain antibody protein
CC given in an exemplification of the invention.
XX
SQ Sequence 99 AA;
Query Match 76.8%; Score 43; DB 9; Length 9;
Best Local Similarity 66.7%; Pred. No. 2e+06;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 HOYSKLPWT 9
    |||||
Db 1 HOYERSPWT 9

RESULT 35
AEA17138
ID AEA17138 standard; protein; 109 AA.
XX
XX AC AEA17138;
XX
DT 28-JUL-2005 (first entry)
XX
DE Human TNF-alpha variable light chain antibody protein Seq 8.
XX
XX antibody; antibody production; tumor necrosis factor-alpha; cytokine;
KW rheumatoid arthritis; antiarthritic; antirheumatic; antiinflammatory.
XX
XX Homo sapiens.
OS
XX WO2005047329-A1.
FN
PD 26-MAY-2005.
XX
PF 16-NOV-2004; 2004WO-KR002964.
XX
PR 17-NOV-2003; 2003KR-00080950.
XX
PA (YUHA-) YUHAN CORP.
XX
PI Kang HI, Ko IY, Song MY, Kim CS, Park SK, Lee JS, Yoo TH;
PI Na KI;
XX
DR WPI; 2005-372349/38.
XX
PF New antibody variable region of a monoclonal antibody specifically
PT binding to human tumor necrosis factor-alpha, useful as regulator for
PT controlling inflammatory cytokines in rheumatoid arthritis or for
PT treating rheumatoid arthritis.
XX
PS Claim 3; SEQ ID NO 8; 21pp; English.
XX
CC This invention relates to a novel antibody variable region of a
CC monoclonal antibody specifically binding to human tumor necrosis factor
CC (TNF)-alpha comprising at least one heavy chain variable region and a
CC light chain variable region. Specifically, it refers to a recombinant
CC vector pTK11-Hv comprising DNA encoding these heavy and light chain
CC variable regions, as well as a transformant Escherichia coli. The present
CC invention describes an antibody variable region of a monoclonal antibody
CC that specifically binds to human tumor necrosis factor-alpha, and is
CC useful as a direct or indirect regulator for controlling inflammatory
CC cytokines in rheumatoid arthritis. Accordingly, the pharmaceutical
CC compositions derived thereof are TNF-alpha modulators that exhibit
CC antiarthritic and antirheumatic activities and as such can be used for
CC treating rheumatoid arthritis. This polypeptide sequence is the human TNF
CC -alpha light chain antibody protein given in an exemplification of the
CC invention.
XX
SQ Sequence 109 AA;
Query Match 76.8%; Score 43; DB 9; Length 109;
Best Local Similarity 66.7%; Pred. No. 10;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 HOYSKLPWT 9
    |||||
Db 90 HOYERSPWT 98

RESULT 36
ABP43158
ID ABP43158 standard; protein; 215 AA.
XX
XX AC ABP43158;
XX
```

DT 22-AUG-2002 (first entry)  
 XX Human ovarian antigen HVVIC185, SEQ ID NO:4290.  
 KW Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;  
 KW ovarian cancer; breast cancer; tumour; reproductive system disorder;  
 KW infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;  
 KW PCOS; ovarian cyst; dysmenorrhea; endocrine disorder; infection;  
 KW inflammatory condition; immune disorder; blood disorder;  
 KW cardiovascular disorder; respiratory disorder; neurological disorder;  
 KW gastrointestinal disorder; urinary system disorder; drug screening;  
 KW gene therapy; chromosome mapping; forensic analysis;  
 KW antibody preparation; cytostatic; immunomodulatory; neuroprotective;  
 KW antiinflammatory; gynaecological; reproductive.  
 XX Homo sapiens.  
 OS  
 XX WO200200677-A1.  
 PN  
 XX 03-JAN-2002.  
 PD  
 XX 07-JUN-2001; 2001WO-US018569.  
 PF  
 XX 07-JUN-2000; 2000US-0209467P.  
 PR  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 PA  
 XX Birse CE, Rosen CA;  
 PI WPI; 2002-147878/19.  
 DR N-PSDB; ABQ56235.  
 DR  
 XX Isolated nucleic acid molecules encoding novel ovarian polypeptides,  
 PT useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian  
 PT cancer), immune disorders, cardiovascular disorders and neurological  
 PT diseases.  
 PT  
 XX Claim 11; SEQ ID NO 4290; 2922pp; English.  
 PS  
 XX The invention relates to 2175 novel human ovarian antigens (ABP41054-  
 CC ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also  
 CC encompasses polypeptides 90% identical and polynucleotides 95% identical  
 CC to the sequences of the invention. The invention additionally relates to  
 CC recombinant vectors and host cells comprising human ovarian antigen  
 CC polynucleotides, antibodies against human ovarian antigens, and the use  
 CC of ovarian antigen polynucleotides and polypeptides in diagnosing,  
 CC treating, prognosing or preventing various ovary and/or breast-related  
 CC disorders. Such conditions include ovarian cancer and breast cancer, and  
 CC metastatic tumours of ovarian or breast origin, reproductive system  
 CC disorders (e.g., infertility, disorders of pregnancy, anovulation,  
 CC polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine  
 CC disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic  
 CC shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and  
 CC vaginitis), immune disorders (e.g. congenital and acquired  
 CC immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),  
 CC blood-related disorders (e.g., anaemia), cardiovascular disorders,  
 CC respiratory disorders, neurological disorders, gastrointestinal disorders  
 CC and urinary system disorders. Ovarian antigen polypeptides and  
 CC polynucleotides may also be used in screening for compounds which  
 CC modulate ovarian antigen expression or activity. The polynucleotides may  
 CC further be used for gene therapy, chromosome mapping, in the  
 CC identification of individuals and in forensic analysis, and the  
 CC polypeptides may be used as food additives or to prepare antibodies  
 CC useful in disease diagnosis, drug targeting and phenotyping. The present  
 CC sequence represents a human ovarian antigen of the invention. Note: The  
 CC sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 215 AA;  
 Query Match 76.8%; Score 43; DB 5; Length 215;  
 Best Local Similarity 100.0%; Pred. No. 21;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 YSKLPWT 9  
 DB 196 YSKLPWT 202  
 |||||  
 |||||  
 RESULT 37  
 ADO07305  
 ID ADO07305 standard; protein; 107 AA.  
 XX  
 AC ADO07305;  
 XX  
 DT 15-JUL-2004 (first entry)  
 XX  
 DE Human proteolytic A26-JK1 light chain, used in catalytic antibody.  
 XX  
 KW Catalytic antibody; human; antibody; protease; gene therapy.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Region 1..23  
 FT /label= FR1  
 FT /note= "Framework region 1"  
 FT  
 FT Active-site 1  
 FT /note= "Possible Glu component of catalytic triad"  
 FT Region 24..34  
 FT /label= CDR1  
 FT /note= "Complementarity determining region 1"  
 FT  
 FT Active-site 26  
 FT /note= "Possible Ser component of catalytic triad"  
 FT Active-site 28  
 FT /note= "Possible Ser component of catalytic triad"  
 FT Active-site 31  
 FT /note= "Possible Ser component of catalytic triad"  
 FT Active-site 32  
 FT /note= "Possible Ser component of catalytic triad"  
 FT Active-site 34  
 FT /note= "Possible His component of catalytic triad"  
 FT Region 35..49  
 FT /label= FR2  
 FT /note= "Framework region 2"  
 FT  
 FT Region 50..56  
 FT /label= CDR2  
 FT /note= "Complementarity determining region 2"  
 FT  
 FT Active-site 52  
 FT /note= "Possible Ser component of catalytic triad"  
 FT Active-site 54  
 FT /note= "Possible Ser component of catalytic triad"  
 FT Active-site 56  
 FT /note= "Possible Ser component of catalytic triad"  
 FT Region 57..88  
 FT /label= FR3  
 FT /note= "Framework region 3"  
 FT  
 FT Region 89..95  
 FT /label= CDR3  
 FT /note= "Complementarity determining region 3"  
 FT  
 FT Active-site 89  
 FT /note= "Possible His component of catalytic triad"  
 FT Active-site 91  
 FT /note= "Possible Ser component of catalytic triad"  
 FT Active-site 92  
 FT /note= "Possible Ser component of catalytic triad"  
 FT Active-site 93  
 FT /note= "Possible Ser component of catalytic triad"  
 XX  
 PN WO2004033658-A2.  
 XX  
 PD 22-APR-2004.  
 XX  
 XX 09-OCT-2003; 2003WO-US032214.  
 XX

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PR 10-OCT-2002; 2002US-0417979P.
XX (INTE-) INTEGRIGEN INC.
XX
XX Smider V, Larrick JW;
XX
XX WPI: 2004-340921/31.
XX N-PSDB; ADO07304.
XX
XX Novel recombinant catalytic polypeptide useful for cleaving target
XX proteins or for treating or preventing cancers, comprises a human
XX antibody light chain operably joined to a heterologous antibody heavy
XX chain.
XX
XX Claim 62; SEQ ID NO 24; 92pp; English.
XX
XX The present sequence is the protein sequence of a human light chain
XX variable region (VL), denoted A26-JK1, that is preferred for use in
XX recombinant catalytic polypeptides of the invention. VL genes encoding
XX potentially catalytic variable regions were cloned by PCR from human
XX genomic DNA following analysis of the human kappa repertoire for genes
XX containing putative serine protease triads. Several genes were
XX identified, including A26. Catalytic polypeptides of the invention
XX comprise a human antibody light chain operably joined to a heterologous
XX antibody heavy chain. The light chain has a serine protease dyad and
XX endopeptidase activity, and the heavy chain has a predetermined
XX specificity for a target protein. By joining 2 heterologous human
XX antibody chains, one of which supplies the catalytic activity to
XX hydrolyse polypeptides and the other the binding specificity for a target
XX protein, the invention provides for the construction of a repertoire of
XX proteases with customised protein substrate specificities of potentially
XX unlimited number and thus makes possible the effective treatment and/or
XX prevention of any medical condition attributable to the presence or
XX overexpression of an identified protein. The invention also provides
XX nucleic acids encoding the catalytic antibodies (which can be used for
XX gene therapy), host cells, transgenic non-human animals, and methods of
XX cleaving a target protein (in vitro or in vivo) using a recombinant
XX catalytic polypeptide. It also provides a library of recombinant
XX catalytic polypeptides with altered enzymatic activity, and a method of
XX altering the enzymatic activity of the recombinant catalytic polypeptides
XX by mutating at least one complementarity determining region of the heavy
XX chain.
XX
XX SQ Sequence 107 AA;
XX
XX Query Match 75.0%; Score 42; DB 8; Length 107;
XX Best Local Similarity 77.8%; Pred. No. 15;
XX Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 1 HQYSKLPWT 9
XX ||| |||||
XX Db 89 HQSSSLPWT 97
XX
XX RESULT 38
XX ADO07307
XX ID ADO07307 standard; protein; 107 AA.
XX AC ADO07307;
XX
XX DT 15-JUL-2004 (first entry)
XX
XX DE Human proteolytic A10-JK1 light chain, used in catalytic antibody.
XX
XX KW Catalytic antibody; human; antibody; protease; gene therapy.
XX
XX OS Homo sapiens.
XX
XX XH Key Location/Qualifiers
XX FH 1..23
XX FT Region /label= FR1
XX FT /note= "Framework region 1"
XX FT Active-site
XX

```

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FT Region
FT /note= "Possible Glu component of catalytic triad"
FT 24..34
FT /label= CDR1
FT /note= "Complementarity determining region 1"
FT 26
FT Active-site
FT /note= "Possible Ser component of catalytic triad"
FT 28
FT Active-site
FT /note= "Possible Ser component of catalytic triad"
FT 31
FT Active-site
FT /note= "Possible Ser component of catalytic triad"
FT 32
FT Active-site
FT /note= "Possible Ser component of catalytic triad"
FT 34
FT Active-site
FT /note= "Possible His component of catalytic triad"
FT 35..49
FT Region
FT /label= FR2
FT /note= "Framework region 2"
FT 50..56
FT Region
FT /label= CDR2
FT /note= "Complementarity determining region 2"
FT 52
FT Active-site
FT /note= "Possible Ser component of catalytic triad"
FT 54
FT Active-site
FT /note= "Possible Ser component of catalytic triad"
FT 56
FT Active-site
FT /note= "Possible Ser component of catalytic triad"
FT 57..88
FT Region
FT /label= FR3
FT /note= "Framework region 3"
FT 89..95
FT Region
FT /label= CDR3
FT /note= "Complementarity determining region 3"
FT 89
FT Active-site
FT /note= "Possible His component of catalytic triad"
FT 91
FT Active-site
FT /note= "Possible Ser component of catalytic triad"
FT 92
FT Active-site
FT /note= "Possible Ser component of catalytic triad"
FT 93
FT Active-site
FT /note= "Possible Ser component of catalytic triad"
XX WO2004033658-A2.
XX PN
XX 22-APR-2004.
XX PD
XX
XX 09-OCT-2003; 2003WO-US032214.
XX PF
XX
XX 10-OCT-2002; 2002US-0417979P.
XX PR
XX (INTE-) INTEGRIGEN INC.
XX PA
XX Smider V, Larrick JW;
XX PI
XX WPI: 2004-340921/31.
XX DR N-PSDB; ADO07306.
XX
XX Novel recombinant catalytic polypeptide useful for cleaving target
XX proteins or for treating or preventing cancers, comprises a human
XX antibody light chain operably joined to a heterologous antibody heavy
XX chain.
XX
XX Claim 62; SEQ ID NO 26; 92pp; English.
XX
XX The present sequence is the protein sequence of a human light chain
XX variable region (VL), denoted A10-JK1, that is preferred for use in
XX recombinant catalytic polypeptides of the invention. VL genes encoding
XX potentially catalytic variable regions were cloned by PCR from human
XX genomic DNA following analysis of the human kappa repertoire for genes
XX containing putative serine protease triads. Several genes were
XX identified, including A10. Catalytic polypeptides of the invention
XX comprise a human antibody light chain operably joined to a heterologous
XX antibody heavy chain. The light chain has a serine protease dyad and
XX endopeptidase activity, and the heavy chain has a predetermined

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PI Cattaneo A, Covaceuszach S, Lamba D;
XX WPI; 2005-479446/48.
DR N-PSDB; AEB12543.
XX
PT Humanizing VH and VL variable regions of an animal antibody of known
PT sequence comprises pre-selecting a series of 0 to n possible frameworks
PT acceptors of human origin or humanized antibodies.
XX
XX Disclosure; SEQ ID NO 24; 69pp; English.
XX
PS The invention describes a method of humanizing VH and VL variable regions
CC of an animal antibody of known sequence. The method comprises: if not
CC available, obtaining the crystallographic structure of the VH and VL
CC regions of the animal antibody; pre-selecting a series of 0 to n possible
CC frameworks acceptors of human origin or humanized antibodies, whose
CC structure was determined experimentally with a resolution of no less than
CC 3 angstroms, based on the highest level of homology and identity with the
CC primary sequence of the framework of the animal antibody; conducting a
CC structural comparison between the VH and VL variable regions of the
CC animal antibody and the regions VH and VL obtained, respectively and
CC calculating for each comparison the RMS, to identify the region VH and
CC the region VL of human origin with the smaller RMS; inserting in
CC appropriate position the sequences of the regions CDR of the animal
CC antibody in the human sequences identified; and if necessary, retromutate
CC one or more amino acid residues of the human VH and VL regions. Also
CC described are: a humanized animal antibody obtained by the method; an
CC anti-NGF humanized animal antibody obtainable by the method; and anti-
CC TrkA humanized antibody obtainable by the method. The method is useful
CC for humanizing VH and VL variable regions of an animal antibody of known
CC sequence. This is the amino acid sequence of the light chain variable
CC region from the murine form of antibody MNAC13.
XX
SQ Sequence 106 AA;

Query Match 73.2%; Score 41; DB 9; Length 106;
Best Local Similarity 66.7%; Pred. No. 23;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HOYSKLPWT 9
Db ||:| |||
88 HQWSSYPWT 96

RESULT 41
AEB12558
ID AEB12558 standard; protein; 106 AA.
XX
AC AEB12558;
XX
DT 08-SEP-2005 (first entry)
XX
DE Humanized MNAC13 antibody light chain variable region SEQ ID NO 38.
XX
KW antibody engineering; X-ray crystallography; antibody therapy;
KW diagnostic; MNAC13; light chain variable region.
XX
OS Synthetic.
XX
PN WO2005061540-A2.
XX
PD 07-JUL-2005.
XX
PF 23-DEC-2004; 2004WO-IT000722.
XX
PR 24-DEC-2003; 2003IT-RM000601.
XX
PA (LAYL-) LAY LINE GENOMICS SPA.
XX (SCUO-) SCUOLA INT SUPERIORE DI STUDI AVANZATI.
XX Cattaneo A, Covaceuszach S, Lamba D;
XX WPI; 2005-479446/48.
DR

Query Match 73.2%; Score 41; DB 9; Length 106;
Best Local Similarity 66.7%; Pred. No. 23;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HOYSKLPWT 9
Db ||:| |||
88 HQWSSYPWT 96

RESULT 42
AEA89805
ID AEA89805 standard; protein; 108 AA.
XX
AC AEA89805;
XX
DT 25-AUG-2005 (first entry)
XX
DE Antibody activity-related mouse TAL36 protein region SeqID28.
XX
KW antibody engineering; cytostatic; apoptosis stimulation; cancer;
KW therapeutic.
XX
OS Mus musculus.
XX
PN WO2005056798-A1.
XX
PD 23-JUN-2005.
XX
PF 10-DEC-2004; 2004WO-JP018493.
XX
PR 12-DEC-2003; 2003JP-00415760.
XX
PA (CHUS ) CHUGAI SEIYAKU KK.
XX
PI Ohtomo T, Yabuta N, Tsumoda H, Tsuchiya M;
XX WPI; 2005-479085/48.
XX
PT Reinforcing activity of antibody e.g. antihuman Mpl antibody by coupling
PT heavy chain variable domains to light chain variable domains by linker,
PT to produce single chain polypeptide.
XX

```



PS Example 2; SEQ ID NO 28; 44pp; Japanese.

CC This invention relates to a novel method of reinforcing activity of an antibody, for example antihuman Mpl antibody. The method comprises coupling 2 or more heavy chain variable domains to 2 or more light chain variable domains by a linker to produce a single chain polypeptide, or coupling a first polypeptide having a heavy chain and light chain variable domain of an antibody and a second polypeptide having a heavy chain and light chain variable domain of an antibody by a linker. The invention may be useful for the development of compounds with a cytostatic activity acting as a stimulator of apoptosis. The method is useful for reinforcing activity of an antibody which may be useful for treating cancer. The method enables an increase in the agonistic activity of the antibody, which is highly stable. The present sequence is that of a region of a mouse protein which was used in the exemplification of the invention.

XX SQ Sequence 108 AA;

Query Match 73.2%; Score 41; DB 9; Length 108;  
 Best Local Similarity 66.7%; Pred. No. 23;  
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HOYSKLPWT 9  
 ||:| |||  
 Db 90 HQWSSYPWT 98

RESULT 43  
 AEA44098  
 ID AEA44098 standard; protein; 108 AA.  
 AC AEA44098;  
 XX  
 DT 25-AUG-2005 (first entry)  
 XX  
 DE Anti-TPO antibody associated variable light chain SEQ ID NO 163.  
 XX  
 KW hemostatic; single chain antibody; protein purification;  
 KW antibody engineering; antibody production; thrombocytopenia; hemostatic;  
 KW hematological disease; light chain variable region.  
 XX  
 OS Unidentified.  
 XX  
 PN WO2005056604-A1.  
 XX  
 PD 23-JUN-2005.  
 XX  
 PF 10-DEC-2004; 2004WO-JP018506.  
 XX  
 PR 12-DEC-2003; 2003JP-00415746.  
 PR 12-MAR-2004; 2004JP-00071763.  
 PR 27-AUG-2004; 2004JP-00248323.  
 XX  
 PA (CHUS ) CHUGAI SEIYAKU KK.  
 XX  
 PI Tsunoda H, Nakano K, Orita T, Tsuchiya M, Hirata Y;  
 XX  
 WIPI; 2005-445149/45.  
 XX  
 PT Anti-Mpl antibodies including antihuman Mpl antibody and variants like genetically-engineered antihuman Mpl diabody, applicable in drug compositions for use in chemotherapy of thrombocytopenia and other diseases associated with Mpl mutation.  
 PT  
 PT  
 PS Claim 22; SEQ ID NO 163; 106pp; Japanese.

CC The invention describes an antibody is a single-chain polypeptide with TPO (thrombopoietin) receptor (Mpl)-binding activity that contains the 2 heavy-chain variable regions and 2 light-chain variable regions. Also described are: a chimeric antibody for binding with Mpl; an antibody for binding with soluble Mpl; antibodies for binding with human Mpl and monkey Mpl; antibodies with agonistic activity against human Mpl and

CC monkey Mpl; antibodies with binding activity for soluble Mpl; antibodies with TPO agonistic activity; antibodies containing a heavy-chain variable region with CDR (complementary-determinant regions 1, 2 and 3); antibodies containing a light-chain variable region with CDR 1, 2 and 3; antibodies containing heavy and light-chain variable regions with CDR 1, 2 and 3 selected from the already-specified groups in 18 combinations; antibodies containing a heavy-chain variable region with FR1, 2, 3 and 4; antibodies containing a light-chain variable region FR1, 2, 3 and 4; epitope-recognizing antibodies that can recognize the antibodies with the heavy and light-chain variable regions and amino acid sequences; antibodies that can recognize the amino acid moiety in human Mpl from positions 26-274; polynucleotides encoding these antibodies; polynucleotides hybridizable with the polynucleotides that encode the antibodies under stringent conditions and the antibodies containing by which have equivalent activity as such antibodies; vectors containing these polynucleotides; host cells carrying such polynucleotides or vectors; and drug compositions containing these antibodies. The antibodies are applicable in drug compositions for use in chemotherapy of thrombocytopenia and other diseases associated with Mpl mutation such as congenital amegakaryocytic thrombocytopenia. These antibodies can include antihuman Mpl antibody and variants like genetically-engineered antihuman Mpl diabody and (humanized) antihuman Mpl sc(Fv)2. Such antibodies are soluble to enhance binding ability. The diabody and sc(Fv)2 show high agonistic activity against antihuman Mpl antibody, such activity of which is comparable or superior to that of the natural ligand, human TPO. This sequence represents an anti-TPO antibody light chain variable region.

XX SQ Sequence 108 AA;

Query Match 73.2%; Score 41; DB 9; Length 108;  
 Best Local Similarity 66.7%; Pred. No. 23;  
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HOYSKLPWT 9  
 ||:| |||  
 Db 90 HQWSSYPWT 98

RESULT 44  
 AAB48936  
 ID AAB48936 standard; protein; 113 AA.  
 XX  
 AC AAB48936;  
 XX  
 DT 16-MAR-2001 (first entry)  
 XX  
 DE Anti-TrkA murine monoclonal antibody MNAC13 light chain variable region.  
 XX  
 KW Murine monoclonal antibody MNAC13; light chain variable region; VL;  
 KW human TrkA antagonist; NGF receptor; nerve growth factor;  
 KW neurological pathology; acute pain; chronic pain; analgesic; neuroma;  
 KW cancer; TrkA-expressing tumour; gene therapy; in vivo imaging; diagnosis.  
 XX  
 OS Mus sp.  
 XX  
 PN WO200073344-A2.  
 XX  
 PD 07-DEC-2000.  
 XX  
 PF 26-MAY-2000; 2000WO-IT000218.  
 XX  
 PR 26-MAY-1999; 99IT-RM0000333.  
 XX  
 PA (SIRS-) SIRS SOC ITAL RICERCA SCI SRL.  
 XX  
 PI Novak MM;  
 XX  
 DR WIPI; 2001-061515/07.  
 DR N-PSDB; AAC87642.  
 XX  
 PT Monoclonal antibody and its derivatives specific to high affinity tyrosine kinase receptor of nerve growth factor useful for treating and diagnosing neuropathological disorders such as pain, neuromas, TrkA

PT expressing neoplastic tumors.

XX Claim 2; Page; 33pp; English.

XX The invention relates to a murine monoclonal antibody, MNAC13, which

CC recognises the human nerve growth factor (NGF) receptor tyrosine kinase,

CC TrkA, and acts as an antagonist of NGF/TrkA binding. MNAC13 has a light

CC chain variable region (VL) as given in AAB48936, and a heavy chain

CC variable region (VH) as given in AAB48937. The invention also encompasses

CC synthetic derivatives of monoclonal antibody MNAC13, such as the single

CC chain antibody, scFvMNAC13 (AAB48934), which comprises the VL and VH

CC regions of MNAC13 in one polypeptide chain. The invention additionally

CC relates to pharmaceutical compositions comprising the antibody or

CC antibody derivatives of the invention, engineered eukaryotic cells able

CC to express the MNAC13 antibody or its derivatives, and a diagnostic

CC composition comprising the antibody or its derivatives for in vivo

CC imaging. NGF antagonist (inhibitor of binding of NGF to TrkA receptor The

CC MNAC13 monoclonal antibody and its derivatives are useful for treating

CC neurological pathologies such as acute or chronic pain, neuromas, and

CC TrkA-expressing neoplastic tumours. A composition comprising MNAC13 or

CC its derivatives with a diagnostically acceptable carrier is useful for in

CC vivo imaging diagnostics. The present sequence represents the light chain

CC variable region of the anti-TrkA murine monoclonal antibody MNAC13. Note:

CC The present sequence is derived from that of the single chain antibody

CC scFvMNAC13 shown on pages 32-33 and the information given in claim 2

XX

SQ Sequence 113 AA;

Query Match 73.2%; Score 41; DB 4; Length 113;

Best Local Similarity 66.7%; Pred. No. 24;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HQYSKLPWT 9

DB 89 HQWSSYPWT 97

RESULT 45

ADSI4282

ID ADS14282 standard; protein; 255 AA.

XX

AC ADS14282;

XX

DT 16-DEC-2004 (first entry)

XX

DE Murine protein relating to the invention SEQ ID NO:8.

XX

KW variant receptor; antidiabetic; haemostatic; endocrine; thrombocytopenia;

KW type II diabetes; laron syndrome; thrombopoietin.

XX

OS Mus musculus.

XX

PN WO2004081048-A1.

XX

PD 23-SEP-2004.

XX

PF 12-MAR-2004; 2004WO-JP003334.

XX

PR 13-MAR-2003; 2003JP-00067832.

XX

PA (CHUS) CHUGAI SEIYAKU KK.

XX

PI Tsuchiya M, Hirata Y;

XX

DR WPI; 2004-677525/66.

XX

DR N-PSDB; ADS14281.

XX

XX Novel ligand having agonist activity with respect to variant receptor

PT e.g., variant thrombopoietin receptor, useful for treating disease

PT resulting due to variant receptor such as congenital non-megakaryocyte

PT thrombocytopenia.

XX

PS Example 4; SEQ ID NO 8; 132pp; Japanese.

XX The invention relates to a novel ligand (preferably an antibody) (1)

CC having agonist activity with respect to a variant receptor. A ligand of

CC the invention has antidiabetic, haemostatic, and endocrine-gen. activity.

CC The ligand is useful for treating the disease caused due to variant

CC receptor, which involves combining the ligand/antibody with the variant

CC receptor, where the disease is congenital non-megakaryocyte

CC thrombocytopenia. A ligand of the invention is useful for transmitting a

CC signal to a variant receptor, which involves combining the variant

CC receptor with the ligand. The invention is useful for treating diseases

CC resulting due to variation receptor, such as type II diabetes and laron

CC syndrome. The ligand enables signal transduction function of

CC thrombopoietin, with respect to variant receptor. The present sequence is

CC used in the exemplification of the invention.

XX

SQ Sequence 255 AA;

Query Match 73.2%; Score 41; DB 8; Length 255;

Best Local Similarity 66.7%; Pred. No. 55;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HQYSKLPWT 9

DB 229 HQWSSYPWT 237

RESULT 46

AAB48934

ID AAB48934 standard; protein; 295 AA.

XX

AC AAB48934;

XX

DT 16-MAR-2001 (first entry)

XX

DE Anti-TrkA single chain antibody scFvMNAC13.

XX

KW Single chain antibody; murine monoclonal antibody MNAC13; scFvMNAC13;

KW human TrkA antagonist; NGF receptor; nerve growth factor;

KW neurological pathology; acute pain; chronic pain; analgesic; neuroma;

KW cancer; TrkA-expressing tumour; gene therapy; in vivo imaging; diagnosis.

XX

OS Mus sp.

OS Synthetic.

XX

PN WO2000073344-A2.

XX

PD 07-DEC-2000.

XX

PF 26-MAY-2000; 2000WO-IT000218.

XX

PR 26-MAY-1999; 99IT-RM000333.

XX

PA (SIRS-) SIRS SOC ITAL RICERCA SCI SRL.

XX

PI Novak MM;

XX

DR WPI; 2001-061515/07.

XX

DR N-PSDB; AAC87642.

XX

PT Monoclonal antibody and its derivatives specific to high affinity

PT tyrosine kinase receptor of nerve growth factor useful for treating and

PT diagnosing neuropathological disorders such as pain, neuromas, TrkA

PT expressing neoplastic tumors.

XX

PS Claim 8; Page 32-33; 33pp; English.

XX

CC The invention relates to a murine monoclonal antibody, MNAC13, which

CC recognises the human nerve growth factor (NGF) receptor tyrosine kinase,

CC TrkA, and acts as an antagonist of NGF/TrkA binding. MNAC13 has a light

CC chain variable region (VL) as given in AAB48936, and a heavy chain

CC variable region (VH) as given in AAB48937. The invention also encompasses

CC synthetic derivatives of monoclonal antibody MNAC13, such as the single

CC chain antibody, scFvMNAC13 (AAB48934), which comprises the VL and VH

CC regions of MNAC13 in one polypeptide chain. The invention additionally  
 CC relates to pharmaceutical compositions comprising the antibody or  
 CC antibody derivatives of the invention, engineered eukaryotic cells able  
 CC to express the MNAC13 antibody or its derivatives, and a diagnostic  
 CC composition comprising the antibody or its derivatives for in vivo  
 CC imaging. NGF antagonist (inhibitor of binding of NGF to TrkA receptor The  
 CC MNAC13 monoclonal antibody and its derivatives are useful for treating  
 CC neurological pathologies such as acute or chronic pain, neuromas, and  
 CC TrkA-expressing neoplastic tumours. A composition comprising MNAC13 or  
 CC its derivatives with a diagnostically acceptable carrier is useful for in  
 CC vivo imaging diagnostics. The present sequence represents the anti-TrkA  
 CC single chain antibody scFvMNAC13

XX Sequence 295 AA;

Query Match 73.2%; Score 41; DB 4; Length 295;  
 Best Local Similarity 66.7%; Pred. NO. 64;  
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HQYSKLPWT 9  
 ||:| |||  
 Db 110 HQWSSYPWT 118

RESULT 47

ADSL14288  
 ID ADS14288 standard; protein; 519 AA.

XX AC ADS14288;

XX DT 16-DEC-2004 (first entry)

XX DE Murine protein relating to the invention SEQ ID NO:14.

XX KW variant receptor; antidiabetic; haemostatic; endocrine; thrombocytopenia;  
 XX type II diabetes; laron syndrome; thrombopoietin.

XX OS Mus musculus.

XX PN WO2004081048-A1.

XX PD 23-SEP-2004.

XX PF 12-MAR-2004; 2004WO-JP003334.

XX PR 13-MAR-2003; 2003JP-00067832.

XX PA (CHUS ) CHUGAI SEIYAKU KK.

XX PI Tsuchiya M, Hirata Y;

XX DR WPI; 2004-677525/66.

XX DR N-PSDB; ADS14287.

XX PT Novel ligand having agonist activity with respect to variant receptor  
 PT e.g., variant thrombopoietin receptor, useful for treating disease  
 PT resulting due to variant receptor such as congenital non-megakaryocyte  
 PT thrombocytopenia.

XX PS Disclosure; SEQ ID NO 14; 132pp; Japanese.

XX CC The invention relates to a novel ligand (preferably an antibody) (I)  
 CC having agonist activity with respect to a variant receptor. A ligand of  
 CC the invention has antidiabetic, haemostatic and endocrine-gen. activity.  
 CC The ligand is useful for treating the disease caused due to variant  
 CC receptor, which involves combining the ligand/antibody with the variant  
 CC receptor, where the disease is congenital non-megakaryocyte  
 CC thrombocytopenia. A ligand of the invention is useful for transmitting a  
 CC signal to a variant receptor, which involves combining the variant  
 CC receptor with the ligand. The invention is useful for treating diseases  
 CC resulting due to variation receptor, such as type II diabetes and laron  
 CC syndrome. The ligand enables signal transduction function of  
 CC thrombopoietin, with respect to variant receptor. The present sequence is

CC used in the exemplification of the invention.

SQ Sequence 519 AA;

Query Match 73.2%; Score 41; DB 8; Length 519;  
 Best Local Similarity 66.7%; Pred. NO. 1.1e+02;  
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HQYSKLPWT 9

||:| |||  
 Db 239 HQWSSYPWT 247

RESULT 48

ADR69579  
 ID ADR69579 standard; peptide; 8 AA.

XX AC ADR69579;

XX DT 18-NOV-2004 (first entry)

XX DE Novel hybrid antigen-related peptide SeqID1159.

XX KW hybrid antigen; antigenic domain; infectious agent; tumour antigen;  
 KW binding domain; heat shock protein; antimicrobial; cytostatic; vaccine;  
 KW gene therapy; infectious disease; cancer.

XX OS Unidentified.

XX PN WO2004071457-A2.

XX PD 26-AUG-2004.

XX PF 13-FEB-2004; 2004WO-US004340.

XX PR 13-FEB-2003; 2003US-0447142P.

XX PR 11-APR-2003; 2003US-0462469P.

XX PR 18-APR-2003; 2003US-0463746P.

XX PR 16-SEP-2003; 2003US-0503417P.

XX PR 12-FEB-2004; 2004US-00776521.

XX PA (MOJA-) MOJAVE THERAPEUTICS INC.

XX PI Fletchner J, Prince-Cohane K, Mehta S, Slusarewicz P, Andjelic S;  
 PI Barber B;

XX DR WPI; 2004-625768/60.

XX PT New hybrid antigens comprising an antigenic domain and improved heat  
 PT shock protein-binding domains, useful for preventing or treating  
 PT infectious diseases or cancer.

XX PS Disclosure; SEQ ID NO 1159; 56pp; English.

XX CC This invention relates to a novel hybrid antigen which comprises at least  
 CC one antigenic domain of an infectious agent or tumour antigen and a  
 CC binding domain that non-covalently binds to a heat shock protein. The  
 CC invention may be useful for the production of compounds with an  
 CC antimicrobial or cytostatic activity. In addition, the invention may  
 CC prove useful for the production of a vaccine or for gene therapy. The  
 CC composition and methods disclosed are useful for preventing or treating  
 CC infectious diseases or cancer. The present sequence is that of a heat  
 CC shock protein binding domain peptide which was used in the  
 CC exemplification of the invention.

SQ Sequence 8 AA;

Query Match 71.4%; Score 40; DB 8; Length 8;  
 Best Local Similarity 62.5%; Pred. NO. 2e+06;  
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 HQYSKLPW 8

||:| |||

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Db          1 HSYNRLPW 8

RESULT 49
ADU08271
ID ADU08271 standard; peptide; 8 AA.
XX
XX
AC ADU08271;
XX
XX
DT 13-JAN-2005 (first entry)
XX
XX Heat shock protein binding domain #21.
XX
XX Hybrid antigen; antigenic domain; infectious agent; tumour antigen;
KW binding domain; heat shock protein; hep; immune response;
KW infectious disease; cancer; cytostatic; antimicrobial; immunostimulant.
XX
XX Unidentified.
XX
XX WO2004091493-A2.
XX
XX 28-OCT-2004.
XX
XX 09-APR-2004; 2004WO-US010983.
XX
XX 11-APR-2003; 2003US-0462469P.
XX 18-APR-2003; 2003US-0463746P.
XX 16-SEP-2003; 2003US-0503417P.
XX 12-FEB-2004; 2004US-00776521.
XX 13-FEB-2004; 2004WO-US004340.
XX 08-APR-2004; 2004US-00820067.
XX
XX (MOJA-) MOJAVE THERAPEUTICS INC.
XX
XX Flechtner JB, Prince-Cohane K, Mehta S, Slusaregicz P, Andjelic S;
XX Barber BH;
XX
XX WPI; 2004-775516/76.
XX
XX Hybrid antigen useful for treating an infectious disease or cancer,
XX comprises an antigenic domain from the infectious agent or cancer joined
XX to a heat shock protein binding domain through an improved linker
XX peptide.
XX
XX Disclosure; SEQ ID NO 1159; 99pp; English.
XX
XX The invention relates to hybrid antigens comprising at least one
XX antigenic domain of an infectious agent or tumour antigen, at least one
XX binding domain that non-covalently binds to a heat shock protein (hep),
XX and at least one peptide linker between them. Also disclosed are: (a) a
XX composition for inducing an immune response to an infectious agent or
XX tumour antigen comprising at least one of the hybrid antigens or a
XX complex of at least one heat shock protein and at least one of the hybrid
XX antigens, (b) a method for inducing an immune response to an infectious
XX agent or tumour antigen by administering a hybrid antigen and a heat
XX shock protein, where the hybrid antigen and the heat shock protein are
XX non-covalently bound, and (c) treating an infectious disease or cancer by
XX administering a hybrid antigen and a heat shock protein. The heat shock
XX protein is preferably hep70. The composition is administered via oral or
XX parenteral route. The hybrid antigen is useful in preparing a composition
XX for treating or preventing cancer or infectious disease. The new peptide
XX linkers give the antigens improved activity. Note: Many of the SEQ ID Nos
XX are replicated more than once in the specification but the sequences of
XX these replicated SEQ ID Nos are not the same. This sequence represents a
XX heat shock protein binding sequence.
XX
XX Sequence 8A;
XX
XX Query Match 71.4%; Score 40; DB 8; Length 8;
XX Best Local Similarity 62.5%; Pred. NO. 2e+06;
XX Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
XX
XX 1 HQYSKLPW 8

Query Match 71.4%; Score 40; DB 3; Length 9;
Best Local Similarity 75.0%; Pred. NO. 2e+06;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYSKLPWT 9
Db 2 QYSVFWT 9
Search completed: April 6, 2006, 09:03:57
Job time : 84.8136 secs
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GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: April 6, 2006, 08:56:41 ; Search time 9 Seconds  
(without alignments)  
96.217 Million cell updates/sec

Title: US-10-089-500-8

Perfect score: 56

Sequence: 1 HQYSLPWT 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : PIR 80:\*

1: Pirl:\*

2: Pirl:\*

3: Pirl:\*

4: Pirl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	48	85.7	111	2	G38740
2	48	85.7	111	2	E38740
3	45	80.4	111	2	A38740
4	45	80.4	111	2	C38740
5	42	75.0	128	2	A47159
6	42	75.0	141	2	A49134
7	39	69.6	108	1	KLHUME
8	39	69.6	258	2	AF2204
9	38	67.9	288	2	T36237
10	38	67.9	363	2	T39701
11	38	67.9	581	2	C39768
12	38	67.9	602	1	ACHU
13	38	67.9	603	2	S70849
14	38	67.9	1289	1	RMKRR3
15	37	66.1	108	1	KLHUAU
16	37	66.1	134	1	K4HU17
17	37	66.1	136	2	A49137
18	37	66.1	190	2	T31291
19	37	66.1	402	2	S47329
20	37	66.1	585	2	T47364
21	37	66.1	821	2	H71475
22	37	66.1	823	2	C81739
23	37	66.1	1582	2	A56248
24	36	64.3	103	2	S18731
25	36	64.3	111	1	KVMS13
26	36	64.3	518	2	D96681
27	36	64.3	588	2	T26193
28	35	62.5	106	2	S20262
29	35	62.5	109	2	S26336

30	35	62.5	125	2	S40333	Ig kappa chain V-J
31	35	62.5	140	2	H69405	hypothetical prote
32	35	62.5	296	2	B87293	hydrolase, probabl
33	35	62.5	312	2	T27004	hypothetical prote
34	35	62.5	318	2	B83527	hypothetical prote
35	35	62.5	376	2	T46096	hypothetical prote
36	35	62.5	413	2	T18945	hypothetical prote
37	35	62.5	431	2	A89761	hypothetical prote
38	35	62.5	440	2	T41138	hypothetical prote
39	35	62.5	492	2	T18221	chromosome condensa
40	35	62.5	535	2	JCS762	cytokine-inducible
41	35	62.5	549	2	B83149	probable acyl-CoA
42	35	62.5	574	2	B29677	complement C9 prec
43	35	62.5	609	2	AE2062	gamma-glutamyltran
44	35	62.5	788	1	JDLVHH	DNA-directed DNA p
45	35	62.5	1102	2	S28104	probable DNA-direc
46	34.5	61.6	641	2	JC7331	gamma-glutamyltran
47	34	60.7	64	2	G82775	hypothetical prote
48	34	60.7	64	2	AE2772	hypothetical prote
49	34	60.7	88	2	PL0261	Ig kappa chain V r
50	34	60.7	91	2	S17628	Ig kappa chain V r
51	34	60.7	106	2	PL0260	Ig kappa chain V r
52	34	60.7	107	2	B48677	Ig kappa chain V-J
53	34	60.7	107	2	B49026	Ig kappa chain V r
54	34	60.7	107	2	G72868	Acortf-149 protein
55	34	60.7	108	1	KVMS73	Ig kappa chain V r
56	34	60.7	130	1	KVMSM4	Ig kappa chain pre
57	34	60.7	142	2	S28757	cytochrome-c oxida
58	34	60.7	173	2	S58632	hypothetical prote
59	34	60.7	215	2	JF0242	Ig kappa chain NIG
60	34	60.7	249	2	JQ0274	hypothetical 29K p
61	34	60.7	316	2	AF0457	pantothenate kinas
62	34	60.7	346	2	T41973	glycoprotein M - h
63	34	60.7	378	2	D83381	hypothetical prote
64	34	60.7	429	2	T34466	hypothetical prote
65	34	60.7	431	2	T04956	hypothetical prote
66	34	60.7	471	2	T18944	hypothetical prote
67	34	60.7	473	2	H69761	conserved hypothet
68	34	60.7	525	2	F96674	FlG16.8 (imported
69	34	60.7	547	2	S64332	probable membrane
70	34	60.7	568	2	S58286	gamma-glutamyltran
71	34	60.7	574	2	T05002	probable gamma-glu
72	34	60.7	577	2	T05001	probable gamma-glu
73	34	60.7	632	2	T32454	hypothetical prote
74	34	60.7	729	2	S76065	hypothetical prote
75	34	60.7	930	2	E96600	protein F14J16.20
76	33.5	59.8	578	2	D87371	gamma-glutamyltran
77	33	58.9	77	2	G95393	protein (imported
78	33	58.9	90	2	A02020	hypothetical prote
79	33	58.9	97	2	PH1085	Ig light chain V r
80	33	58.9	106	2	PL0259	Ig kappa chain V r
81	33	58.9	106	2	T41886	ACHNPV orf149 - Bo
82	33	58.9	108	2	C30608	Ig kappa chain V-I
83	33	58.9	118	2	T03036	Ig light chain - h
84	33	58.9	128	2	S40379	Ig kappa chain V-J
85	33	58.9	129	1	K3HUI1	Ig kappa chain pre
86	33	58.9	149	2	A11824	hypothetical prote
87	33	58.9	159	2	T28751	hypothetical prote
88	33	58.9	176	2	JH0607	trypsin inhibitor
89	33	58.9	212	2	T46600	nitrogen metabolic
90	33	58.9	289	2	AH1846	sulfate transport
91	33	58.9	315	2	T23824	hypothetical prote
92	33	58.9	334	2	A83342	conserved hypothet
93	33	58.9	341	2	S63666	platelet activatin
94	33	58.9	341	2	S43252	platelet-activatin
95	33	58.9	342	2	A40191	platelet-activatin
96	33	58.9	342	2	S13638	Vgl embryonic grow
97	33	58.9	360	2	A29619	squamosa promoter
98	33	58.9	373	2	T52593	hypothetical prote
99	33	58.9	375	2	T00929	protein kinase SMK
100	33	58.9	379	2	S46711	
101	33	58.9	388	2	S48879	
102	33	58.9	388	2	S48879	

103	33	58.9	392	1	FOLJGA	gag polyprotein -	176	32	57.1	557	2	D83478	gamma-glutamyltran
104	33	58.9	392	1	FOLJGB	gag polyprotein -	177	32	57.1	560	2	A82220	hypothetical prote
105	33	58.9	393	2	S29356	gag protein - bovi	178	32	57.1	578	2	T02232	hypothetical prote
106	33	58.9	411	2	A12939	conserved hypotet	179	32	57.1	586	2	T49441	gamma-glutamyltran
107	33	58.9	411	2	F98342	hypothetical prote	180	32	57.1	587	2	E96702	unknown protein, 6
108	33	58.9	422	2	G90259	hypothetical prote	181	32	57.1	591	2	F70871	probable membrane
109	33	58.9	422	2	H90275	hypothetical prote	182	32	57.1	593	2	S72769	B1496 Fl 14 protei
110	33	58.9	435	1	EFUC1A	translation elonga	183	32	57.1	613	2	T52465	hypothetical prote
111	33	58.9	460	2	F84764	hypothetical prote	184	32	57.1	614	2	S68236	betaine/GABA trans
112	33	58.9	481	2	T37505	hypothetical prote	185	32	57.1	614	2	A41757	betaine transport
113	33	58.9	488	1	S11910	nitrogen metabolic	186	32	57.1	637	2	T13432	gamma-glutamyltran
114	33	58.9	533	2	F70551	hypothetical prote	187	32	57.1	707	2	E84973	polyribonucleotide
115	33	58.9	536	2	A34596	transcription fact	188	32	57.1	721	2	D82934	ATP-dependent zinc
116	33	58.9	553	2	T03858	hypothetical prote	189	32	57.1	732	2	T25937	hypothetical prote
117	33	58.9	559	2	D95055	PTS system, lactos	190	32	57.1	788	2	T26967	hypothetical prote
118	33	58.9	608	2	T29778	hypothetical prote	191	32	57.1	797	2	AB3410	organic solvent to
119	33	58.9	779	2	AG1978	hypothetical prote	192	32	57.1	900	2	G96617	probable disease r
120	33	58.9	781	2	AF2516	adenylate cyclase	193	32	57.1	907	2	F96617	probable disease r
121	33	58.9	877	2	C64809	ybgB protein - Eac	194	32	57.1	1053	2	I55534	VLA-3 alpha subuni
122	33	58.9	1073	2	B36429	integrin alpha-6 c	195	32	57.1	1056	2	C96661	kinesin-like prote
123	33	58.9	1091	2	A41543	integrin alpha-6 c	196	32	57.1	1095	2	AD0301	conserved hypotet
124	33	58.9	1104	2	JH0181	nitrite reductase	197	32	57.1	1098	2	S36868	alpha, alpha-trehal
125	33	58.9	1135	1	JO1928	G2-G1 polyprotein	198	32	57.1	1249	2	T14150	vesicle associated
126	33	58.9	3147	2	T21328	hypothetical prote	199	32	57.1	1471	2	T40117	myosin-2 isoform -
127	32.5	58.0	583	2	G87261	gamma-glutamyltran	200	32	57.1	1579	2	S25329	carboxypeptidase Y
128	32.5	58.0	910	2	A32560	outer membrane pro	201	31	55.4	66	2	S67984	muscarinic toxin a
129	32.5	58.0	911	2	A47675	68K outer membrane	202	31	55.4	82	2	G89446	hypothetical prote
130	32.5	58.0	922	2	S15204	pertactin - Bordet	203	31	55.4	91	2	S37515	ig kappa chain v r
131	32	57.1	89	2	S17471	hypothetical prote	204	31	55.4	100	2	S29590	ig kappa chain v r
132	32	57.1	92	2	S37533	ig kappa chain v r	205	31	55.4	106	2	C97329	probable transcript
133	32	57.1	98	2	S19974	ig kappa chain v r	206	31	55.4	108	1	K1HUKU	ig kappa chain v-i
134	32	57.1	98	2	PH1061	ig light chain v r	207	31	55.4	115	2	S19350	probable membrane
135	32	57.1	107	2	PL0270	ig kappa chain v r	208	31	55.4	122	2	G95904	hypothetical prote
136	32	57.1	107	2	PL0272	ig kappa chain v r	209	31	55.4	127	2	S04574	ig kappa chain pre
137	32	57.1	107	2	PL0271	ig kappa chain v r	210	31	55.4	136	2	T49673	hypothetical prote
138	32	57.1	107	2	PL0269	ig kappa chain v r	211	31	55.4	157	2	E72468	hypothetical prote
139	32	57.1	133	2	A54379	beta 1.4 N-acetyl	212	31	55.4	174	2	T02276	hypothetical prote
140	32	57.1	134	2	T04045	hypothetical prote	213	31	55.4	201	2	JQ0949	proteinase inhibit
141	32	57.1	143	1	KEMS	hypothetical prote	214	31	55.4	213	2	S07999	probable membrane
142	32	57.1	162	1	RFNWA	epsilon-casein pre	215	31	55.4	215	2	H85580	hypothetical prote
143	32	57.1	162	1	B41841	phycoerythrocyanin	216	31	55.4	241	2	F64865	murein hydrolase E
144	32	57.1	162	2	AC1872	phycoerythrocyanin	217	31	55.4	241	2	H90839	murein transglycos
145	32	57.1	188	2	JC1065	coat protein - bee	218	31	55.4	241	2	H85697	murein transglycos
146	32	57.1	192	2	A10688	probable bacteriop	219	31	55.4	245	2	I51323	proteolipid protei
147	32	57.1	203	2	T23943	hypothetical prote	220	31	55.4	254	2	H89772	hypothetical prote
148	32	57.1	216	2	AH0685	probable lipoprote	221	31	55.4	261	1	QBBLP	recombination prot
149	32	57.1	223	1	KASHS2	alpha-s2-casein pr	222	31	55.4	261	2	A10617	bacteriophage reco
150	32	57.1	223	2	I46995	alpha-s2-casein C	223	31	55.4	261	2	G90775	recombination prot
151	32	57.1	223	2	JN0547	alpha-s2-casein pr	224	31	55.4	261	2	H85637	recombination prot
152	32	57.1	234	2	T51666	myb-related transc	225	31	55.4	261	2	A98004	recombination prot
153	32	57.1	235	2	AF2319	hypothetical prote	226	31	55.4	261	2	E85848	hypothetical prote
154	32	57.1	240	2	T35224	probable nitrate r	227	31	55.4	263	2	AG2222	nitrate transport
155	32	57.1	260	2	S76509	hypothetical prote	228	31	55.4	264	2	S95259	conserved hypotet
156	32	57.1	278	2	C83552	hypothetical prote	229	31	55.4	264	2	E98124	hypothetical prote
157	32	57.1	290	2	A88616	protein T25C8.3 li	230	31	55.4	267	2	D64351	nitrate transport
158	32	57.1	306	1	S35151	cyclin-suppressing	231	31	55.4	268	1	JQ0961	myb-related protei
159	32	57.1	315	2	T00528	hypothetical prote	232	31	55.4	271	2	T11590	hypothetical prote
160	32	57.1	329	2	S08499	quinone 5-dehydrog	233	31	55.4	271	2	G84030	hema concentration
161	32	57.1	337	2	A82309	quinone oxidoreduc	234	31	55.4	274	2	S30894	nitrate transport
162	32	57.1	368	1	W2WL6	E2 protein - human	235	31	55.4	286	2	AD2185	ATP-binding protei
163	32	57.1	372	2	B64717	LPS biosynthesis p	236	31	55.4	290	2	T18992	hypothetical prote
164	32	57.1	382	2	S36476	E2 protein - human	237	31	55.4	295	2	B41320	hypothetical prote
165	32	57.1	389	2	T47178	hypothetical prote	238	31	55.4	301	2	C97852	tellurium resistan
166	32	57.1	393	2	S27881	beta-alanine synth	239	31	55.4	306	2	D86805	pantothenate kinas
167	32	57.1	398	1	W2WL42	E2 protein - human	240	31	55.4	316	2	S64357	probable membrane
168	32	57.1	420	2	W43297	casein kinase II (	241	31	55.4	318	2	B95883	probable transcript
169	32	57.1	435	2	T01805	hypothetical prote	242	31	55.4	319	2	B82381	transcription regu
170	32	57.1	442	2	A71433	hypothetical prote	243	31	55.4	324	2	H96746	RING-H2 zinc finge
171	32	57.1	443	2	D83265	conserved hypotet	244	31	55.4	333	1	DEHGGT	glyceraldehyde-3-p
172	32	57.1	452	2	S36482	E2 protein - human	245	31	55.4	336	2	E99850	protein F12M16.19
173	32	57.1	533	2	S78529	(N-acetylneuraminy	246	31	55.4	353	2	C96573	gibberellin 20-dio
174	32	57.1	533	2	S53320	(N-acetylneuraminy	247	31	55.4	361	2	T06330	gibberellin 20-dio
175	32	57.1	541	2	A87595	amine oxidase, fla	248	31	55.4	365	2	T06991	gibberellin 20-dio



249	31	55.4	365	2	T06990	gibberellin 20-dio	322	31	55.4	824	2	T44037	helicase [imported
250	31	55.4	367	2	T31750	hypothetical prote	323	31	55.4	839	2	S73548	MG422 homolog C12-
251	31	55.4	370	1	S55333	protein kinase pim	324	31	55.4	843	2	T12689	armadillo segment
252	31	55.4	370	2	T11849	gibberellin 20-oxi	325	31	55.4	853	2	S60178	gag polyprotein ho
253	31	55.4	371	2	T04337	probable gibberell	326	31	55.4	854	2	T14377	s-receptor kinase
254	31	55.4	379	2	T01748	gibberellin 20-oxi	327	31	55.4	868	2	A83547	probable aconitate
255	31	55.4	379	2	T01748	gibberellin 20-oxi	328	31	55.4	1002	2	A85963	transposase - Esch
256	31	55.4	379	2	T06533	probable gibberell	329	31	55.4	1029	2	T02576	transposase - Esch
257	31	55.4	380	2	T48931	gibberellin 20-oxi	330	31	55.4	1030	2	T31452	hypothetical prote
258	31	55.4	382	2	T11847	gibberellin 20-oxi	331	31	55.4	1058	2	A38564	hypothetical prote
259	31	55.4	385	2	T11848	gibberellin 20-oxi	332	31	55.4	1058	2	JC1254	ubiquitin-protein
260	31	55.4	385	2	T06701	hypothetical prote	333	31	55.4	1085	2	S66149	gene pipsqueak pro
261	31	55.4	389	2	AC2268	heterocyst envelop	334	31	55.4	1123	1	SYNCLC	leucine-tRNA ligas
262	31	55.4	394	2	T24749	hypothetical prote	335	31	55.4	1157	2	S38160	NUP133 protein - y
263	31	55.4	403	2	AH2302	hypothetical prote	336	31	55.4	1203	2	T21275	hypothetical prote
264	31	55.4	409	2	T50311	oxalsp2 protein [i	337	31	55.4	1354	2	T13930	tripeptidyl-peptid
265	31	55.4	409	2	T47303	respiratory protei	338	31	55.4	1385	2	S34230	156K protein - Pla
266	31	55.4	410	2	B55523	aromatic dioxygena	339	31	55.4	1488	2	AG2136	polyketide synthas
267	31	55.4	425	2	C97013	probable non-proce	340	31	55.4	1502	2	S53602	carbamoyl-phosphat
268	31	55.4	426	2	A64604	hypothetical prote	341	31	55.4	1547	2	JQ0096	hypothetical 176K
269	31	55.4	436	2	E71493	probable RNA polym	342	31	55.4	1584	2	T22674	hypothetical prote
270	31	55.4	445	2	S42281	S-locus glycoprote	343	31	55.4	2471	2	T42977	large tegument pro
271	31	55.4	445	2	JQ1733	self-incompatibili	344	31	55.4	2957	2	T33152	hypothetical prote
272	31	55.4	449	2	S17780	strK protein - Str	345	31	55.4	3119	2	T18414	protein G377 - mal
273	31	55.4	450	2	I48756	gene Shx protein -	346	31	55.4	3473	1	A46112	genome polyprotein
274	31	55.4	459	2	G85212	hypothetical prote	347	31	55.4	3473	2	S27922	polyprotein - rice
275	31	55.4	463	2	F90422	4-hydroxyputryl-C	348	31	55.4	4540	2	T30838	cytoplasmic dynein
276	31	55.4	472	2	G75298	ribosomal protein	349	30.5	54.5	303	1	CFCYB	carboxypeptidase B
277	31	55.4	483	2	E87345	conserved hypothet	350	30.5	54.5	371	2	AC3440	GTP cyclohydrolase
278	31	55.4	484	2	E83245	potassium uptake p	351	30.5	54.5	380	2	T10898	probable omega-3 f
279	31	55.4	484	2	S62938	hypothetical prote	352	30.5	54.5	1186	2	T19334	hypothetical prote
280	31	55.4	493	2	C87362	hypothetical prote	353	30.5	54.5	4644	1	A38905	dynein heavy chain
281	31	55.4	511	2	T11467	cytochrome-c oxida	354	30	53.6	61	2	S60796	M protein precurs
282	31	55.4	512	1	ODFF1	cytochrome-c oxida	355	30	53.6	74	2	AG2533	hypothetical prote
283	31	55.4	512	1	ODFF1Y	cytochrome-c oxida	356	30	53.6	77	2	T03206	hypothetical prote
284	31	55.4	513	2	T13782	transducin homolog	357	30	53.6	96	2	G38601	ig kappa chain V r
285	31	55.4	519	2	A49367	probable membrane	358	30	53.6	103	2	F83238	probable transcrip
286	31	55.4	523	2	S53401	hypothetical prote	359	30	53.6	107	2	A48677	ig kappa chain V-J
287	31	55.4	532	2	C70581	gene pipsqueak pro	360	30	53.6	108	1	KIHURE	ig kappa chain V-I
288	31	55.4	535	2	S66148	cytochrome c-type	361	30	53.6	114	2	T16365	hypothetical prote
289	31	55.4	552	1	E57987	hypothetical prote	362	30	53.6	124	2	S23662	hypothetical prote
290	31	55.4	552	2	D86101	cytochrome c-type	363	30	53.6	134	2	C75352	conserved hypothet
291	31	55.4	552	2	H91260	cytochrome c-type	364	30	53.6	142	2	S36310	T-cell receptor de
292	31	55.4	564	2	C83742	cytochrome c oxida	365	30	53.6	143	2	S36300	T-cell receptor de
293	31	55.4	574	2	B86005	probable transport	366	30	53.6	156	2	C97097	probable membrane
294	31	55.4	574	2	D91159	probable transport	367	30	53.6	160	2	S00714	phycocyanin 1 alph
295	31	55.4	574	2	E65135	hypothetical 64.6K	368	30	53.6	162	1	CFKCA	C-phycocyanin alph
296	31	55.4	584	1	ALBY	alpha-glucosidase	369	30	53.6	162	1	CFVCA	C-phycocyanin alph
297	31	55.4	584	2	S64627	alpha-glucosidase	370	30	53.6	162	2	T11978	phycocyanin alpha
298	31	55.4	584	2	S46183	gamma-glutamyltran	371	30	53.6	163	1	CFICA	phycocyanin alpha
299	31	55.4	588	2	A82354	DNA-binding regula	372	30	53.6	163	2	B35126	conserved hypothet
300	31	55.4	616	2	I38155	plakoglobin - mous	373	30	53.6	163	2	AF0119	conserved hypothet
301	31	55.4	621	2	S35092	dopamine beta-mono	374	30	53.6	163	2	AD0179	thiol-specific ant
302	31	55.4	621	2	JC1346	ATP binding protei	375	30	53.6	196	2	A47362	hypothetical prote
303	31	55.4	625	2	S58789	hypothetical prote	376	30	53.6	196	2	S69732	isopentenyl pyroph
304	31	55.4	634	2	T18711	hypothetical prote	377	30	53.6	213	2	B84333	hypothetical prote
305	31	55.4	634	2	T18702	hypothetical prote	378	30	53.6	215	2	H69251	sigma-B factor neg
306	31	55.4	638	2	T48380	hypothetical prote	379	30	53.6	216	2	B57255	nitrate reductase
307	31	55.4	652	2	G85024	probable CHP-rich	380	30	53.6	225	2	C90040	Myb DNA binding pr
308	31	55.4	657	2	A11882	nitrate transport	381	30	53.6	256	2	T49254	conserved hypothet
309	31	55.4	659	2	S30893	nrtc protein - Syn	382	30	53.6	265	2	B69820	hypothetical prote
310	31	55.4	667	2	S75959	nitrate transport	383	30	53.6	265	2	F69742	proteasome endopep
311	31	55.4	667	2	AH2165	bicarbonate transp	384	30	53.6	273	2	I38135	exopolysaccharide
312	31	55.4	670	2	S77387	nitrate transport	385	30	53.6	280	2	AF3650	hypothetical prote
313	31	55.4	691	2	S54262	methyl-accepting c	386	30	53.6	281	2	T15980	exopolysaccharide
314	31	55.4	738	2	S35093	plakoglobin - Afri	387	30	53.6	283	2	JC6531	avermectin B 5-O-m
315	31	55.4	744	2	A32905	plakoglobin, demo	388	30	53.6	283	2	T44579	C5-O-methyltransfe
316	31	55.4	765	2	F97123	sporulation protei	389	30	53.6	289	2	A87646	hypothetical prote
317	31	55.4	771	2	T43612	transposase - Yers	390	30	53.6	309	2	B91143	probable membrane
318	31	55.4	781	2	S35099	beta-catenin - Afr	391	30	53.6	309	2	E85988	probable membrane
319	31	55.4	808	2	T23129	hypothetical prote	392	30	53.6	310	2	A30911	probable exported
320	31	55.4	820	2	S33794	hypothetical prote	393	30	53.6	310	2	C55116	hypothetical 34.8
321	31	55.4	824	2	T44222	probable helicase	394	30	53.6	311	2	AF0448	probable Hyd fami

395	30	53.6	318	2	E83019	hypothetical prote	468	30	53.6	615	2	D96499	probable UDP-glucos
396	30	53.6	319	2	S62810	adenine specific D	469	30	53.6	618	2	G59432	MacGAP protein (im
397	30	53.6	320	2	D82241	conserved hypotet	470	30	53.6	619	2	F81532	conserved hypotet
398	30	53.6	323	2	T35035	probable acyl-lacy	471	30	53.6	619	2	E86617	CR58 hypothetical
399	30	53.6	329	2	T44552	hypothetical prote	472	30	53.6	619	2	F72006	CR58 hypothetical
400	30	53.6	342	1	B71051	conserved hypotet	473	30	53.6	657	2	T41546	hypothetical prote
401	30	53.6	342	2	T23224	hypothetical prote	474	30	53.6	657	2	S53414	probable membrane
402	30	53.6	345	2	H70464	hypothetical prote	475	30	53.6	680	2	JC5133	protein-glutamine
403	30	53.6	345	2	C89974	hypothetical prote	476	30	53.6	697	2	T12507	hypothetical prote
404	30	53.6	346	2	H70722	probable transfera	477	30	53.6	697	2	T03722	EX070 protein - mo
405	30	53.6	348	2	AC3546	response regulator	478	30	53.6	736	2	T41629	hypothetical prote
406	30	53.6	352	2	T15981	hypothetical prote	479	30	53.6	744	2	T27674	hypothetical prote
407	30	53.6	354	2	A24782	xiaA protein - Ana	480	30	53.6	753	2	A27041	tyrosine kinase-re
408	30	53.6	364	2	G86574	RNA methyltransfer	481	30	53.6	755	2	T19118	acid phosphatase h
409	30	53.6	364	2	F72048	RNA methyltransfer	482	30	53.6	768	2	T09890	hypothetical prote
410	30	53.6	366	2	D96649	hypothetical prote	483	30	53.6	778	2	A13064	glucose dehydrogen
411	30	53.6	367	1	W2WL11	E2 protein - human	484	30	53.6	778	2	G98221	glucose dehydrogen
412	30	53.6	372	2	C83766	adenine glycosylas	485	30	53.6	781	2	S35091	beta-catenin - mou
413	30	53.6	373	1	AJCHQ	glutamate-ammonia	486	30	53.6	781	2	A38973	beta-catenin - hum
414	30	53.6	379	2	AD1974	thiamin-phosphate	487	30	53.6	787	2	A1692	inner membrane pro
415	30	53.6	381	2	T03923	probable omega-3 f	488	30	53.6	787	2	E71537	probable 60kDa inn
416	30	53.6	382	2	F82335	NlpD-related prote	489	30	53.6	802	2	S49252	penicillin amidase
417	30	53.6	387	2	T19572	hypothetical prote	490	30	53.6	802	2	I39665	penicillin amidase
418	30	53.6	390	1	W2WLRB	E2 protein - cotto	491	30	53.6	806	2	T41930	ribonucleotide red
419	30	53.6	394	2	T19571	hypothetical prote	492	30	53.6	808	2	T14513	hypothetical prote
420	30	53.6	406	2	H63143	coenzyme F420-redu	493	30	53.6	817	2	S33793	hypothetical prote
421	30	53.6	409	2	JW0101	azaarene carbazole	494	30	53.6	817	2	T01866	hypothetical prote
422	30	53.6	416	2	S00828	hypothetical prote	495	30	53.6	868	2	C81200	aconitate hydratase
423	30	53.6	422	2	AH3317	carbamoyl-phosphat	496	30	53.6	868	2	H81775	aconitate hydratase
424	30	53.6	431	2	T07685	omega-3 fatty acid	497	30	53.6	875	1	A36369	1-phosphatidylinos
425	30	53.6	432	2	B84620	hypothetical prote	498	30	53.6	889	2	T47311	hypothetical prote
426	30	53.6	445	2	T23590	hypothetical prote	499	30	53.6	902	2	S61144	glycogen phosphory
427	30	53.6	445	2	T28015	hypothetical prote	500	30	53.6	905	2	T40015	phosphatidylethano
428	30	53.6	447	2	T43750	hypothetical prote	501	30	53.6	911	1	A54809	disease resistance
429	30	53.6	450	2	T23111	hypothetical prote	502	30	53.6	911	2	A39967	inter-alpha-trypsi
430	30	53.6	451	2	G69859	Mg2+ transporter h	503	30	53.6	928	2	T21680	hypothetical prote
431	30	53.6	455	2	C82403	probable oxygen-in	504	30	53.6	944	2	T21673	hypothetical prote
432	30	53.6	462	2	G70015	conserved hypotet	505	30	53.6	947	2	G86557	polymorphic membra
433	30	53.6	464	2	S59898	kynureninase (EC 3	506	30	53.6	947	2	T01238	hypothetical prote
434	30	53.6	464	2	T48675	kynureninase (EC 3	507	30	53.6	947	2	D72067	polymorphic membra
435	30	53.6	465	2	G02652	kynureninase (EC 3	508	30	53.6	954	2	H71427	hypothetical prote
436	30	53.6	470	2	S72279	conserved hypotet	509	30	53.6	971	2	T09210	starch phosphoryla
437	30	53.6	472	2	T31465	cell cycle protein	510	30	53.6	1016	2	T25433	hypothetical prote
438	30	53.6	472	2	AG1986	nifd element site-	511	30	53.6	1017	2	T48126	hypothetical prote
439	30	53.6	475	2	T35697	arabinofuranosidas	512	30	53.6	1054	2	T18304	acid trehalase hom
440	30	53.6	476	2	T35528	probable aminotran	513	30	53.6	1075	2	B96508	hypothetical prote
441	30	53.6	490	2	T36716	probable penicilli	514	30	53.6	1113	2	H84105	hypothetical prote
442	30	53.6	490	2	T23112	hypothetical prote	515	30	53.6	1115	2	T11614	probable poly(A)-s
443	30	53.6	492	2	H70959	hypothetical prote	516	30	53.6	1232	2	T05322	hypothetical prote
444	30	53.6	496	2	JS0732	aspartic proteinase	517	30	53.6	1490	2	T47840	multi resistance p
445	30	53.6	500	2	AD1047	probable amino aci	518	30	53.6	1684	2	T02367	hypothetical prote
446	30	53.6	502	2	A82234	gonadoliberin III-	519	30	53.6	1790	1	S27772	vitellogenin precu
447	30	53.6	503	2	E70602	probable membrane	520	30	53.6	1966	2	T08991	hypothetical prote
448	30	53.6	504	2	T38226	probable serine-th	521	30	53.6	1993	2	T30902	sodium channel SCA
449	30	53.6	514	2	G84724	probable ARI-like	522	30	53.6	2588	2	A12136	peptide synthetase
450	30	53.6	516	2	E71957	ABC transporter, A	523	28.5	52.7	210	2	A56169	ig kappa chain v r
451	30	53.6	516	2	B64551	oligopeptide ABC t	524	29.5	52.7	293	2	S50109	vitellogenin gene-
452	30	53.6	517	2	C89840	conserved hypotet	525	29.5	52.7	348	2	T03530	omega-3 fatty acid
453	30	53.6	524	2	T20471	hypothetical prote	526	29.5	52.7	379	2	JC2555	probable gamma-glu
454	30	53.6	524	2	E64569	phosphoglycerate d	527	29.5	52.7	591	2	F81893	gamma-glutamyltran
455	30	53.6	524	2	C71864	d-3-phosphoglycera	528	29.5	52.7	606	2	D81126	tracheal colonizat
456	30	53.6	542	2	A84725	similar to Ariadne	529	29.5	52.7	672	2	I40333	probable cysteinyl
457	30	53.6	548	2	S33788	Photinus-luciferin	530	29.5	52.7	754	2	S62512	RNA-directed RNA p
458	30	53.6	549	2	AF2378	choline dehydrogen	531	29.5	52.7	757	1	A60008	RNA-directed RNA p
459	30	53.6	572	2	B84958	proline-trNA ligas	532	29.5	52.7	757	1	B60011	RNA-directed RNA p
460	30	53.6	572	2	F90564	conserved hypotet	533	29.5	52.7	757	1	PIIV61	RNA-directed RNA p
461	30	53.6	581	2	S52154	acetyl-CoA synthet	534	29.5	52.7	757	1	PIIV68	RNA-directed RNA p
462	30	53.6	583	2	C97460	choline dehydrogen	535	29.5	52.7	757	2	S06212	glycoprotein H - h
463	30	53.6	595	2	A35919	carotenoid biosynt	536	29	51.8	65	2	PQ0852	hypothetical prote
464	30	53.6	600	2	B66990	probable membrane	537	29	51.8	82	2	AF3441	ig light chain v h
465	30	53.6	604	2	AB1989	hypothetical prote	538	29	51.8	99	2	PH1059	ig light chain v h
466	30	53.6	605	2	S46833	hypothetical prote	539	29	51.8	103	2	PH1043	ig light chain v h
467	30	53.6	610	2	AE2436	penicillin-binding	540	29	51.8	103	2	F82524	hypothetical prote

541	29	51.8	108	2	I39154	Ig kappa chain (BR	614	29	51.8	290	2	S55116	hypothetical prote
542	29	51.8	108	2	S63900	Ig kappa chain (cl	615	29	51.8	293	2	A51517	conserved hypothet
543	29	51.8	109	2	PH0888	Ig kappa chain v r	616	29	51.8	293	2	T32892	hypothetical prote
544	29	51.8	110	2	PH0090	Ig light chain v r	617	29	51.8	296	2	T43930	hypothetical prote
545	29	51.8	112	2	S38716	Ig kappa chain v r	618	29	51.8	295	2	AD1040	putative methyltra
546	29	51.8	112	2	A49715	Ig kappa chain v r	619	29	51.8	297	2	AB2818	UDP-glucose 4-epim
547	29	51.8	114	2	D71048	hypothetical prote	620	29	51.8	299	2	F96828	hypothetical prote
548	29	51.8	117	2	S42466	Ig kappa chain v r	621	29	51.8	300	2	S76855	hypothetical prote
549	29	51.8	122	2	A23980	Ig kappa chain pre	622	29	51.8	301	1	K1BPP4	polynucleotide kin
550	29	51.8	124	2	PC2258	cytochrome P450 pr	623	29	51.8	302	2	S73583	probable lipoprote
551	29	51.8	126	2	A34908	Ig kappa chain pre	624	29	51.8	307	2	E86323	protein F14D16.11
552	29	51.8	132	2	S46373	Ig kappa chain V-J	625	29	51.8	308	2	C86561	phosphatidate cyt1
553	29	51.8	139	2	S40365	Ig kappa chain - h	626	29	51.8	308	2	H72062	phosphatidate cyt1
554	29	51.8	142	2	T33290	very hypothetical	627	29	51.8	310	2	G71240	hypothetical prote
555	29	51.8	153	2	S35204	proteinase 4 - buf	628	29	51.8	310	2	T16827	hypothetical prote
556	29	51.8	156	2	F86661	acetyltransferase	629	29	51.8	312	2	A11881	nitrogen assimilat
557	29	51.8	158	2	E82215	probable chemotaxi	630	29	51.8	313	2	E83543	probable hydrolase
558	29	51.8	162	2	B84018	hypothetical prote	631	29	51.8	314	2	T30523	dihydroorotate deh
559	29	51.8	165	2	E64339	hypothetical prote	632	29	51.8	315	2	H71009	probable prolifera
560	29	51.8	165	2	JE0065	retroviral protein	633	29	51.8	317	2	B97162	phospho-N-acetylm
561	29	51.8	173	2	T18601	hypothetical prote	634	29	51.8	317	2	AF0205	probable exported
562	29	51.8	175	2	S45905	hypothetical prote	635	29	51.8	319	2	T33261	hypothetical prote
563	29	51.8	186	2	E85715	unknown protein en	636	29	51.8	321	2	G75329	conserved hypothet
564	29	51.8	196	2	A69193	hypothetical prote	637	29	51.8	322	2	F90487	maltose ABC transp
565	29	51.8	196	2	G82053	probable fibrial	638	29	51.8	325	2	A71500	probable RNA methy
566	29	51.8	198	2	S64601	hypothetical prote	639	29	51.8	326	2	T11721	conserved hypothet
567	29	51.8	201	2	C96813	hypothetical prote	640	29	51.8	338	2	B97596	UDP-glucose-4-epim
568	29	51.8	202	2	C72621	probable NADH dehy	641	29	51.8	339	2	D70942	probable pfkB prot
569	29	51.8	203	2	A90871	phage superinfecti	642	29	51.8	339	2	T15560	hypothetical prote
570	29	51.8	203	2	D64885	superinfection exc	643	29	51.8	340	2	T32891	hypothetical prote
571	29	51.8	203	2	H85747	superinfection exc	644	29	51.8	340	2	T52386	mitotic checkpoint
572	29	51.8	213	2	S74055	hypothetical prote	645	29	51.8	342	2	T09355	hypothetical prote
573	29	51.8	221	2	C82498	ribosomal large ch	646	29	51.8	344	2	T39023	hypothetical prote
574	29	51.8	221	2	C70704	probable rocd - My	647	29	51.8	345	2	T04016	hypothetical prote
575	29	51.8	222	2	F85176	isomerase like pro	648	29	51.8	346	2	B84123	iron (III) dicitra
576	29	51.8	222	2	H72522	hypothetical prote	649	29	51.8	352	2	C82294	oxidoreductase Taa
577	29	51.8	225	2	A87624	hypothetical prote	650	29	51.8	353	2	F72019	conserved hypothet
578	29	51.8	226	2	AC0176	probable exported	651	29	51.8	353	2	E86604	Fe-S oxidoreductas
579	29	51.8	233	2	C90507	hypothetical prote	652	29	51.8	356	2	A96814	hypothetical prote
580	29	51.8	235	2	H85564	hypothetical prote	653	29	51.8	358	1	S71887	serine/threonine-a
581	29	51.8	235	2	C90714	hypothetical prote	654	29	51.8	358	2	AC0146	probable Branched-
582	29	51.8	235	2	F64799	hypothetical prote	655	29	51.8	361	2	D59107	hypothetical prote
583	29	51.8	235	2	C90714	probable tRNA liga	656	29	51.8	361	2	T02000	homeotic protein K
584	29	51.8	235	2	C85565	probable tRNA liga	657	29	51.8	364	2	S58871	hypothetical prote
585	29	51.8	238	2	T33219	hypothetical prote	658	29	51.8	366	2	T47360	hypothetical prote
586	29	51.8	240	2	C90293	hypothetical prote	659	29	51.8	367	2	B83676	pyruvate dehydroge
587	29	51.8	242	2	AB3523	taurine transport	660	29	51.8	367	2	S55961	hypothetical prote
588	29	51.8	244	2	B83142	hypothetical prote	661	29	51.8	367	2	C71425	hypothetical prote
589	29	51.8	246	2	E70556	probable respirato	662	29	51.8	367	2	G85362	hypothetical prote
590	29	51.8	246	2	I51325	proteolipid protei	663	29	51.8	374	2	E90454	hypothetical prote
591	29	51.8	248	2	AG3275	hexaprenyldihydrox	664	29	51.8	376	2	T40488	hypothetical prote
592	29	51.8	249	2	T21920	hypothetical prote	665	29	51.8	379	2	PC4180	thiazide-sensitiv
593	29	51.8	250	2	AC2988	3-demethylubiquino	666	29	51.8	380	2	JQ2338	omega-3 fatty acid
594	29	51.8	250	2	E98295	dihydroxypolypreny	667	29	51.8	380	2	T20269	hypothetical prote
595	29	51.8	253	2	C75611	transcription regu	668	29	51.8	380	2	T24786	hypothetical prote
596	29	51.8	257	2	S70177	yifE protein - Ver	669	29	51.8	383	2	T06238	omega-3 fatty acid
597	29	51.8	261	1	Q0BEF5	HVLF5 protein - hu	670	29	51.8	385	2	E71238	hypothetical prote
598	29	51.8	264	2	D71037	hypothetical prote	671	29	51.8	385	2	C97277	glycosyltransferas
599	29	51.8	266	2	A45186	homeotic protein G	672	29	51.8	386	2	G88555	protein B0464.7 [1
600	29	51.8	268	2	S00553	MSS18 protein - ye	673	29	51.8	387	2	T16068	hypothetical prote
601	29	51.8	270	2	F86699	protoporphyrinogen	674	29	51.8	391	2	H30308	transposase ISC131
602	29	51.8	273	2	A83546	probable oxidoredu	675	29	51.8	392	2	S37902	hypothetical prote
603	29	51.8	278	2	AC3479	ATP-dependent heli	676	29	51.8	393	2	E90272	transposase ISC131
604	29	51.8	281	2	A97604	probable oxidoredu	677	29	51.8	393	2	B71857	probable lipopolys
605	29	51.8	281	2	AB2826	aldo/keto reductas	678	29	51.8	395	2	B75512	conserved hypothet
606	29	51.8	283	2	T19333	hypothetical prote	679	29	51.8	395	2	C90328	transposase ISC131
607	29	51.8	284	1	E64938	probable aldehyde	680	29	51.8	396	2	S31151	translation elonga
608	29	51.8	284	2	F85788	probable an aldehy	681	29	51.8	398	2	C71857	probable lipopolys
609	29	51.8	285	2	B90940	probable an aldehy	682	29	51.8	403	2	B90290	transposase ISC131
610	29	51.8	285	2	A10711	probable oxidoredu	683	29	51.8	408	2	B90326	transposase ISC131
611	29	51.8	287	2	S74050	hypothetical prote	684	29	51.8	417	2	S74940	hypothetical prote
612	29	51.8	288	2	I78556	membrane glycoprot	685	29	51.8	420	2	A54759	cytochrome ba(3) c
613	29	51.8	289	2	D71235	hypothetical prote	686	29	51.8	421	2	A56550	Krox-20 - African

687	29	51.8	422	2	G87188	phosphoribosylamin	760	29	51.8	545	2	S58973	carboxylesterase (
688	29	51.8	422	2	G70707	probable purD prot	761	29	51.8	547	2	A50047	probable acyl-CoA
689	29	51.8	422	2	AE3333	hypothetical cytos	762	29	51.8	553	2	T06499	Rieske [2Fe-2S] ir
690	29	51.8	423	2	T04915	CDP-diacylglycerol	763	29	51.8	556	2	A81931	probable adhesin N
691	29	51.8	423	2	G85255	CDP-diacylglycerol	764	29	51.8	564	2	T45866	hypothetical prote
692	29	51.8	424	2	T07366	probable phosphati	765	29	51.8	578	2	AH1020	cytochrome c-type
693	29	51.8	431	2	A64658	LPS biosynthesis p	766	29	51.8	580	2	S76846	hypothetical prote
694	29	51.8	431	2	S62528	hypothetical prote	767	29	51.8	585	2	S43718	malate dehydrogena
695	29	51.8	439	1	A48099	transcription fact	768	29	51.8	594	1	E84622	exonuclease ABC c
696	29	51.8	439	2	B72313	glutamine syntheta	769	29	51.8	594	2	B71893	serotonin transpor
697	29	51.8	439	2	I57561	transcription fact	770	29	51.8	607	2	S19585	exonuclease ABC c
698	29	51.8	446	2	G70634	probable lipD prot	771	29	51.8	630	2	T50239	probable gamma-glu
699	29	51.8	447	2	G83324	probable two-compo	772	29	51.8	630	2	S30604	neurotransmitter t
700	29	51.8	447	2	G75201	probable beta-lact	773	29	51.8	631	2	G82035	glucose inhibited
701	29	51.8	448	2	B90498	permease, probable	774	29	51.8	631	2	S87288	hypothetical prote
702	29	51.8	450	2	AG0008	probable membrane	775	29	51.8	635	2	T27014	hypothetical prote
703	29	51.8	451	2	H82063	UDP-N-acetylmuram	776	29	51.8	639	2	T23658	hypothetical prote
704	29	51.8	452	2	S48916	hypothetical prote	777	29	51.8	651	2	E85024	probable CHP-rich
705	29	51.8	455	2	C84133	glutamine syntheta	778	29	51.8	652	2	G96560	hypothetical prote
706	29	51.8	455	2	H70983	hypothetical prote	779	29	51.8	652	2	C70688	probable nitrate x
707	29	51.8	456	2	AG0199	adenylosuccinate l	780	29	51.8	652	2	T02001	hypothetical prote
708	29	51.8	456	2	AE0521	aromatic amino aci	781	29	51.8	658	2	F85024	probable CHP-rich
709	29	51.8	456	2	AF0093	Sodium_sulfate sym	782	29	51.8	662	2	H84984	bo-type ubiquinol
710	29	51.8	459	2	E86176	protein F19P19.10	783	29	51.8	669	2	T17122	hypothetical prote
711	29	51.8	465	2	AE3102	glutamyl-tRNA amid	784	29	51.8	670	2	C84496	probable replicati
712	29	51.8	465	2	E98184	probable amidase P	785	29	51.8	670	2	A85819	hypothetical prote
713	29	51.8	469	2	E95236	glycosyl hydrolase	786	29	51.8	671	1	VCMVCE	env polyprotein -
714	29	51.8	475	2	S65290	clathrin-associate	787	29	51.8	693	2	A41617	dopamine transport
715	29	51.8	476	2	S52746	stearyl-CoA 9-des	788	29	51.8	694	2	T01134	glycoprotein H pre
716	29	51.8	476	2	T45656	hypothetical prote	789	29	51.8	694	2	T44195	glycoprotein H pre
717	29	51.8	478	2	A72721	probable Glycerol	790	29	51.8	694	2	J02383	glycoprotein H - h
718	29	51.8	478	2	T45661	hypothetical prote	791	29	51.8	694	2	T44008	glycoprotein H [im
719	29	51.8	482	2	T43885	cytochrome-c oxida	792	29	51.8	700	2	A90732	probable terminase
720	29	51.8	482	2	T43876	cytochrome-c oxida	793	29	51.8	700	2	D85582	probable terminase
721	29	51.8	482	2	T43879	cytochrome-c oxida	794	29	51.8	707	2	C90999	probable terminase
722	29	51.8	482	2	T43884	cytochrome-c oxida	795	29	51.8	709	2	S73497	cell division prot
723	29	51.8	482	2	T43883	cytochrome-c oxida	796	29	51.8	711	1	A47136	macrophage-stimula
724	29	51.8	482	2	T43886	cytochrome-c oxida	797	29	51.8	716	1	A40332	macrophage-stimula
725	29	51.8	482	2	T45295	cytochrome-c oxida	798	29	51.8	716	1	JC5061	macrophage-stimula
726	29	51.8	482	2	T45296	cytochrome-c oxida	799	29	51.8	720	2	T47221	replication licens
727	29	51.8	484	2	G98100	beta-glucosidase (	800	29	51.8	721	2	T05815	hypothetical prote
728	29	51.8	484	2	T20254	hypothetical prote	801	29	51.8	722	2	B75608	GMC oxidoreductase
729	29	51.8	485	2	A57982	enterobolin (Cytol	802	29	51.8	728	1	S36095	hypothetical prote
730	29	51.8	487	2	G95366	probable NADH2 deh	803	29	51.8	728	1	S36095	transforming prote
731	29	51.8	491	2	T08996	ribulose-1,5-bisph	804	29	51.8	734	1	Y8BYTC	threonine-tRNA lig
732	29	51.8	491	2	A49179	melanoma antigen h	805	29	51.8	775	2	F82887	hypothetical prote
733	29	51.8	492	2	S32951	regulatory protein	806	29	51.8	775	2	S28284	hypothetical prote
734	29	51.8	495	2	S75340	NADH2 dehydrogenas	807	29	51.8	785	2	T51203	related to ser/thr
735	29	51.8	495	2	T08995	ribulose-1,5-bisph	808	29	51.8	787	1	JDVLM2	DNA-directed DNA p
736	29	51.8	499	2	S75893	hypothetical prote	809	29	51.8	788	1	JDVLM2	DNA-directed DNA p
737	29	51.8	503	2	S73843	general amino acid	810	29	51.8	803	2	G36523	FLA17.8 [imported
738	29	51.8	505	2	T35107	hypothetical prote	811	29	51.8	811	2	S57149	probable membrane
739	29	51.8	505	2	T50815	cdc2-like protein	812	29	51.8	819	2	JC7240	two-pore calcium c
740	29	51.8	508	2	T45867	hypothetical prote	813	29	51.8	832	2	H72278	alpha-mannosidase-
741	29	51.8	510	1	W2BE47	protein-serine/thr	814	29	51.8	836	1	JDVLD	DNA-directed DNA p
742	29	51.8	511	2	T45869	hypothetical prote	815	29	51.8	841	1	S39365	outer membrane uah
743	29	51.8	512	1	D70506	hypothetical prote	816	29	51.8	863	2	D88485	protein B0244.7 [i
744	29	51.8	514	2	T21286	hypothetical prote	817	29	51.8	925	2	JC2033	G protein-coupled
745	29	51.8	516	1	S72937	hypothetical prote	818	29	51.8	927	2	T47827	squamosa promoter
746	29	51.8	517	2	G87032	conserved hypotet	819	29	51.8	959	2	E85276	hypothetical prote
747	29	51.8	517	2	T29852	hypothetical prote	820	29	51.8	959	2	T00246	DNA polymerase V -
748	29	51.8	520	2	B95168	GMP synthase [impo	821	29	51.8	964	2	S45944	hypothetical prote
749	29	51.8	520	2	C98034	GMP synthase (glut	822	29	51.8	977	2	E86349	hypothetical prote
750	29	51.8	531	2	T45865	hypothetical prote	823	29	51.8	977	2	T41289	hypothetical prote
751	29	51.8	532	2	T21184	hypothetical prote	824	29	51.8	983	2	AG2381	hypothetical prote
752	29	51.8	534	2	T52649	beta-1,2-xylosyltr	825	29	51.8	989	2	T01519	glycine cleavage s
753	29	51.8	535	2	E96494	protein F7F22.8 [i	826	29	51.8	1002	2	B54145	sodium-chloride tr
754	29	51.8	536	2	T19488	hypothetical prote	827	29	51.8	1011	2	T17430	tol protein - Neur
755	29	51.8	541	2	T35143	probable monooxyge	828	29	51.8	1011	2	T40851	hypothetical prote
756	29	51.8	541	2	T45563	hypothetical prote	829	29	51.8	1021	2	G01202	NaCl electrotransport
757	29	51.8	542	2	AH2191	hypothetical prote	830	29	51.8	1021	2	E90733	hypothetical prote
758	29	51.8	545	2	S58978	carboxylesterase (	831	29	51.8	1021	2	G85583	probable tail comp
759	29	51.8	545	2	S58972	carboxylesterase (	832	29	51.8	1023	2	A47296	thiazide-sensitive

833	29	51.8	1025	2	I59331	thyrotropin-releas	906	28	50.0	111	1	KVMS80	Ig kappa chain V r
834	29	51.8	1025	2	E86355	hypothetical prote	907	28	50.0	111	2	S23628	Ig kappa chain V r
835	29	51.8	1045	1	SUS8MM	serine proteinase	908	28	50.0	111	2	B72722	hypothetical prote
836	29	51.8	1045	2	A29840	serine proteinase	909	28	50.0	112	2	S51148	antibody light cha
837	29	51.8	1054	2	S54473	TPS3 protein - yea	910	28	50.0	117	2	AC1991	hypothetical prote
838	29	51.8	1089	2	E82987	hypothetical prote	911	28	50.0	118	2	S12627	Ig lambda chain pr
839	29	51.8	1100	1	DDBYD1	RAD1 protein - yea	912	28	50.0	121	2	G64315	hypothetical prote
840	29	51.8	1100	2	T21544	hypothetical prote	913	28	50.0	123	2	E97918	conserved hypotet
841	29	51.8	1106	2	T31742	hypothetical prote	914	28	50.0	123	2	F95047	conserved hypotet
842	29	51.8	1112	2	T28082	hypothetical prote	915	28	50.0	124	2	S40348	Ig kappa chain V-J
843	29	51.8	1121	2	C87973	hypothetical prote	916	28	50.0	136	2	G75482	hypothetical prote
844	29	51.8	1125	2	E90598	protein Y43F8C.12	917	28	50.0	138	2	A83960	hypothetical prote
845	29	51.8	1131	2	A23944	membrane nuclease	918	28	50.0	138	2	T49371	hypothetical prote
846	29	51.8	1153	2	T26883	chitin synthase (E	919	28	50.0	139	2	H82962	hypothetical prote
847	29	51.8	1159	2	T43461	hypothetical prote	920	28	50.0	139	2	B72206	ferredoxin - therm
848	29	51.8	1163	2	T24855	probable phosphodi	921	28	50.0	140	2	T31641	hypothetical prote
849	29	51.8	1132	2	T13424	hypothetical prote	922	28	50.0	143	2	JQ0446	hypothetical 15.7K
850	29	51.8	1221	2	A44978	DNA topoisomerase	923	28	50.0	147	1	H82121	histidine triad fa
851	29	51.8	1222	2	T22490	hypothetical prote	924	28	50.0	149	1	XAACP3	pepin inhibitor 3
852	29	51.8	1276	2	F96753	Similar to downy m	925	28	50.0	152	2	H83578	hypothetical prote
853	29	51.8	1276	2	S69048	probable membrane	926	28	50.0	156	2	E82931	hypothetical prote
854	29	51.8	1311	2	G86471	unknown protein [i	927	28	50.0	156	2	E84230	dihydrofolate redu
855	29	51.8	1357	2	S61187	probable ABC trans	928	28	50.0	159	1	H71493	dihydrofolate redu
856	29	51.8	1469	2	T50210	probable ABC trans	929	28	50.0	163	2	T47559	60S ribosomal prot
857	29	51.8	1640	2	H88094	protein F39E9.2 [i	930	28	50.0	167	2	G70436	hypothetical prote
858	29	51.8	1808	2	T15089	hypothetical prote	931	28	50.0	168	2	T41994	spliced glycoprote
859	29	51.8	1816	2	F83901	hypothetical prote	932	28	50.0	169	2	A83077	probable signal pe
860	29	51.8	1824	2	T07589	hypothetical prote	933	28	50.0	171	2	G86480	hypothetical prote
861	29	51.8	1896	1	RNPF2L	disease resistance	934	28	50.0	171	2	C90247	hypothetical prote
862	29	51.8	2091	2	A97077	DNA-directed RNA p	935	28	50.0	172	2	G82987	secreted protein H
863	29	51.8	2116	2	T49818	hypothetical prote	936	28	50.0	172	2	T46498	hypothetical prote
864	29	51.8	2145	2	S61041	glutamate synthase	937	28	50.0	172	2	B97877	hypothetical prote
865	29	51.8	2591	2	T30288	glutamate synthase	938	28	50.0	179	2	AG0999	transposase (orf1)
866	29	51.8	2628	2	T28651	pristinamycin I sy	939	28	50.0	180	2	AH3614	probable membrane
867	29	51.8	2769	1	UIBO	hemagglutinin A -	940	28	50.0	184	2	S73640	hypothetical prote
868	29	51.8	4464	2	D87755	thryoglobulin prec	941	28	50.0	188	2	JC4680	inorganic diphosph
869	28.5	50.9	62	2	D95110	protein T2E12.4 [i	942	28	50.0	189	2	B71511	vascular endotheli
870	28.5	50.9	62	2	B97379	hypothetical prote	943	28	50.0	190	2	B36729	2-C-methyl-D-eryth
871	28.5	50.9	219	2	T10509	hypothetical prote	944	28	50.0	190	2	AC3040	hypothetical prote
872	28.5	50.9	231	2	T27396	phosphoglycolate p	945	28	50.0	190	2	A99246	conserved hypotet
873	28.5	50.9	231	2	AH0262	hypothetical prote	946	28	50.0	196	2	A83008	conserved hypotet
874	28.5	50.9	301	2	D64938	conserved hypotet	947	28	50.0	197	2	T16370	hypothetical prote
875	28.5	50.9	301	2	A99940	hypothetical prote	948	28	50.0	198	2	A97395	hypothetical prote
876	28.5	50.9	301	2	E85788	hypothetical prote	949	28	50.0	198	2	AC2613	hypothetical prote
877	28.5	50.9	366	2	A35074	hypothetical prote	950	28	50.0	206	2	B82173	conserved hypotet
878	28.5	50.9	446	2	E82975	gamma-glutamyltran	951	28	50.0	207	2	JQ0788	conserved hypotet
879	28.5	50.9	513	2	JC5920	conserved hypotet	952	28	50.0	207	2	JC4679	chloramphenicol O-
880	28.5	50.9	558	2	S58226	potassium channel	953	28	50.0	211	1	ASLJMS	vascular endotheli
881	28.5	50.9	568	1	A05225	nodU protein - Rhi	954	28	50.0	212	2	S49807	nef protein - siml
882	28.5	50.9	568	1	S05532	gamma-glutamyltran	955	28	50.0	217	2	D96013	hypothetical prote
883	28.5	50.9	568	2	JC4570	gamma-glutamyltran	956	28	50.0	218	2	H69005	probable partial t
884	28.5	50.9	569	1	EKHUEX	gamma-glutamyltran	957	28	50.0	219	2	S38865	hypothetical prote
885	28.5	50.9	581	2	S28439	gamma-glutamyltran	958	28	50.0	219	2	T21218	Ig kappa chain - m
886	28.5	50.9	635	2	T23465	modulation protein	959	28	50.0	222	2	B64354	hypothetical prote
887	28.5	50.9	757	1	P11V34	hypothetical prote	960	28	50.0	227	2	B64617	hypothetical prote
888	28.5	50.9	1011	2	T51399	RNA-directed RNA p	961	28	50.0	228	2	G64573	hypothetical prote
889	28	50.0	17	2	B44923	DNA-directed RNA p	962	28	50.0	231	2	C71532	protein phosphatas
890	28	50.0	28	2	A60752	carboxypeptidase 3	963	28	50.0	231	2	S62530	probable ribonucle
891	28	50.0	35	2	E38601	outer membrane pro	964	28	50.0	233	2	T35186	hypothetical prote
892	28	50.0	52	2	D90532	Ig kappa chain V r	965	28	50.0	234	2	A61547	ribonuclease HII -
893	28	50.0	62	2	H64443	hypothetical prote	966	28	50.0	234	2	A61547	proteinase (EC 3.4
894	28	50.0	65	2	S03858	hypothetical prote	967	28	50.0	238	2	E70412	phosphoribosylform
895	28	50.0	68	2	C97874	carboxypeptidase A	968	28	50.0	238	2	H87299	NEF protein - siml
896	28	50.0	68	2	C97874	degenerate transpo	969	28	50.0	239	2	S54852	hypothetical prote
897	28	50.0	99	2	S36053	Ig lambda chain -	970	28	50.0	239	2	H72667	nef protein - siml
898	28	50.0	99	2	S36051	Ig lambda chain -	971	28	50.0	244	2	S61208	hypothetical prote
899	28	50.0	99	2	S36052	Ig lambda chain -	972	28	50.0	246	2	S54853	NEF protein - siml
900	28	50.0	99	2	PH1058	Ig lambda chain -	973	28	50.0	247	1	QBEEF1	nef protein - siml
901	28	50.0	99	2	PH1058	Ig light chain V r	974	28	50.0	250	2	S54849	NEF protein - siml
902	28	50.0	101	2	D82931	hypothetical prote	975	28	50.0	250	2	S54851	nef protein - siml
903	28	50.0	105	2	T46263	hypothetical prote	976	28	50.0	251	2	S61207	NEF protein - siml
904	28	50.0	108	1	K1HUBI	Ig kappa chain V-I	977	28	50.0	251	2	AF2281	hypothetical prote
905	28	50.0	108	2	JQ1549	VI protein - Panic	978	28	50.0	251	2	S54867	nef protein - siml
	28	50.0	109	2	PH0093	Ig kappa chain V r	979	28	50.0	251	2		

979 28 50.0 254 2 S03071 hypothetical prote  
 980 28 50.0 254 2 S40702 hypothetical prote  
 981 28 50.0 254 2 T43494 hypothetical prote  
 982 28 50.0 255 2 F86025 hypothetical prote  
 983 28 50.0 256 2 H65150 hypothetical 29.7  
 984 28 50.0 256 2 E91179 hypothetical prote  
 985 28 50.0 257 2 B70702 hypothetical prote  
 986 28 50.0 257 2 T21848 hypothetical prote  
 987 28 50.0 259 2 T11567 nef protein - simi  
 988 28 50.0 259 2 T49291 hypothetical prote  
 989 28 50.0 260 2 C98084 degenerate transpo  
 990 28 50.0 262 2 D90400 hypothetical prote  
 991 28 50.0 263 1 ASL7MA nef protein - simi  
 992 28 50.0 263 1 ASL7RT nef protein - simi  
 993 28 50.0 263 2 T11556 nef protein - simi  
 994 28 50.0 263 2 S03069 hypothetical prote  
 995 28 50.0 265 2 AH0775 hydroxyethylthiao  
 996 28 50.0 265 2 T28061 hypothetical prote  
 997 28 50.0 266 2 D95373 TRM17a probable tr  
 998 28 50.0 267 2 AH1077 PTS system, fructo  
 999 28 50.0 267 2 AG1435 conserved hypothet  
 1000 28 50.0 274 2 H95101

## ALIGNMENTS

RESULT 1  
 G38740  
 IG kappa chain V region (Py69) - mouse  
 C:Species: Mus musculus (house mouse)  
 C>Date: 18-Oct-1991 #sequence\_revision 18-Oct-1991 #text\_change 09-Jul-2004  
 C:Accession: G38740  
 R:Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.  
 J. Biol. Chem. 266, 6607-6613, 1991  
 A:Title: Heavy and light chain variable region sequences and antibody properties of anti  
 A:Reference number: A38740; MUID:91177923; PMID:1706720  
 A:Accession: G38740  
 A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra  
 A:Molecule type: mRNA  
 A:Residues: 1-111 <RUF>  
 A:Cross-references: UNIPROT:Q91WS9; UNIPARC:UPI0000176CDA  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:19-93/Domain: immunoglobulin homology <IMM>

Query Match 85.7%; Score 48; DB 2; Length 111;  
 Best Local Similarity 100.0%; Pred. No. 0.13;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 QYSKLPWT 9  
 Db 93 QYSKLPWT 100  
 RESULT 2  
 E38740  
 IG kappa chain V region (Py54) - mouse  
 C:Species: Mus musculus (house mouse)  
 C>Date: 18-Oct-1991 #sequence\_revision 18-Oct-1991 #text\_change 09-Jul-2004  
 C:Accession: E38740  
 R:Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.  
 J. Biol. Chem. 266, 6607-6613, 1991  
 A:Title: Heavy and light chain variable region sequences and antibody properties of anti  
 A:Reference number: A38740; MUID:91177923; PMID:1706720  
 A:Accession: E38740  
 A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra  
 A:Molecule type: mRNA  
 A:Residues: 1-111 <RUF>  
 A:Cross-references: UNIPROT:Q91WS9; UNIPARC:UPI0000176CDB  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:19-93/Domain: immunoglobulin homology <IMM>

Query Match 85.7%; Score 48; DB 2; Length 111;  
 Best Local Similarity 100.0%; Pred. No. 0.13;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 QYSKLPWT 9  
 Db 93 QYSKLPWT 100  
 RESULT 3  
 A38740  
 IG kappa chain V region (Py20) - mouse  
 C:Species: Mus musculus (house mouse)  
 C>Date: 18-Oct-1991 #sequence\_revision 18-Oct-1991 #text\_change 09-Jul-2004  
 C:Accession: A38740  
 R:Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.  
 J. Biol. Chem. 266, 6607-6613, 1991  
 A:Title: Heavy and light chain variable region sequences and antibody properties of anti  
 A:Reference number: A38740; MUID:91177923; PMID:1706720  
 A:Accession: A38740  
 A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra  
 A:Molecule type: mRNA  
 A:Residues: 1-111 <RUF>  
 A:Cross-references: UNIPROT:Q91WS9; UNIPARC:UPI0000176CD9  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:19-93/Domain: immunoglobulin homology <IMM>

Query Match 80.4%; Score 45; DB 2; Length 111;  
 Best Local Similarity 87.5%; Pred. No. 0.46;  
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 QYSKLPWT 9  
 Db 93 QYSKLPWT 100  
 RESULT 4  
 C38740  
 IG kappa chain V region (Py2) - mouse  
 C:Species: Mus musculus (house mouse)  
 C>Date: 18-Oct-1991 #sequence\_revision 18-Oct-1991 #text\_change 09-Jul-2004  
 C:Accession: C38740  
 R:Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.  
 J. Biol. Chem. 266, 6607-6613, 1991  
 A:Title: Heavy and light chain variable region sequences and antibody properties of anti  
 A:Reference number: A38740; MUID:91177923; PMID:1706720  
 A:Accession: C38740  
 A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra  
 A:Molecule type: mRNA  
 A:Residues: 1-111 <RUF>  
 A:Cross-references: UNIPROT:Q91WS9; UNIPARC:UPI0000176CDB  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:19-93/Domain: immunoglobulin homology <IMM>

Query Match 80.4%; Score 45; DB 2; Length 111;  
 Best Local Similarity 87.5%; Pred. No. 0.46;  
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 QYSKLPWT 9  
 Db 93 QYSKLPWT 100  
 RESULT 5  
 A47159  
 Ig lambda chain V region (CEA-specific maird T84.66) - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C>Date: 21-Sep-1993 #sequence\_revision 18-Nov-1994 #text\_change 21-Jan-2000  
 C:Accession: A47159  
 R:Gaída, F.J.; Pieper, D.; Roder, U.W.; Shively, J.E.; Wagener, C.; Neumaier, M.

J. Biol. Chem. 268, 14138-14145, 1993  
 A:Title: Molecular characterization of a cloned idiotypic cascade containing a network a  
 A:Reference number: A47159; MUID:93300804; PMID:7686150  
 A:Accession: A47159  
 A:Status: preliminary  
 A:Molecule type: DNA; protein  
 A:Residues: 1-128 <GAI>  
 A:Cross-references: UNIPARC:UPI00001767A5  
 A:Experimental source: hybridoma 6G6.C4  
 A:Note: sequence extracted from NCBI backbone (NCBIN:134419, NCBIP:134420)  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:36-110/Domain: immunoglobulin homology <IMM>

Query Match 75.0%; Score 42; DB 2; Length 128;  
 Best Local Similarity 66.7%; Pred. No. 1.8;  
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 HOYSKLPWT 9  
 |||||  
 Db 109 HQYDNPWT 117  
 |||||

RESULT 6  
 A49134  
 Ig kappa chain V-1 region (ISE) - human (fragment)  
 C:Species: Homo sapiens (man)  
 C:Date: 19-Dec-1993 #sequence\_revision 18-Nov-1994 #text\_change 21-Jan-2000  
 C:Accession: A49134; S25115  
 R:Rocca, A.; Khamlichi, A.A.; Aucouturier, P.; Noel, L.H.; Denoroy, L.; Preud'homme, J.L  
 Clin. Exp. Immunol. 91, 505-509, 1993  
 A:Title: Primary structure of a variable region of the V kappa I subgroup (ISE) in light  
 A:Reference number: A49134; MUID:93185310; PMID:7680298  
 A:Accession: A49134  
 A:Status: preliminary  
 A:Molecule type: mRNA; protein  
 A:Residues: 1-141 <ROC>  
 A:Cross-references: UNIPARC:UPI0000116098; EMBL:X67322; NID:G33268; PIDN:CAA47736.1; PID  
 A:Note: sequence extracted from NCBI backbone (NCBIP:127088)  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:38-112/Domain: immunoglobulin homology <IMM>

Query Match 75.0%; Score 42; DB 2; Length 141;  
 Best Local Similarity 66.7%; Pred. No. 2;  
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 HOYSKLPWT 9  
 |||||  
 Db 111 HQYDSYPWT 119  
 |||||

RESULT 7  
 K1HUWE  
 Ig kappa chain V-1 region (WEA) - human  
 C:Species: Homo sapiens (man)  
 C:Date: 03-Aug-1984 #sequence\_revision 03-Aug-1984 #text\_change 09-Jul-2004  
 C:Accession: A01876  
 R:Goni, F.; Frangione, B.  
 Proc. Natl. Acad. Sci. U.S.A. 80, 4837-4841, 1983  
 A:Title: Amino acid sequence of the Fv region of a human monoclonal IgM (protein WEA) wi  
 A:Reference number: A93964; MUID:83273707; PMID:6410398  
 A:Accession: A01876  
 A:Molecule type: protein  
 A:Residues: 1-108 <GON>  
 A:Cross-references: UNIPROT:P01610; UNIPARC:UPI000012E14C  
 A:Comment: This chain was obtained from a monoclonal antibody against 3,4-pyruvylated ga  
 C:Genetics:  
 A:Gene: GDB:ICKV1  
 A:Cross-references: GDB:I36264  
 A:Map position: 2p12-2p12  
 C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap  
 hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la

C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer  
 F:16-90/Domain: immunoglobulin homology <IMM>  
 F:23-88/Disulfide bonds: #status predicted

Query Match 69.6%; Score 39; DB 1; Length 108;  
 Best Local Similarity 75.0%; Pred. No. 5.4;  
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QYSKLPWT 9  
 |||||  
 Db 90 QYSSFPWT 97  
 |||||

RESULT 8  
 AF2204  
 beta-carotene ketolase [imported] - Nostoc sp. (strain PCC 7120)  
 C:Species: Nostoc sp. PCC 7120  
 A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120  
 C:Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 09-Jul-2004  
 C:Accession: AF2204  
 R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi  
 Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, E  
 DNA Res. 8, 205-213, 2001  
 A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium An  
 A:Reference number: AB1807; MUID:21595285; PMID:11759840  
 A:Accession: AF2204  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-258 <KUR>  
 A:Cross-references: UNIPROT:O8YSA0; UNIPARC:UPI00000CE6D5; GB:BA000019; PIDN:BA074888.1;  
 A:Experimental source: strain PCC 7120  
 C:Genetics:  
 A:Gene: alr3189  
 C:Superfamily: beta-carotene ketolase

Query Match 69.6%; Score 39; DB 2; Length 258;  
 Best Local Similarity 62.5%; Pred. No. 13;  
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYSKLPW 8  
 |||||  
 Db 240 HEYPQLPW 247  
 |||||

RESULT 9  
 T36237  
 probable phosphotransferase - Streptomyces coelicolor  
 C:Species: Streptomyces coelicolor  
 C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004  
 C:Accession: T36237  
 R:Oliver, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.  
 submitted to the EMBL Data Library, March 1999  
 A:Reference number: Z21577  
 A:Accession: T36237  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-288 <OLI>  
 A:Cross-references: UNIPROT:O9X8F0; UNIPARC:UPI00000DAF93; EMBL:AL049573; PIDN:CAB40335.  
 A:Experimental source: strain A3(2)  
 C:Genetics:  
 A:Gene: SC08DB:SCE39.27c

Query Match 67.9%; Score 38; DB 2; Length 288;  
 Best Local Similarity 75.0%; Pred. No. 23;  
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 HOYSKLPW 8  
 |||||  
 Db 256 HVYSDLPW 263  
 |||||

RESULT 10



T33701  
Lipoate-protein ligase A - fission yeast (Schizosaccharomyces pombe)  
C:Species: Schizosaccharomyces pombe  
C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004  
C:Accession: T33701  
R:Wood, V.; Skelton, J.; Churcher, C.M.; Rajandream, M.A.; Barrell, B.G.  
submitted to the EMBL Data Library, July 1999  
Reference number: Z21870  
A:Accession: T33701  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-363 <WO>  
A:Cross-references: UNIPROT:O13629; UNIPARC:UPI000006A57A; EMBL:AL109652; PIDN:CAB51768.  
A:Experimental source: strain 972h-; cosmid c17A3  
C:Genetics:  
A:Gene: p1038  
A:Map position: 2

Query Match 67.9%; Score 38; DB 2; Length 363;  
Best Local Similarity 55.6%; Pred. No. 29;  
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 HOYSKLPWT 9  
|:|:|  
Db 322 HELSSIPWT 330

RESULT 11  
C39768  
cholinesterase (EC 3.1.1.8) - rabbit  
N:Alternate names: butyrylcholinesterase  
C:Species: Oryctolagus cuniculus (domestic rabbit)  
C:Date: 14-Feb-1992 #sequence\_revision 01-Mar-1996 #text\_change 09-Jul-2004  
C:Accession: S10255; C39768  
R:Jbilo, O.; Chatonnet, A.  
Nucleic Acids Res. 18, 3990, 1990  
A:Title: Complete sequence of rabbit butyrylcholinesterase.  
A:Reference number: S10255; MUID:90326526; PMID:2374720  
A:Accession: S10255  
A:Status: translation not shown  
A:Molecule type: DNA  
A:Residues: 1-581 <JBI>  
A:Cross-references: UNIPROT:P21927; UNIPARC:UPI0000127869; EMBL:X52090; NID:g1476; PIDN:  
R:Arpagaus, M.; Chatonnet, A.; Masson, P.; Newton, M.; Vaughan, T.A.; Bartels, C.F.; Nog  
J. Biol. Chem. 266, 6966-6974, 1991  
A:Title: Use of the polymerase chain reaction for homology probing of butyrylcholinester  
A:Reference number: C39768; MUID:91201348; PMID:2016308  
A:Accession: C39768  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 75-215 <ARP>  
A:Cross-references: UNIPARC:UPI000016C540; GB:M62779; NID:g164788; PIDN:AAA31169.1; PID:  
C:Genetics:  
A:Introns: 485/2; 541/1  
C:Superfamily: cholinesterase; cholinesterase homology  
C:Keywords: carboxylic ester hydrolase; glycoprotein  
F:35-535/Domain: cholinesterase homology <CHE>

Query Match 67.9%; Score 38; DB 2; Length 581;  
Best Local Similarity 75.0%; Pred. No. 47;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYSKLPW 8  
|:|:|  
Db 430 HRSSKLPW 437

RESULT 12  
ACHU  
cholinesterase (EC 3.1.1.8) precursor [validated] - human  
N:Alternate names: acylcholine acylhydrolase; butyrylcholinesterase; choline esterase II  
C:Species: Homo sapiens (man)  
C:Date: 30-Jun-1987 #sequence\_revision 23-Feb-1996 #text\_change 09-Jul-2004

C:Accession: A33769; A26613; A33887; A34668; A00772  
R:Arpagaus, M.; Kott, M.; Vatsis, K.P.; Bartels, C.F.; La Du, B.N.; Lockridge, O.  
Biochemistry 29, 124-131, 1990  
A:Title: Structure of the gene for human butyrylcholinesterase. Evidence for a single co  
A:Reference number: A33769; MUID:90212557; PMID:2322535  
A:Accession: A33769  
A:Molecule type: DNA  
A:Residues: 'MSVQSNLQAGAAACISPKYMIPTPCKLHLCRESEIN', 1-602 <ARP>  
A:Cross-references: UNIPROT:P06276; UNIPARC:UPI0000172799; GB:M32391; GB:J02879  
A:Note: two ATG codons found upstream of Met-1 do not lie in a favorable context for tra  
R:Prody, C.A.; Zevin-Sonkin, D.; Gnatt, A.; Goldberg, O.; Soreq, H.  
Proc. Natl. Acad. Sci. U.S.A. 84, 3555-3559, 1987  
A:Title: Isolation and characterization of full-length cDNA clones coding for cholineste  
A:Reference number: A26613; MUID:87231856; PMID:3035536  
A:Accession: A26613  
A:Molecule type: mRNA  
A:Residues: 1-133,'D', 135-602 <PRO>  
A:Cross-references: UNIPARC:UPI000017279A  
R:McIlernan, C.; Adkins, S.; Chatonnet, A.; Vaughan, T.A.; Bartels, C.F.; Kott, M.; Rose  
Proc. Natl. Acad. Sci. U.S.A. 84, 6682-6686, 1987  
A:Title: Brain cDNA clone for human cholinesterase.  
A:Reference number: A33887; MUID:88016155; PMID:3477799  
A:Accession: A33887  
A:Molecule type: mRNA  
A:Residues: 'MSVQSNLQAGAAACISPKYMIPTPCKLHLCRESEIN', 1-602 <MCT>  
A:Cross-references: UNIPARC:UPI000017279B  
A:Note: two ATG codons found upstream of Met-1 do not lie in a favorable context for tra  
R:Nogueira, C.P.; McGuire, M.C.; Graesser, C.; Bartels, C.F.; Arpagaus, M.; Van der Spek,  
Am. J. Hum. Genet. 46, 934-942, 1990  
A:Title: Identification of a frameshift mutation responsible for the silent phenotype of  
A:Reference number: A34668; MUID:90252779; PMID:2339692  
A:Accession: A34668  
A:Molecule type: DNA  
A:Residues: 143-145,'VSNWNIITCL' <NOG>  
A:Cross-references: UNIPARC:UPI000017279C  
A:Note: frameshift mutant in codon for residue 145 (Gly)  
R:Lockridge, O.; Bartels, C.F.; Vaughan, T.A.; Wong, C.K.; Norton, S.E.; Johnson, L.L.  
J. Biol. Chem. 262, 549-557, 1987  
A:Title: Complete amino acid sequence of human serum cholinesterase.  
A:Reference number: A00772; MUID:87109144; PMID:3542989  
A:Accession: A00772  
A:Molecule type: protein  
A:Residues: 29-602 <LOC>  
A:Cross-references: UNIPARC:UPI000004B875  
A:Experimental source: plasma  
C:Comment: Cholinesterase is present in most cells (except erythrocytes).  
C:Genetics:  
A:Gene: GDB:BCHE; CHE1  
A:Cross-references: GDB:120558; OMIM:177400  
A:Map position: 3q26.1-3q26.2  
A:Introns: 506/2; 562/1  
C:Function:  
A:Description: hydrolyzes acylcholines to choline and a carboxylic acid  
A:Note: this cholinesterase is highly reactive with organophosphate esters  
C:Superfamily: cholinesterase; cholinesterase homology  
C:Keywords: carboxylic ester hydrolase; glycoprotein; homotetramer  
F:1-28/Domain: signal sequence #status predicted <SIG>  
F:29-602/Product: cholinesterase #status experimental <MAT>  
F:56-556/Domain: cholinesterase homology <CHE>  
F:45,85,134,269,284,369,483,509,514/Binding site: carbohydrate (Asn) (covalent) #status  
F:226/Active site: Ser #status experimental

Query Match 67.9%; Score 38; DB 1; Length 602;  
Best Local Similarity 75.0%; Pred. No. 49;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYSKLPW 8  
|:|:|  
Db 451 HRSSKLPW 458

RESULT 13  
S70849



```

cholinesterase (EC 3.1.1.8) - mouse
N;Alternate names: butyrylcholine esterase
C;Species: Mus musculus (house mouse)
C;Date: 28-Oct-1996 #sequence_revision 08-Nov-1996 #text_change 09-Jul-2004
C;Accession: S70849; S15680; A39768
R;Taylor, P.
submitted to the EMBL Data Library, August 1992
A;Reference number: S70849
A;Accession: S70849
A;Molecule type: nucleic acid
A;Residues: 1-603 <TAY>
A;Cross-references: UNIPROT:Q03311; UNIPARC:UPI0000029829; EMBL:M99492; NID:g191579; PID:
R;Rachinsky, T.L.; Camp, S.; Li, Y.; Ekstroem, T.J.; Newton, M.; Taylor, P.
Neuron 5, 317-327, 1990
A;Title: Molecular cloning of mouse acetylcholinesterase: tissue distribution of alterna
A;Reference number: JH0314; MUID:90380429; PMID:2400605
A;Accession: S15680
A;Status: nucleic acid sequence not shown
A;Molecule type: nucleic acid
A;Residues: 30-128, P',130-603 <RAC>
A;Cross-references: UNIPARC:UPI00001758EE; EMBL:M99492
R;Arpagaus, M.; Chatonnet, A.; Masson, P.; Newton, M.; Vaughan, T.A.; Bartels, C.F.; Nog
J. Biol. Chem. 266, 6966-6974, 1991
A;Title: Use of the polymerase chain reaction for homology probing of butyrylcholinester
A;Reference number: A39768; MUID:91201348; PMID:2016308
A;Accession: A39768
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 97-128, 'P',130-237 <RAP>
A;Cross-references: UNIPARC:UPI00001758EF
C;Superfamily: cholinesterase; cholinesterase homology
C;Keywords: carboxylic ester hydrolase; glycoprotein
F:57-57/Domain: cholinesterase homology <CHE>

Query Match 67.9%; Score 38; DB 2; Length 603;
Best Local Similarity 75.0%; Pred. No. 49;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYSKLPW 8
|: |||||
Db 452 HRSSKLPW 459

RESULT 14
RMXRR3
mRNA guanylyltransferase (EC 2.7.7.50) - reovirus type 3
N;Alternate names: lambda 2 protein; mRNA capping enzyme
C;Species: reovirus type 3
A;Note: host Homo sapiens (man)
C;Accession: A28471
R;Seliger, L.S.; Zheng, K.; Shatkin, A.J.
J. Biol. Chem. 262, 16289-16293, 1987
A;Title: Complete nucleotide sequence of reovirus L2 gene and deduced amino acid sequenc
A;Reference number: A28471; MUID:88058999; PMID:2824487
A;Accession: A28471
A;Molecule type: DNA
A;Residues: 1-1289 <SEL>
A;Cross-references: UNIPROT:P11079; UNIPARC:UPI0000111321
C;Genetics:
A;Map position: segment L2
C;Superfamily: reovirus mRNA guanylyltransferase
C;Keywords: core protein; mRNA capping; nucleotidyltransferase; transcription

Query Match 67.9%; Score 38; DB 1; Length 1289;
Best Local Similarity 66.7%; Pred. No. 11e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HOYSKLPWT 9
|: |||||
Db 659 HQHSSLTWT 667

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RESULT 15
KHUUAU
Ig kappa chain V-I region (Au) - human
C;Species: Homo sapiens (man)
C;Date: 24-Apr-1984 #sequence_revision 02-Jul-1998 #text_change 09-Jul-2004
C;Accession: A91653; A01862; S02573
R;Schiechl, H.; Hilsechmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 353, 345-370, 1972
A;Title: Die Primaerstruktur einer monoklonalen Immunglobulin-L-Kette vom kappa-Typ, Su
A;Reference number: A91653; MUID:72189444; PMID:5028201
A;Accession: A91653
A;Molecule type: protein
A;Residues: 1-108 <SCH>
A;Cross-references: UNIPROT:P01594; UNIPARC:UPI000012E13E
A;Note: the C region of this chain has the Inv (3) marker
R;Fehlhammer, H.; Schiffer, M.; Epp, O.; Colman, P.M.; Lattman, E.E.; Schwager, P.; Stei
Biophys. Struct. Mech. 1, 139-146, 1975
A;Title: The structure determination of the variable portion of the Bence-Jones protein
A;Reference number: A90729; MUID:77022433; PMID:1234024
A;Contents: annotation; X-ray crystallography
A;Note: the structure of the V region was determined by molecular replacement methods u
R;Steiner, V.; Chang, J.Y.
FEBS Lett. 222, 6-10, 1987
A;Title: Chemical modification of the carboxyl groups of protein substrates enhances the
A;Reference number: S02572; MUID:88005152; PMID:3115831
A;Contents: annotation
C;Comment: This is a Bence Jones protein.
C;Genetics:
A;Gene: GDB:IGKV1
A;Cross-references: GDB:136264
A;Map position: 2p12-2p12
C;Complex: an immunoglobulin heterotetramer subunit consists of two identical light (k)
chain disulfide bonds; in some cases, such as IgA and IgM, the subunits associate into 1:
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>
F:23-88/Disulfide bonds: #status predicted

Query Match 66.1%; Score 37; DB 1; Length 108;
Best Local Similarity 75.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QYSKLPWT 9
|: |||||
Db 90 QYDYLPT 97

RESULT 16
KHUUL7
Ig kappa chain precursor V-IV region (B17) - human
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 21-Jan-2000
C;Accession: A01905
R;Marsh, P.; Mills, F.; Gould, H.
Nucleic Acids Res. 13, 6531-6544, 1985
A;Title: Detection of a unique human VkapaiV germline gene by a cloned cDNA probe.
A;Reference number: A01905; MUID:86041854; PMID:2997713
A;Accession: A01905
A;Molecule type: mRNA
A;Residues: 1-134 <MAR>
A;Cross-references: UNIPARC:UPI000017370A
A;Note: the sequence was determined from the differentiated gene
A;Note: the authors translated the codon TGC for residue 76 as Trp
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (k)
chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1:
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-134/Product: Ig kappa chain V-IV region (B17) #status predicted <MAT>
F:21-43/Region: framework 1
F:36-116/Domain: immunoglobulin homology <IMM>
F:44-60/Region: complementarity-determining 1
F:61-75/Region: framework 2

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F;76-82/Region: complementarity-determining 2  
F;83-114/Region: framework 3  
F;115-121/Region: complementarity-determining 3  
F;122-134/Region: framework 4  
F;143-114/Dsulfide bonds: #status predicted

Query Match 66.1%; Score 37; DB 1; Length 134;  
Best Local Similarity 75.0%; Pred. No. 15;  
Matches 6; Conservative 0; Mismatches 2; Indels

Qy 2 QYSKLPWT 9  
Db 116 QYYNLPWT 123

## RESULT 17

A49137  
 Ig kappa chain precursor V region - human  
 C:Species: Homo sapiens (man)  
 C:Date: 19-Dec-1993 #sequence\_revision 18-Nov-1994 #text\_change 21-Jan-2000  
 C:Accession: A49137; S24479  
 R:Khamlichi, A.A.; Soutourier, P.; Silvain, C.; Bauwens, M.; Touchard, G.; Preud'homme, Clin. Exp. Immunol. 87, 122-126, 1992  
 A:Title: Primary structure of a monoclonal kappa chain in myeloma with light chain deposits  
 A:Reference number: A49137; MUID:92127887; PMID:1733627  
 A:Accession: A49137  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-136 <KHA>  
 A:Cross-references: UNIPARC:UPI0000116015; GB:X64135; GB:S79324; NID:g33059; PIDN:CAA454  
 A:Note: sequence extracted from NCBI backbone (NCBIN:79324, NCBIP:79325)  
 R:Cogne, M.C.C.

Query Match 66.1%; Score 37; DB 2; Length 136;  
Best Local Similarity 75.0%; Pred. No. 16;  
Matches 6: Conservative 0; Mismatches 2; Indels

Qy 2 QYSKLPWT 9  
D**b** 116 QYSTAPWT 123

RESIT.T 18

K23001 18  
 T31291  
 hypothetical protein 1251 - Sphingomonas aromaticivorans plasmid pNL1  
 C:Species: Sphingomonas aromaticivorans  
 C:Date: 11-Jan-2000 #sequence\_revision 11-Jan-2000 #text\_change 09-Jul-2004  
 C:Accession: T31291  
 R:Romine, M.F.; Spillwell, L.C.; Wong, K.K.; Thurston, S.J.; Sisk, E.C.; Sensen, C.W.; G  
 submitted to the EMBL Data Library, July 1998  
 A:Description: Complete sequence of a 184 kb catabolic plasmid from Sphingomonas aromatic  
 A:Reference number: Z20992  
 A:Accession: T31291  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-190 <ROW>  
 A:Cross-references: UNIPROT:O85999; UNIPARC:UPI000005C9FC; EMBL:AF079317; NID:G3378261;  
 C:Genetics:  
 A:Genome: plasmid pNL1  
 A:Note: orf1251

Query Match	66.1%;	Score 37;	DB 2;	Length 190;
Best Local Similarity	75.0%;	Pred. No. 22;		

	Matches	6;	Conservative	0;	Mismatches	2;	Indels	0;	Gaps	0;
Qy	1	HOYSKLEW	8							
Db	114	HQVRKLEW	121							

## RESULT 19

S47329  
OXAL protein precursor - yeast (*Saccharomyces cerevisiae*)  
N:Alternate names: PET1402 protein; protein YER154W  
C:Species: *Saccharomyces cerevisiae*  
C>Date: 02-Dec-1994 #sequence revision 02-Dec-1994 #text change 09-Jul-2004  
C/Accession: S47329; S50657; S46384; A36328; S51575; S12291  
R:Pratje, E.  
submitted to the EMBL Data Library, August 1993  
A:Reference number: S47329  
A:Accession: S47329  
A:Molecule type: DNA  
A:Residues: 1-402 <PRA>  
A:Cross-references: UNIPROT:P39952; UNIPARC:UPI0000130F59; EMBL:X74456; NID:  
R:Dietrich, F.S.  
submitted to the EMBL Data Library, December 1994  
A:Description: The sequence of *S. cerevisiae* cosmid 8229, 9115, 9132, 9981  
A:Reference number: S50657  
A:Accession: S50657  
A:Molecule type: DNA  
A:Residues: 1-402 <DIE>  
A:Cross-references: UNIPARC:UPI0000130F59; EMBL:U18917; NID:q603377; PID:q66  
R:Bonnefoy, N.; Chalvet, F.; Hamel, P.; Stonimski, P.P.; Dujardin, G.  
J. Mol. Biol. 239, 201-212, 1994  
A:Title: OXAL1, a *Saccharomyces cerevisiae* nuclear gene whose sequence is co  
A:Reference number: S46384; MUID:94254098; PMID:8196054

Query Match	Score 37;	DB 2;	Length 402;
Best Local Similarity	66.1%		
Matches	75.0%		
6: Conservative			
0: Mismatches			
2: Indels			
0: Gaps			
0: Gaps			

Qy 1 HQYSKLPW 8  
db 121 HVYSGLPW 128

## RESULT 20

T47364  
 hypothetical protein F7M19.70 - Arabidopsis thaliana  
 C:Species: Arabidopsis thaliana (mouse-ear cress)  
 C:Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 09-Jul-2004  
 C:Accession: T47364  
 R:Nyakatura, G.; Fartmann, B.; Dauner, D.; Sterr, W.; Holland, R.; Weicheelgartner, M.; Mayer, K.F.X.  
 submitted to the Protein Sequence Database, April 2000  
 A:Reference number: Z24458  
 A:Accession: T47364  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-585 <NYA>  
 A:Cross-references: UNIPROT:Q9M255; UNIPARC:UPI00000A2909; EMBL:AL1138643  
 A:Experimental source: cultivar Columbia; BAC clone F7M19  
 C:Genetics:  
 A:Map position: 3  
 A:Introns: 101/3; 233/2; 328/3; 361/2  
 A>Note: F7M19.70

Query Match 66.1%; Score 37; DB 2; Length 585;  
 Best Local Similarity 75.0%; Pred. No. 71;  
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QYSKLPWT 9  
 ||| |||  
 DB 568 QYQKPWT 575

RESULT 21  
 H71475  
 probable chlrr phosphoprotein - Chlamydia trachomatis (serotype D, strain UW3/Cx)  
 C:Species: Chlamydia trachomatis  
 C:Date: 13-Sep-1998 #sequence\_revision 13-Sep-1998 #text\_change 09-Jul-2004  
 C:Accession: H71475  
 R:Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell, Science 282, 754-759, 1998  
 A:Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trachomatis  
 A:Reference number: A71570; MUID:99000809; PMID:9784136  
 A:Accession: H71475  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-821 <ARN>  
 A:Cross-references: UNIPROT:O84749; UNIPARC:UPI00000D339A; GB:AE001346; GB:AE001273; NID  
 A:Experimental source: serotype D, strain UW-3/Cx  
 C:Genetics:  
 A:Gene: CT744

Query Match 66.1%; Score 37; DB 2; Length 821;  
 Best Local Similarity 75.0%; Pred. No. 1e+02;  
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 HOYSKLPW 8  
 ||| |||  
 DB 273 HALSKLPW 280

RESULT 22  
 C81739  
 conserved hypothetical protein TC0120 [imported] - Chlamydia muridarum (strain Nigg)  
 C:Species: Chlamydia muridarum, Chlamydia trachomatis MoPn  
 C:Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 09-Jul-2004  
 C:Accession: C81739  
 R:Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, Nucleic Acids Res. 28, 1397-1406, 2000  
 A:Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.  
 A:Reference number: A81500; MUID:20150255; PMID:10684935  
 A:Accession: C81739  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-823 <TET>  
 A:Cross-references: UNIPROT:Q9PLI0; UNIPARC:UPI00000577DC; GB:AE002279; GB:AE002160; NID

A:Experimental source: strain Nigg (MoPn)  
 C:Genetics:  
 A:Gene: TC0120

Query Match 66.1%; Score 37; DB 2; Length 823;  
 Best Local Similarity 75.0%; Pred. No. 1e+02;  
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 HOYSKLPW 8  
 ||| |||  
 DB 272 HALSKLPW 279

RESULT 23  
 A56248  
 sulfonyleurea receptor - golden hamster  
 C:Species: Mesocricetus auratus (golden hamster)  
 C:Date: 05-May-1995 #sequence\_revision 05-May-1995 #text\_change 31-Dec-2004  
 C:Accession: A56248  
 R:Aguiar-Bryan, L.; Nichols, C.G.; Wechsler, S.W.; Clement IV, J.P.; Boyd III, A.E.; G Science 268, 423-426, 1995  
 A:Title: Cloning of the beta cell high-affinity sulfonyleurea receptor: a regulator of insulin secretion  
 A:Reference number: A56248; MUID:95232532; PMID:7716547  
 A:Accession: A56248  
 A:Status: preliminary; not compared with conceptual translation  
 A:Molecule type: mRNA  
 A:Residues: 1-1582 <AGU>  
 A:Cross-references: UNIPARC:UPI000014EB40; GB:L40623  
 C:Keywords: ATP; glycoprotein; nucleotide binding; P-loop  
 F:2-1582/Product: sulfonyleurea receptor #status experimental <MAT>  
 F:696-906/Domain: ATP-binding cassette homology <ABCI>  
 F:713-720/Region: nucleotide-binding motif A (P-loop)  
 F:1362-1555/Domain: ATP-binding cassette homology <ABC2>  
 F:1379-1386/Region: nucleotide-binding motif A (P-loop)  
 F:10/Binding site: carbonylate (Asn) (covalent) #status experimental

Query Match 66.1%; Score 37; DB 2; Length 1582;  
 Best Local Similarity 62.5%; Pred. No. 2e+02;  
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYSKLPW 8  
 ||| |||  
 DB 991 HORAKLPW 998

RESULT 24  
 S18731  
 IG kappa chain V-J region (MSI-N17) - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C:Date: 19-Mar-1997 #sequence\_revision 05-Dec-1998 #text\_change 23-Jul-1999  
 C:Accession: S18731  
 R:Hirama, T.; Takeshita, S.; Yoshida, Y.; Yamagishi, H. Immunol. Lett. 27, 19-24, 1991  
 A:Title: Structure of extrachromosomal circular DNAs generated by immunoglobulin light chain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into la C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light chain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into la C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:11-85/Domain: immunoglobulin homology <IMV>  
 F:18-83/Disulfide bonds: #status predicted

Query Match 64.3%; Score 36; DB 2; Length 103;  
 Best Local Similarity 75.0%; Pred. No. 18;  
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYSKLPWT 9  
 |.|||||  
 Db 85 QHSYLPWT 92

RESULT 25  
 KMS13  
 Ig kappa chain V region (PC2413) - mouse  
 C:Species: Mus musculus (house mouse)  
 C>Date: 01-Sep-1981 #sequence\_revision 01-Sep-1981 #text\_change 09-Jul-2004  
 C:Accession: A01932  
 R:Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.  
 Nature 276, 785-790, 1978  
 A:Title: Rearrangement of genetic information may produce immunoglobulin diversity.  
 A:Reference number: A93204; MUID:79073152; PMID:103003  
 A:Accession: A01932  
 A:Molecule type: protein  
 A:Residues: 1-111 <WEI>  
 A:Cross-references: UNIPROT:P01657; UNIPARC:UPI000002A0EC  
 C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer  
 F:16-94/Domain: immunoglobulin homology <IMM>  
 F:23-92/Disulfide bonds: #status predicted

Query Match 64.3%; Score 36; DB 1; Length 111;  
 Best Local Similarity 55.6%; Pred. No. 19;  
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 HQYSKLPWT 9  
 |||:||||  
 Db 93 HQTKVPWT 101

RESULT 26  
 D96681  
 protein F1E22.2 [imported] - Arabidopsis thaliana  
 C:Species: Arabidopsis thaliana (mouse-ear cress)  
 C>Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004  
 C:Accession: D96681  
 R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, J.; Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Dewar, K.; Hansen, N.F.; Hughes, B.; Huizar, L.  
 Nature 408, 816-820, 2000  
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziani, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, K.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
 A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
 A:Reference number: A86144; MUID:21016719; PMID:11130712  
 A:Accession: D96681  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-518 <STO>  
 A:Cross-references: UNIPROT:Q9SH20; UNIPARC:UPI0000048400; GB:AE0051173; NID:96686412; PMID:11130712  
 C:Genetics:  
 A:Map position: 1  
 A:Superfamily: Escherichia coli tryptase-like proteinase degS; GLGF domain homology; tryptase

Query Match 64.3%; Score 36; DB 2; Length 518;  
 Best Local Similarity 85.7%; Pred. No. 95;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HQYSKLP 7  
 |||:||||  
 Db 387 HQYDKLP 393

RESULT 27  
 T26193

hypothetical protein W05E10.4 - Caenorhabditis elegans  
 C:Species: Caenorhabditis elegans  
 C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
 C:Accession: T26193  
 R:Mortimore, B.  
 submitted to the EMBL Data Library, July 1996  
 A:Reference number: Z20168  
 A:Accession: T26193  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-588 <WIL>  
 A:Cross-references: UNIPROT:Q23176; UNIPARC:UPI000007E829; EMBL:Z77670; PIDN:CA801250.1  
 A:Experimental source: clone W05E10  
 C:Genetics:  
 A:Gene: CESP:W05E10.4  
 A:Map position: 5  
 A:Introns: 25/3; 37/2; 71/1; 103/2; 133/1; 299/3; 329/3; 428/3; 479/3; 504/3; 523/3  
 C:Superfamily: human alpha,alpha-trehalase

Query Match 64.3%; Score 36; DB 2; Length 588;  
 Best Local Similarity 71.4%; Pred. No. 1.1e+02;  
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 QYSKLPW 8  
 :||:||||  
 Db 568 KYAKLPW 574

RESULT 28  
 PLO262  
 Ig kappa chain V region (anti-DNA, 60VK) - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C>Date: 16-Sep-1992 #sequence\_revision 16-Sep-1992 #text\_change 21-Jan-2000  
 C:Accession: PLO262  
 R:Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A.; J. Exp. Med. 171, 265-297, 1990  
 A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic hypermutation  
 A:Reference number: PLO231; MUID:90111618; PMID:2104919  
 A:Accession: PLO262  
 A:Molecule type: mRNA  
 A:Residues: 1-106 <SHL>  
 A:Cross-references: UNIPARC:UPI0000176CC2  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:1-23/Region: framework 1  
 F:16-90/Domain: immunoglobulin homology <IMM>  
 F:24-34/Region: complementarity-determining 1  
 F:35-49/Region: framework 2  
 F:50-56/Region: complementarity-determining 2  
 F:57-88/Region: framework 3  
 F:89-97/Region: complementarity-determining 3  
 F:98-106/Region: framework 4

Query Match 62.5%; Score 35; DB 2; Length 106;  
 Best Local Similarity 62.5%; Pred. No. 27;  
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 QYSKLPWT 9  
 ||:||||  
 Db 90 QVASYPWT 97

RESULT 29  
 S26336  
 Ig light chain V region - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C>Date: 19-Mar-1998 #sequence\_revision 19-Mar-1998 #text\_change 21-Jan-2000  
 C:Accession: S26336  
 R:Stark, S.E.; Caton, A.J.  
 J. Exp. Med. 174, 613-624, 1991  
 A:Title: Antibodies that are specific for a single amino acid interchange in a protein are not cross-reactive  
 A:Reference number: S26309; MUID:91341421; PMID:1908510  
 A:Accession: S26336

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A:Molecule type: mRNA
A:Residues: 1-109 <STA>
A:Cross-references: UNIPARC:UPI00001769AF; EMBL:X59201
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-95/Domain: immunoglobulin homology <IMM>

Query Match 62.5%; Score 35; DB 2; Length 109;
Best Local Similarity 55.6%; Pred. No. 28;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 HOYSKLPWT 9
   |||
   |||
Db 94 HQHYSTPWT 102

RESULT 30
S40333
IG kappa chain V-J region - human
C:Species: Homo sapiens (man)
C>Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40333
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40333
A>Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-125 <KLE>
A:Cross-references: UNIPARC:UPI0000116153; EMBL:X72443; NID:G441354; PIDN:CAA51111.1; PI
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:34-108/Domain: immunoglobulin homology <IMM>

Query Match 62.5%; Score 35; DB 2; Length 125;
Best Local Similarity 62.5%; Pred. No. 33;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 QYSKLPWT 9
   |||
   |||
Db 108 QYNSYPWT 115

RESULT 31
H69405
Hypothetical protein AF1249 - Archaeoglobus fulgidus
C:Species: Archaeoglobus fulgidus
C>Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C:Accession: H69405
R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A:Authors: Uterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.
Smith, H.O.; Woese, C.R.; Venter, J.C.
A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo
A:Reference number: A69250; MUID:98049343; PMID:9389475
A:Accession: H69405
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-140 <KLE>
A:Cross-references: UNIPROT:Q29019; UNIPARC:UPI0000056DD4; GB:AE001018; GB:AE000782; NID
C:Superfamily: Archaeoglobus fulgidus hypothetical protein AF1249

Query Match 62.5%; Score 35; DB 2; Length 140;
Best Local Similarity 66.7%; Pred. No. 37;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 HOYSKLPWT 9
   |||
   |||
Db 36 HNGIKLPWT 44

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RESULT 32
B87293
Hydrolase, probable [imported] - Caulobacter crescentus
C:Species: Caulobacter crescentus
C>Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 12-Jul-2004
C:Accession: B87293
R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.F.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A:Title: Complete Genome Sequence of Caulobacter crescentus.
A:Reference number: A87249; MUID:21173698; PMID:11259647
A:Accession: B87293
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-296 <STO>
A:Cross-references: UNIPROT:Q9AB76; UNIPARC:UPI00000C6PFE; GB:AE005673; NID:gl3421508; P
C:Genetics:
A:Gene: CC0355
C:Superfamily: tropinesterase

Query Match 62.5%; Score 35; DB 2; Length 296;
Best Local Similarity 71.4%; Pred. No. 80;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 YSKLPWT 9
   |||
   |||
Db 144 YAKAPWT 150

RESULT 33
T27004
Hypothetical protein Y486A.14 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T27004
R:Wall, M.
submitted to the EMBL Data Library, September 1999
A:Reference number: Z20297
A:Accession: T27004
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-312 <WIL>
A:Cross-references: UNIPROT:Q9U2A0; UNIPARC:UPI000017BC8E; EMBL:AL110490; NID:e1542263;
A:Experimental source: clone Y48B6A
C:Genetics:
A:Gene: CESP:Y48B6A.14
A:Introns: 132/1; 210/1; 288/3

Query Match 62.5%; Score 35; DB 2; Length 312;
Best Local Similarity 83.3%; Pred. No. 85;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 YSKLPW 8
   |||
   |||
Db 19 YSRLPW 24

RESULT 34
B83527
Hypothetical protein PA0955 [imported] - Pseudomonas aeruginosa (strain PA01)
C:Species: Pseudomonas aeruginosa
C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C:Accession: B83527
R:Stover, C.K.; Pham, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A:Reference number: A82950; MUID:20437337; PMID:10984043
A:Accession: B83527
A>Status: preliminary

```

A:Molecule type: DNA  
A:Residues: 1-318 <STO>  
A:Cross-references: UNIPROT:Q9I503; UNIPARC:UPI00000C51DB; GB:AE004529; GB:AE004091; NID  
A:Experimental source: strain PA01  
C:Genetics:  
A:Gene: PA0955

Query Match 62.5%; Score 35; DB 2; Length 318;  
Best Local Similarity 71.4%; Pred. No. 86;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYSLPW 8  
|||:|  
Db 166 EYSLPW 172

RESULT 35  
T46096  
hypothetical protein T25B15.30 - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C>Date: 04-Feb-2000 #sequence\_revision 04-Feb-2000 #text\_change 09-Jul-2004  
C:Accession: T46096  
R:Alcaraz, J.P.; Clabault, G.; Cottet, A.; Mache, R.; Mewes, H.W.; Lemcke, K.; Mayer, K.  
submitted to the Protein Sequence Database, January 2000  
A:Reference number: Z23021  
A:Accession: T46096  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-376 <ALC>  
A:Cross-references: UNIPROT:Q9FT56; UNIPARC:UPI00000A2BEC; EMBL:AL132972  
A:Experimental source: cultivar Columbia; BAC clone T25B15  
C:Genetics:  
A:Map position: 3  
A:Introns: 31/1; 51/2; 60/3; 76/2; 106/3; 163/1; 191/2; 226/3; 252/1; 274/3; 298/1; 326/  
A:Note: T25B15.30

Query Match 62.5%; Score 35; DB 2; Length 376;  
Best Local Similarity 83.3%; Pred. No. 1e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 YSKLPW 8  
|||:|  
Db 83 YSRLPW 88

RESULT 36  
T18945  
hypothetical protein C05C10.4 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C:Accession: T18945  
R:Matthews, P.  
submitted to the EMBL Data Library, February 1995  
A:Reference number: Z19049  
A:Accession: T18945  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-413 <WIL>  
A:Cross-references: UNIPROT:Q09451; UNIPARC:UPI0000131F24; EMBL:Z48178; PIDN:CAA88205.1;  
A:Experimental source: clone C05C10  
C:Genetics:  
A:Gene: CESP:C05C10.4  
A:Map position: 2  
A:Introns: 31/3; 96/3; 128/1; 155/3; 185/3; 255/1; 313/3; 360/3; 407/3  
C:Superfamily: mammalian acid phosphatase

Query Match 62.5%; Score 35; DB 2; Length 413;  
Best Local Similarity 83.3%; Pred. No. 1.1e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 YSKLPW 8  
|||:|  
Db 225 YAKLPW 230

RESULT 37  
A89761  
hypothetical protein [imported] - Staphylococcus aureus (strain N315)

C:Species: Staphylococcus aureus  
C>Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 09-Jul-2004  
C:Accession: A89761  
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc  
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;  
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.  
Lancet 357, 1225-1240, 2001

A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.  
A:Reference number: A89758; MUID:21311952; PMID:11418146

A:Accession: A89761  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-431 <KUR>  
A:Cross-references: UNIPROT:Q9XB68; UNIPARC:UPI00000D4731; GB:BA0000018; PID:GL3699942; P;  
A:Experimental source: strain N315  
C:Genetics:  
A:Gene: SA0024

Query Match 62.5%; Score 35; DB 2; Length 431;  
Best Local Similarity 83.3%; Pred. No. 1.2e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 YSKLPW 8  
|||:|  
Db 77 YSKVPW 82

RESULT 38  
T44138  
hypothetical protein [imported] - Staphylococcus aureus (fragment)  
C:Species: Staphylococcus aureus  
C>Date: 21-Jan-2000 #sequence\_revision 21-Jan-2000 #text\_change 09-Jul-2004  
C:Accession: T44138  
R:Rito, T.; Katayama, Y.; Hiramatsu, K.  
Antimicrob. Agents Chemother. 43, 1449-1458, 1999  
A:Title: Cloning and nucleotide sequence determination of the entire mec DNA of pre-meth  
A:Reference number: Z22733; MUID:99278010; PMID:10348769

A:Accession: T44138  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-440 <ITO>  
A:Cross-references: UNIPROT:Q9XB68; UNIPARC:UPI000017A091; EMBL:D86934; PIDN:BAA82240.1  
A:Experimental source: strain N315

Query Match 62.5%; Score 35; DB 2; Length 440;  
Best Local Similarity 83.3%; Pred. No. 1.2e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 YSKLPW 8  
|||:|  
Db 86 YSKVPW 91

RESULT 39  
T18221  
chromosome condensation regulator protein - yeast (Candida albicans)  
C:Species: Candida albicans  
C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C:Accession: T18221  
R:Barrell, B.G.; Rajandream, M.A.  
submitted to the EMBL Data Library, November 1998

A:Reference number: Z18831  
A:Accession: T18221  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-492 <BAR>  
A:Cross-references: UNIPROT:O94013; UNIPARC:UPI000006A886; EMBL:AL033396; PIDN:CAA21948.  
C:Genetics:

A;Note: Rccl-like  
C;Superfamily: pheromone response pathway component SRM1

Query Match 62.5%; Score 35; DB 2; Length 492;  
Best Local Similarity 85.7%; Pred. No. 1.4e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYSKLPW 7  
| | | | |  
DB 31 HSYSKLPW 37

RESULT 40  
JC5762  
cytokine-inducible SH2 protein 4 - human  
C;Species: Homo sapiens (man)  
C;Date: 24-Jan-1998 #sequence\_revision 13-Mar-1998 #text\_change 09-Jul-2004  
C;Accession: JC5762  
R;Masuhara, M.; Sakamoto, H.; Matsumoto, A.; Suzuki, R.; Yasukawa, H.; Mitsui, K.; Wakid  
Biochem. Biophys. Res. Commun. 239, 439-446, 1997  
A;Title: Cloning and characterization of novel CIS family genes.  
A;Reference number: JC5760; MUID:98008857; PMID:9344848  
A;Accession: JC5762  
A;Status: nucleic acid sequence not shown  
A;Molecule type: mRNA  
A;Residues: 1-535 <MAS>  
A;Cross-references: UNIPROT:O14544; UNIPARC:UPI0000135B68; DBJ:AB006968; NID:G2463524;  
C;Comment: This protein plays a role in the negative regulation of cytokine signaling by  
F;384-461/Domain: SH2 homology <SH2>

Query Match 62.5%; Score 35; DB 2; Length 535;  
Best Local Similarity 62.5%; Pred. No. 1.5e+02;  
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 HOYSKLPW 8  
| | | | |  
DB 130 HHYSPAPW 137

RESULT 41  
B83149  
probable acyl-CoA dehydrogenase PA3972 [imported] - Pseudomonas aeruginosa (strain PA01)  
C;Species: Pseudomonas aeruginosa  
C;Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 09-Jul-2004  
C;Accession: B83149  
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; B  
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,  
.; Lory, S.; Olson, M.V.  
Nature 406, 959-964, 2000  
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho  
A;Reference number: A82950; MUID:20437337; PMID:10984043  
A;Accession: B83149  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-549 <STO>  
A;Cross-references: UNIPROT:Q9HX44; UNIPARC:UPI00000C5BA9; GB:AE004815; GB:AE004091; NID  
A;Experimental source: strain PA01  
C;Genetics:  
A;Gene: PA3972

Query Match 62.5%; Score 35; DB 2; Length 549;  
Best Local Similarity 55.6%; Pred. No. 1.5e+02;  
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 HOYSKLPWT 9  
| | | | |  
DB 101 HELPSLPWT 109

RESULT 42  
B29677  
complement C9 precursor - rainbow trout (fragment)  
C;Species: Oncorhynchus mykiss (rainbow trout)

C;Date: 31-Dec-1988 #sequence\_revision 03-Oct-1995 #text\_change 21-Jul-2000  
C;Accession: B29677; A56929  
R;Stanley, K.K.; Herz, J.  
EMBO J. 6, 1951-1957, 1987  
A;Title: Topological mapping of complement component C9 by recombinant DNA techniques  
A;Reference number: A29677; MUID:88004404; PMID:2443347  
A;Accession: B29677  
A;Molecule type: mRNA  
A;Residues: 1-49, 'V', '51-63, 'A', '65-525, 'RVFLEKGNWSVGQQAARVENV' <ST2>  
A;Cross-references: UNIPARC:UPI0000177AA0; EMBL:X05474; NID:G64310; PID:G755800  
A;Note: the authors' translation is shown for residues 50 and 64; this sequence has been  
R;Tomlinson, S.; Stanley, K.K.; Esser, A.F.  
Dev. Comp. Immunol. 17, 67-76, 1993  
A;Title: Domain structure, functional activity, and polymerization of trout complement  
A;Reference number: A56929; MUID:93193801; PMID:8449252  
A;Accession: A56929  
A;Molecule type: mRNA  
A;Residues: 523-574 <TOM>  
A;Cross-references: UNIPARC:UPI0000177AA1; GB:S56372; NID:G266296; PIDN:AAB25728.1; PID  
A;Note: sequence extracted from NCBI backbone (NCBIN:127123, NCBIPI:127125)  
A;Note: authors' translation is shown for residues 523 and 558  
C;Superfamily: complement C9; EGF homology; LDL receptor ligand-binding repeat homology  
C;Keywords: complement alternate pathway; complement pathway; cytolysis; glycoprotein;  
F;17-72/Domain: thrombospondin type 1 repeat homology <THR1>  
F;79-112/Domain: LDL receptor ligand-binding repeat homology <LDL3>  
F;479-510/Domain: EGF homology <EGF>  
F;530-574/Domain: thrombospondin type 1 repeat homology <THR2>

Query Match 62.5%; Score 35; DB 2; Length 574;  
Best Local Similarity 50.0%; Pred. No. 1.6e+02;  
Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 HOYSKLPW 8  
| | | | |  
DB 167 NEYNRLPW 174

RESULT 43  
AE2062  
gamma-glutamyltranspeptidase [imported] - Nostoc sp. (strain PCC 7120)  
C;Species: Nostoc sp. PCC 7120  
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120  
C;Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 09-Jul-2004  
C;Accession: AE2062  
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguch  
Nakazaki, N.; Shimpou, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, A  
DNA Res. 8, 205-213, 2001  
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium An  
A;Reference number: AB1807; MUID:21595285; PMID:11759840  
A;Accession: AE2062  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-609 <KUR>  
A;Cross-references: UNIPROT:Q8YVC7; UNIPARC:UPI00000CE2D7; GB:BA000019; PIDN:BAB73750.1  
A;Experimental source: strain PCC 7120  
C;Genetics:  
A;Gene: alr2051  
C;Superfamily: gamma-glutamyltransferase

Query Match 62.5%; Score 35; DB 2; Length 609;  
Best Local Similarity 71.4%; Pred. No. 1.7e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYSKLPW 8  
| | | | |  
DB 163 RYGLKLPW 169

RESULT 44  
JDVLHH  
DNA-directed DNA polymerase (EC 2.7.7.7) - heron hepatitis virus  
C;Species: heron hepatitis virus, HHV  
A;Note: host Ardea cinerea (gray heron)



C>Date: 30-Sep-1989 #sequence\_revision 30-Sep-1989 #text\_change 09-Jul-2004

C:Accession: A30082

R:Sprengel, R.; Kaleta, E.F.; Will, H.

J. Virol. 62, 3832-3839, 1988

A>Title: Isolation and characterization of a hepatitis B virus endemic in herons.

A:Reference number: A93037; MUID:88333160; PMID:3418788

A:Accession: A30082

A:Molecule type: DNA

A:Residues: 1-788 <SPR>

A:Cross-references: UNIPROT:P13846; UNIPARC:UPI00001297F3; GB:M22056; NID:g325452; PIDN:

C:Superfamily: hepatitis virus DNA-directed DNA polymerase

C:Keywords: DNA biosynthesis; nucleotidyltransferase

Query Match 62.5%; Score 35; DB 1; Length 788;

Best Local Similarity 71.4%; Pred. No. 2.2e+02;

Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 QYSKLPW 8

:.:|||||

Db 725 KFSKLPW 731

RESULT 45

S28104

Probable DNA-directed RNA polymerase (EC 2.7.7.6) - gill mushroom (Agaricus bitorquis) P

C:Species: Agaricus bitorquis

C>Date: 28-May-1993 #sequence\_revision 28-May-1993 #text\_change 09-Jul-2004

C:Accession: S28104

R:Robison, M.M.; Royer, J.C.; Horgen, P.A.

Curr. Genet. 19, 495-502, 1991

A>Title: Homology between mitochondrial DNA of Agaricus bisporus and an internal portion

A:Reference number: S28103; MUID:91347410; PMID:1879001

A:Accession: S28104

A>Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-1102 <ROB>

A:Cross-references: UNIPROT:P33539; UNIPARC:UPI00001347D6; EMBL:Z11513

C:Genetics:

A:Genome: plasmid

C:Keywords: mitochondrion; nucleotidyltransferase; transcription

Query Match 62.5%; Score 35; DB 2; Length 1102;

Best Local Similarity 71.4%; Pred. No. 3.2e+02;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 YSKLPWT 9

:.:|||||

Db 665 YDKLPWS 671

RESULT 46

JC7331

gamma-glutamyltransferase (EC 2.3.2.2) homolog - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 08-Sep-2000 #sequence\_revision 08-Sep-2000 #text\_change 15-Sep-2000

C:Accession: JC7331

R:Yamaguchi, T.; Takei, N.; Araki, K.; Ishii, K.; Nagan, T.; Ichikawa, T.; Kumanishi, T

J. Biochem. 128, 101-106, 2000

A>Title: Molecular characterization of a novel gamma-glutamyl transpeptidase homologue f

A:Reference number: JC7331

A:Accession: JC7331

A:Molecule type: mRNA

A:Residues: 1-641 <YAM>

A:Cross-references: UNIPARC:UPI000017C90F; GB:AF244973

A:Experimental source: brain

C:Comment: This enzyme is a membrane-bound glycoenzyme that is involved in the metabolis

glutathione.

C:Genetics:

A:Gene: gthp

C:Keywords: aminoacyltransferase; brain; glutathione; glycolysis; membrane bound

Query Match 61.6%; Score 34.5; DB 2; Length 641;

Best Local Similarity 60.0%; Pred. No. 2.2e+02;

Matches 6; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

QY 1 HQ-YSKLPWT 9

|||:|||||

Db 222 HOLYGRLEWS 231

RESULT 47

G82775

hypothetical protein XF0690 [imported] - Xylella fastidiosa (strain 9a5c)

C:Species: Xylella fastidiosa

C>Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 09-Jul-2004

C:Accession: G82775

R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen

Nature 406, 151-157, 2000

A>Title: The genome sequence of the plant pathogen Xylella fastidiosa.

A:Reference number: A82515; MUID:20365717; PMID:10910347

A>Note: for a complete list of authors see reference number A59328 below

A:Accession: G82775

A>Status: Preliminary

A:Molecule type: DNA

A:Residues: 1-64 <SIM>

A:Cross-references: UNIPROT:Q9PFG9; UNIPARC:UPI00000C24CE; GB:AE003912; GB:AE003849; NID:

A:Experimental source: strain 9a5c

R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A

Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H

sub-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S.

submitted to GenBank, June 2000

A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm

J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigr

chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.P.; Marino, C.L.; Marques, M.V.; Martins, E

A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.

Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; de Oliveira, R.C.; Palmieri, D.A

A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir

M.; Tshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z

A:Reference number: A59328

A:Contents: annotation

C:Genetics:

A:Gene: XF0690

Query Match 60.7%; Score 34; DB 2; Length 64;

Best Local Similarity 62.5%; Pred. No. 25;

Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 HOYSKLPW 8

|||:|||||

Db 16 HYYSSRPW 23

RESULT 48

A82772

hypothetical protein Atu1593 [imported] - Agrobacterium tumefaciens (strain C58, Dupont)

C:Species: Agrobacterium tumefaciens

C>Date: 11-Jan-2002 #sequence\_revision 11-Jan-2002 #text\_change 09-Jul-2004

C:Accession: A82772

R:Wood, D.W.; Stutbal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L

erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell

; Karp, P.; Romero, P.; Zhang, S.

Science 294, 2317-2323, 2001

A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,

ster, E.W.

A>Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A:Reference number: A82577; MUID:21608550; PMID:11743193

A:Accession: A82772

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-64 <KUR>

A:Cross-references: UNIPROT:Q8UF09; UNIPARC:UPI00000D1BEE; GB:AE008688; PIDN:JAL42595.1;

A:Experimental source: strain C58 (Dupont)

C:Genetics:

A:Gene: Atu1593

A:Map position: circular chromosome



```
Query Match          60.7%; Score 34; DB 2; Length 64;
Best Local Similarity 71.4%; Pred. No. 25;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 HQYSKLP 7
      ||| | :|
Db      47 HQYKIP 53

RESULT 49
PL0261
Ig kappa chain V region (anti-DNA, DP15VK) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 09-May-1997
C:Accession: PL0261
R:Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A.
J. Exp. Med. 171, 265-297, 1990
A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic
A:Reference number: PL0231; MUID:90111618; PMID:2104919
A:Accession: PL0261
A:Molecule type: mRNA
A:Residues: 1-88 <SHL>
A:Cross-references: UNIPARC:UPI000176D7B
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-5/Region: framework 1
F:6-16/Region: complementarity-determining 1
F:17-31/Region: framework 2
F:32-38/Region: complementarity-determining 2
F:39-70/Region: framework 3
F:71-79/Region: complementarity-determining 3
F:80-88/Region: framework 4

Query Match          60.7%; Score 34; DB 2; Length 88;
Best Local Similarity 62.5%; Pred. No. 34;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      2 QYSKLPWT 9
      ||| : |||
Db      72 QYASSPWT 79

RESULT 50
SI7628
Ig kappa chain V region - mouse
C:Species: Mus musculus (house mouse)
C>Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Accession: SI7628
R:Clackson, T.; Hoogenboom, H.R.; Griffiths, A.D.; Winter, G.
Nature 352, 624-628, 1991
A:Title: Making antibody fragments using phage display libraries.
A:Reference number: SI7230; MUID:91326098; PMID:1907718
A:Accession: SI7628
A>Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-91 <CLA>
A:Cross-references: UNIPARC:UPI0001767F4
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:8-81/Domain: immunoglobulin homology <IMM>

Query Match          60.7%; Score 34; DB 2; Length 91;
Best Local Similarity 55.6%; Pred. No. 35;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      1 HQYSKLPWT 9
      ||| : |||
Db      80 HQNSYPWT 88

Search completed: April 6, 2006, 08:58:22
Job time : 17 secs
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GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: April 6, 2006, 08:55:21 ; Search time 59.7966 Seconds

(without alignments)  
106.189 Million cell updates/sec

Title: US-10-089-500-8

Perfect score: 56

Sequence: 1 HQYSKLPWT 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

Uniprot 05.80.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	44	78.6	107	Q9JL84_MOUSE	Q9JL84 mus musculus
2	43	76.8	229	Q5C491_SCHJA	Q5C491 schistosoma
3	43	76.8	770	Q9T0Y1_SCHJA	Q9T0Y1 lactobacilli
4	42	75.0	275	Q5D8M7_SCHJA	Q5D8M7 schistosoma
5	41	73.2	572	Q6BN22_DEBHA	Q6BN22 debaryomyce
6	40	71.4	623	Q8XVB0_RALSO	Q8XVB0 ralstonia s
7	39	69.6	108	Q9JL84_MOUSE	Q9JL84 mus musculus
8	39	69.6	258	Q8Y8A0_ANASP	Q8Y8A0 anabaena sp
9	39	69.6	315	Q5E4B3_VIBF1	Q5E4B3 vibrio fisc
10	39	69.6	351	Q9V8T8_DROME	Q9V8T8 drosophila
11	39	69.6	626	Q5BCZ0_EMENI	Q5BCZ0 aspergillus
12	39	69.6	1080	Q4P5B6_USTMA	Q4P5B6 ustilago ma
13	39	69.6	1376	Q5CUY1_CRYPP	Q5CUY1 cryptospori
14	38	67.9	157	Q4PJG3_USTMA	Q4PJG3 ustilago ma
15	38	67.9	288	Q9X8F0_STRCO	Q9X8F0 streptomyce
16	38	67.9	336	Q7NAA3_PHOLL	Q7NAA3 photorhabd
17	38	67.9	349	Q9GKJ6_PIG	Q9GKJ6 sus scrofa
18	38	67.9	363	Q13629_SCHPO	Q13629 schizosach
19	38	67.9	386	Q6FGG0_CANGA	Q6FGG0 candida gla
20	38	67.9	389	Q89UG7_BRAJA	Q89UG7 bradyrhizob
21	38	67.9	433	Q6SV30_MANSJM	Q6SV30 mannhelmia
22	38	67.9	434	Q75B85_ASHGO	Q75B85 ashbya gos
23	38	67.9	581	CHLE_RABIT	P21927 oryctolagus
24	38	67.9	597	Q9JKC1_RAT	Q9JKC1 rattus norv
25	38	67.9	602	CHLE_HUMAN	P06776 homo sapien
26	38	67.9	602	Q5R7Z4_PONPY	Q5R7Z4 pongo pygma
27	38	67.9	603	CHLE_MOUSE	Q03311 mus musculus
28	38	67.9	603	Q543J3_MOUSE	Q543J3 mus musculus
29	38	67.9	603	Q902K8_CHICK	Q902K8 gallus gall
30	38	67.9	657	Q6M124_BDEBA	Q6M124 bdellovibri
31	38	67.9	698	Q8MT38_9NEOP	Q8MT38 papilio xut

32	38	67.9	1036	2	Q6CJY8_KLJLA	Q6CJY8 kluyveromyc
33	38	67.9	1069	2	Q4P862_USTMA	Q4P862 ustilago ma
34	38	67.9	1289	1	MCE_REOVD	P11079 reovirus ty
35	38	67.9	1289	2	Q91RA1_REOVD	Q91RA1 reovirus ty
36	38	67.9	1326	2	Q5CJX7_CRYHO	Q5CJX7 cryptospori
37	37	66.1	108	1	KV1B_HUMAN	P01594 homo sapien
38	37	66.1	108	2	Q9CTV5_MOUSE	Q9CTV5 mus musculu
39	37	66.1	134	1	KV4C_HUMAN	P06314 homo sapien
40	37	66.1	134	2	Q8VDD0_MOUSE	Q8VDD0 mus musculu
41	37	66.1	190	2	Q8S999_SPHAR	Q8S999 sphingomona
42	37	66.1	242	2	Q9PU09_LATCH	Q9PU09 latimeria c
43	37	66.1	245	2	Q8UUT6_BRARE	Q8UUT6 brachydanio
44	37	66.1	330	2	Q6MQC7_BDEBA	Q6MQC7 bdellovibri
45	37	66.1	331	2	Q5AK74_CANAL	Q5AK74 candida alb
46	37	66.1	388	2	Q9FLA1_ARATH	Q9FLA1 arabidopsis
47	37	66.1	402	1	OXA1_YEAST	P39952 saccharomyc
48	37	66.1	402	2	Q46434_CHLTR	Q46434 chlamydia t
49	37	66.1	408	2	Q52011_NOCFA	Q52011 nocardia fa
50	37	66.1	444	2	Q56955_9PAPI	Q56955 human papil
51	37	66.1	517	2	Q50P46_ENTHI	Q50P46 entamoeba h
52	37	66.1	532	2	Q7QFL1_ANOGA	Q7QFL1 anopheles g
53	37	66.1	542	2	Q5OLW2_ENTHI	Q5OLW2 entamoeba h
54	37	66.1	578	2	Q5OV82_ENTHI	Q5OV82 entamoeba h
55	37	66.1	585	2	Q9M255_ARATH	Q9M255 arabidopela
56	37	66.1	586	2	Q5OPH5_ENTHI	Q5OPH5 entamoeba h
57	37	66.1	683	2	Q922P1_MOUSE	Q922P1 mus musculu
58	37	66.1	755	2	Q8KBB5_CHLTE	Q8KBB5 chlorobium
59	37	66.1	810	2	Q655L5_ORYSA	Q655L5 oryza sativ
60	37	66.1	821	2	Q84749_CHLTR	Q84749 chlamydia t
61	37	66.1	823	2	Q9PLI0_CHLMU	Q9PLI0 chlamydia m
62	37	66.1	893	2	Q4WYB5_ASFPFU	Q4WYB5 aspergillus
63	37	66.1	909	2	Q6FGE3_MOUSE	Q6FGE3 mus musculu
64	37	66.1	965	2	Q8AIW2_BACTN	Q8AIW2 bacteroides
65	37	66.1	1087	2	Q8BNE2_MOUSE	Q8BNE2 mus musculu
66	37	66.1	1122	2	Q7F2F8_ORYSA	Q7F2F8 oryza sativ
67	37	66.1	1129	2	Q8XL11_CLOPE	Q8XL11 clostridium
68	37	66.1	1138	2	Q672G3_TSNVS	Q672G3 tomato spot
69	37	66.1	1141	2	Q672G6_TSNVS	Q672G6 tomato spot
70	37	66.1	1556	2	Q70X90_RAT	Q70X90 rattus norv
71	37	66.1	1575	2	Q70X89_RAT	Q70X89 rattus norv
72	37	66.1	1581	1	ABCC8_CRICR	Q09427 cricetus cr
73	37	66.1	1581	1	ABCC8_RAT	Q09429 rattus norv
74	37	66.1	2367	2	Q7X970_ORYSA	Q7X970 oryza sativ
75	37	66.1	16223	2	Q8IR22_DROME	Q8IR22 drosophila
76	36.5	65.2	298	2	Q4T4V7_TETNG	Q4T4V7 tetraodon n
77	36.5	65.2	338	2	Q6MKH4_BDEBA	Q6MKH4 bdellovibri
78	36.5	65.2	358	2	Q53B83_NEROL	Q53B83 nerium olea
79	36.5	65.2	535	2	Q4SJB8_TETNG	Q4SJB8 tetraodon n
80	36.5	65.2	536	2	Q7Q0N5_ANOGA	Q7Q0N5 anopheles g
81	36	64.3	29	2	Q4YM09_PLABE	Q4YM09 plasmodium
82	36	64.3	86	2	Q5KXR3_GBOKA	Q5KXR3 geobacillus
83	36	64.3	95	2	Q864R3_CANFA	Q864R3 canis famli
84	36	64.3	111	1	KV3E_MOUSE	P01657 mus musculu
85	36	64.3	121	2	Q6ZU99_HUMAN	Q6ZU99 homo sapien
86	36	64.3	124	2	Q841T1_STRTR	Q841T1 streptococc
87	36	64.3	124	2	Q9S4L2_STRSL	Q9S4L2 streptococc
88	36	64.3	124	2	Q5M1D3_STRT1	Q5M1D3 streptococc
89	36	64.3	124	2	Q5M5W9_STRT2	Q5M5W9 streptococc
90	36	64.3	137	2	Q7NLX3_GLOVI	Q7NLX3 gloeobacter
91	36	64.3	140	2	Q48404_KLEOX	Q48404 klebsiella
92	36	64.3	143	2	Q722A0_LISMP	Q722A0 listeria mo
93	36	64.3	145	2	Q6RYT3_LEISHA	Q6RYT3 leishmania
94	36	64.3	149	2	Q6G380_BAHE	Q6G380 bartonella
95	36	64.3	158	2	Q6BZ44_DBBHA	Q6BZ44 debaryomyce
96	36	64.3	186	2	Q5FMJ1_LACAC	Q5FMJ1 lactobacilli
97	36	64.3	190	2	Q88CZ5_PSEPK	Q88CZ5 pseudomonas
98	36	64.3	193	2	Q8VAJ0_WSSV	Q8VAJ0 white spot
99	36	64.3	198	2	Q5GV81_XANOR	Q5GV81 xanthomonas
100	36	64.3	198	2	Q4UPT1_XANCP	Q4UPT1 xanthomonas
101	36	64.3	198	2	Q8P481_XANCP	Q8P481 xanthomonas
102	36	64.3	198	2	Q8PFT8_XANAC	Q8PFT8 xanthomonas
103	36	64.3	256	2	Q7RWY3_NEUCR	Q7RWY3 neurospora
104	36	64.3	276	2	Q7MD65_VIBVY	Q7MD65 vibrio vuln

105	36	64.3	317	2	Q4KH99_PSEF5	Q4kh99_pseudomonas	178	35	62.5	339	2	Q6H009_PREDI	Q6h009_fremyella d
106	36	64.3	332	2	Q8THB7_METAC	Q8thb7_methanosarc	179	35	62.5	348	2	Q5XI39_RAT	Q5xi39_rattus norv
107	36	64.3	337	2	Q4HZA8_GIBZE	Q4hza8_gibberella	180	35	62.5	376	2	Q9FRK9_HUMAN	Q9frk9_homo sapien
108	36	64.3	349	2	Q4QDP2_LEIMA	Q4qdp2_leishmania	181	35	62.5	376	2	Q9FT36_ARATH	Q9ft36_arabidopsis
109	36	64.3	362	2	Q6IZD9_SOYBN	Q6izd9_glycine max	182	35	62.5	390	2	Q9IES1_9PAPI	Q9ies1_cottontail
110	36	64.3	363	1	PYRD_CORDI	Q6nh79_corynebacte	183	35	62.5	399	2	Q7MPY8_VIBVY	Q7mpy8_vibrio vuln
111	36	64.3	387	2	Q5PBA0_SOYBN	Q5fba0_glycine max	184	35	62.5	413	1	PPAW_CABEL	Q09451_caenorhabdi
112	36	64.3	416	2	Q6G3Q5_BARHE	Q6g3q5_bartonella	185	35	62.5	418	2	Q6WS49_STAAU	Q6we49_staphylococ
113	36	64.3	420	2	Q7SEX3_NEUCR	Q7sex3_neurospora	186	35	62.5	418	2	Q8NYW2_STAAW	Q8nyw2_staphylococ
114	36	64.3	439	2	Q8TKM4_METAC	Q6k3x6_oryza sativ	187	35	62.5	418	2	Q8NYX1_STAAU	Q8nyx1_staphylococ
115	36	64.3	439	2	Q8TKM4_METAC	Q8tkm4_methanosarc	188	35	62.5	419	2	Q9KJCS_STAAU	Q9kjc5_staphylococ
116	36	64.3	450	2	Q04481_ARATH	Q04481_arabidopsis	189	35	62.5	420	2	Q5ZGM3_9NEOP	Q5zgm3_sesamia non
117	36	64.3	454	2	Q7NA43_PHOLL	Q7na43_photorhabdu	190	35	62.5	426	2	Q6FYK4_BAROU	Q6fyk4_bartonella
118	36	64.3	458	2	Q4EXR9_TETNG	Q4xrx9_tetradodon n	191	35	62.5	426	2	Q6GLU9_BARHE	Q6glu9_bartonella
119	36	64.3	484	2	Q5AU01_EMENI	Q5au01_aspergillus	192	35	62.5	430	2	Q8BQV4_MOUSE	Q8bqv4_mus musculu
120	36	64.3	484	2	Q4S2B8_TETNG	Q4s2b8_tetradodon n	193	35	62.5	431	2	Q5ZGM5_9NEOP	Q5zgm5_sesamia non
121	36	64.3	497	2	Q4UTU5_XANCP	Q4utu5_xanthomonas	194	35	62.5	431	2	Q9XB68_STAAU	Q9xb68_staphylococ
122	36	64.3	497	2	Q8P9U0_XANCP	Q8p9u0_xanthomonas	195	35	62.5	431	2	Q6GDA6_STAAU	Q6gd46_staphylococ
123	36	64.3	497	2	Q8PLM0_XANAC	Q8plm0_xanthomonas	196	35	62.5	431	2	Q6GK90_STAAU	Q6gk90_staphylococ
124	36	64.3	500	2	Q8TX42_METKA	Q8tx42_methanopyru	197	35	62.5	431	2	Q5HK24_STAAU	Q5hk24_staphylococ
125	36	64.3	501	2	Q5GYQ6_XANOR	Q5gyq6_xanthomonas	198	35	62.5	431	2	Q5HJX0_STAAC	Q5hjx0_staphylococ
126	36	64.3	530	2	Q9SHZ0_ARATH	Q9shz0_arabidopsis	199	35	62.5	431	2	Q7A304_STAAU	Q7a304_staphylococ
127	36	64.3	530	2	Q6NBQ2_RHOPA	Q6nbq2_rhodopseudo	200	35	62.5	431	2	Q7A8D6_STAAU	Q7a8d6_staphylococ
128	36	64.3	547	1	LNT_BDEBA	P61032_bdellovibri	201	35	62.5	433	2	Q5ZGM1_9NEOP	Q5zgm1_sesamia non
129	36	64.3	579	2	Q82HB8_STRAW	Q82hb8_streptomyce	202	35	62.5	440	2	Q5ZGM7_9NEOP	Q5zgm7_sesamia non
130	36	64.3	588	2	Q23176_CAEEL	Q23176_caenorhabdi	203	35	62.5	464	1	RCC1_CANAL	P52499_candida alb
131	36	64.3	622	1	SC6A4_DROME	P51905_drosophila	204	35	62.5	467	2	Q6A9S2_PROAC	Q6a9s2_propionibac
132	36	64.3	739	2	Q6CKC7_KJULA	Q6ckc7_kluyveromyc	205	35	62.5	480	2	Q5NRK9_ZYMMO	Q5nrk9_zymomonas m
133	36	64.3	866	2	Q7S0I0_NEUCR	Q7s0i0_neurospora	206	35	62.5	487	2	Q4I8B1_GIBZE	Q4i8b1_gibberella
134	36	64.3	1019	2	Q5SGD5_XENTR	Q5sgd5_xenopus tro	207	35	62.5	491	2	Q9HF93_CANAL	Q9hf93_candida alb
135	36	64.3	1030	2	Q9VM32_DROME	Q9vm32_drosophila	208	35	62.5	492	2	Q94013_CANAL	Q94013_candida alb
136	36	64.3	1036	2	Q8MQK6_DROME	Q8mqk6_drosophila	209	35	62.5	498	2	Q6BZ47_DBBHA	Q6bz47_debaryomyce
137	36	64.3	1041	2	Q5B5P1_EMENI	Q5b5p1_aspergillus	210	35	62.5	499	1	MATK_MACCO	Q8mex7_macrozamia
138	36	64.3	1099	2	Q9VM31_DROME	Q9vm31_drosophila	211	35	62.5	510	2	Q5K028_ORYLA	Q5k028_oryzias lat
139	36	64.3	1271	2	Q4QDS3_LEIMA	Q4qds3_leishmania	212	35	62.5	514	1	MATK_LEPPR	Q8mex8_lepidozamia
140	36	64.3	1746	2	Q4I3U5_GIBZE	Q4i3u5_gibberella	213	35	62.5	521	2	Q7XWZ4_ORYSA	Q7xwz4_oryza sativ
141	36	64.3	2101	2	Q5L196_GEOKA	Q5l196_geobacillus	214	35	62.5	521	2	Q7XWZ6_ORYSA	Q7xwz6_oryza sativ
142	36	64.3	2367	2	Q7SC21_NEUCR	Q7sc21_neurospora	215	35	62.5	528	2	Q4LLS0_9BURK	Q4lle0_burkholderi
143	35	62.5	56	2	Q4XKM0_PLACH	Q4xkm0_plasmodium	216	35	62.5	529	2	Q5SHD9_CRYNE	Q5shd9_cryptococcu
144	35	62.5	92	2	Q8M8G9_9GENT	Q8m8g9_potallia res	217	35	62.5	529	2	Q5K6X8_CRYNE	Q5k6x8_cryptococcu
145	35	62.5	93	2	Q8M8J3_9GENT	Q8m8j3_potallia ana	218	35	62.5	532	2	Q7T2B1_BRARE	Q7t2b1_brachydanio
146	35	62.5	118	2	Q87M31_VIBPA	Q87mj1_vibrio para	219	35	62.5	533	1	SOC56_MOUSE	Q91ly0_mus musculu
147	35	62.5	132	2	Q7RPS4_PLAYO	Q7rps4_plasmodium	220	35	62.5	533	2	Q8VENS_MOUSE	Q8ven5_m suppresso
148	35	62.5	140	1	Y1249_ARCFU	Q29019_archaeoglob	221	35	62.5	533	2	Q6DDY4_XENLA	Q6ddy4_xenopus lae
149	35	62.5	142	2	Q7IAD8_9NUCL	Q7iad8_mamestra co	222	35	62.5	535	1	SOC56_HUMAN	Q14544_homo sapien
150	35	62.5	142	2	Q8QM79_9NUCL	Q8qm79_mamestra co	223	35	62.5	535	2	Q8WUM3_HUMAN	Q8wum3_homo sapien
151	35	62.5	142	2	Q8QLG0_NPVMC	Q8qlg0_mamestra co	224	35	62.5	535	2	Q5RCM6_PONPY	Q5rcm6_pongo pygma
152	35	62.5	170	2	Q5XVB9_ARATH	Q5xvb9_arabidopsis	225	35	62.5	543	2	Q7MV36_PORGI	Q7mv36_porphyromon
153	35	62.5	184	2	Q7RR60_PLAYO	Q7rr60_plasmodium	226	35	62.5	549	2	Q9HX44_PSEAE	Q9hx44_pseudomonas
154	35	62.5	209	2	Q8FU06_METMA	Q8fu06_methanosarc	227	35	62.5	550	2	Q6AYG9_RAT	Q6ayg9_rattus norv
155	35	62.5	219	2	Q8TQ49_METAC	Q8tq49_methanosarc	228	35	62.5	553	2	Q7W120_BORPA	Q7w120_bordetella
156	35	62.5	219	2	Q5A595_CANAL	Q5a595_candida alb	229	35	62.5	553	2	Q7WNO9_BORBR	Q7wnq9_bordetella
157	35	62.5	234	2	Q4RM66_RAT	Q4rm66_rattus norv	230	35	62.5	567	2	Q5FTJ7_GLUOX	Q5ftj7_gluconobact
158	35	62.5	270	2	Q57UA2_9TRYP	Q57ua2_trypanosoma	231	35	62.5	572	2	Q4XZG8_PLACH	Q4xzg8_plasmodium
159	35	62.5	270	2	Q4QIF7_LEIMA	Q4qif7_leishmania	232	35	62.5	574	1	CHLE_HORSE	P81908_equus cabal
160	35	62.5	270	2	Q7SL74_ORYSA	Q7sl74_oryza sativ	233	35	62.5	574	1	C09_ONCMY	P06682_oncorhynchu
161	35	62.5	294	2	Q5M721_ARATH	Q5m721_arabidopsis	234	35	62.5	575	2	Q6AW46_MOUSE	Q6aw46_mus musculu
162	35	62.5	294	2	Q9VYU0_ARATH	Q9vyu0_arabidopsis	235	35	62.5	585	1	VMD2_HUMAN	Q76090_homo sapien
163	35	62.5	296	2	Q9AB76_CAUCR	Q9ab76_caulobacter	236	35	62.5	585	2	Q53Y09_HUMAN	Q53yv9_homo sapien
164	35	62.5	300	2	Q6S979_9VIRU	Q6s979_casava com	237	35	62.5	585	2	Q4R348_MACFA	Q4r348_macaca faec
165	35	62.5	306	2	Q31249_ACIAD	Q31249_acinetobact	238	35	62.5	589	2	Q4PDC7_USTMA	Q4pdc7_ustilago ma
166	35	62.5	314	2	Q6CIU1_YARLI	Q6ciu1_yarrowia li	239	35	62.5	593	2	Q8LI54_SYNP7	Q8lie4_synechococc
167	35	62.5	315	2	Q4IT45_AZOVI	Q4it45_azotobacter	240	35	62.5	593	2	Q5N1B9_SYNP6	Q5n1b9_oncorhynchu
168	35	62.5	318	2	Q91503_PSEAE	Q91503_pseudomonas	241	35	62.5	601	2	Q4QZ25_ONCMY	Q4qz25_oncorhynchu
169	35	62.5	324	2	Q4Q925_LEIMA	Q4q925_leishmania	242	35	62.5	602	2	Q76999_BRAFL	Q76999_branchiostel
170	35	62.5	331	2	Q72VK4_LEPIC	Q72vk4_leptospira	243	35	62.5	602	2	Q9N1N9_HORSE	Q9n1n9_equus cabal
171	35	62.5	331	2	Q8F958_LEPIN	Q8f958_leptospira	244	35	62.5	607	2	Q5TDN8_PYRKO	Q5tdn8_pyrococcus
172	35	62.5	335	2	Q4LGA2_9BURK	Q4lga2_burkholderi	245	35	62.5	609	2	Q8YVC7_ANASP	Q8yvc7_anabaena ep
173	35	62.5	336	2	Q8WZL6_YARLI	Q8wzl6_yarrowia li	246	35	62.5	644	1	K0I53_HUMAN	Q14166_homo sapien
174	35	62.5	336	2	Q4Q923_LEIMA	Q4q923_leishmania	247	35	62.5	650	2	Q4P5K1_USTMA	Q4p5k1_ustilago ma
175	35	62.5	336	2	Q07847_RALSO	Q07847_ralstonia s	248	35	62.5	670	2	Q5W270_9ENTR	Q5w270_serratia sp
176	35	62.5	336	2	Q8XVT9_RALSO	Q8xvt9_ralstonia s	249	35	62.5	725	2	Q5CCP9_PYRPY	Q5ccp9_pyruis pyrifi
177	35	62.5	338	2	Q8A1P2_BACTN	Q8a1p2_bacteroides	250	35	62.5				

251	35	62.5	736	2	Q7NNP9_GLOVI	Q7nnp9 gloebacter	324	34	60.7	360	1	MRAY_RHILQ	Q98kb0 rhizobium 1
252	35	62.5	740	2	Q6F4C9_ORYSA	Q6f4c9 oryza sativ	325	34	60.7	369	2	Q4HXD4_GIBZE	Q4hxd4 gibberella
253	35	62.5	788	1	DPOL_HPBHE	P13846 heron hepac	326	34	60.7	371	1	OMAI_SACSE	Q13375 saccharomyc
254	35	62.5	788	2	P72224_PSEPU	P72224 pseudomonas	327	34	60.7	374	2	QSAGX4_CANAL	Q59qx4 candida alb
255	35	62.5	825	2	Q6B009_BACTU	Q6b009 bacillus th	328	34	60.7	374	2	Q6B214_DEBHA	Q6b214 debaryomyce
256	35	62.5	829	2	Q6B006_BACTU	Q6b006 bacillus th	329	34	60.7	374	2	Q95Y99_CAEEL	Q95y99 caenorhabdi
257	35	62.5	835	2	Q7OTL7_GIALA	Q7otl7 giardia lam	330	34	60.7	378	2	Q9HF74_ASHGO	Q9hf74 ashbya goae
258	35	62.5	872	2	Q6CWC6_KLUJA	Q6cwc6 kluyveromyc	331	34	60.7	378	2	Q91123_PSEAE	Q91123 pseudomonas
259	35	62.5	993	2	Q7SDQ3_NEUCR	Q7sdq3 neurospora	332	34	60.7	379	2	Q8DMU9_STNEL	Q8dmu9 synecococc
260	35	62.5	999	2	Q8C761_MOUSE	Q8c761 mus musculu	333	34	60.7	381	2	Q9VQD6_DROME	Q9vqd6 drosophila
261	35	62.5	1010	2	Q4PAY9_USTMA	Q4pay9 ustilago ma	334	34	60.7	382	2	Q57522_XENLA	Q57522 xenopus lae
262	35	62.5	1102	1	RPOP_AGBT	P33539 agaricus bi	335	34	60.7	382	2	Q57459_XENLA	Q57459 xenopus lae
263	35	62.5	1233	2	Q6FOF7_CANGA	Q6fof7 candida gla	336	34	60.7	388	2	Q6BZP4_YARLI	Q6bzip4 yarrowia li
264	35	62.5	1289	2	Q91RA5_REOVL	Q91ra5 reovirus ty	337	34	60.7	405	2	Q5H910_HUMAN	Q5h910 homo sapien
265	35	62.5	1449	2	Q6S974_9VIRU	Q6s974 caseava com	338	34	60.7	406	2	Q871L4_NEUCR	Q871l4 neurospora
266	35	62.5	1672	2	Q5T4S8_HUMAN	Q5t4s8 homo sapien	339	34	60.7	418	2	Q5B4X5_EMENI	Q5b4x5 aspergillus
267	35	62.5	1678	2	Q9P2N9_HUMAN	Q9p2n9 homo sapien	340	34	60.7	426	1	SMAD7_HUMAN	Q15105 homo sapien
268	35	62.5	4243	2	Q86W11_HUMAN	Q86w11 homo sapien	341	34	60.7	426	1	SMAD7_MOUSE	Q53253 mus musculu
269	35	62.5	5183	2	Q8TDN5_HUMAN	Q8tdn5 homo sapien	342	34	60.7	426	1	SMAD7_RAT	Q88406 rattus norv
270	35	62.5	5183	2	Q5T4S7_HUMAN	Q5t4s7 homo sapien	343	34	60.7	429	2	Q55283_CRYNE	Q55283 cryptococcu
271	34.5	61.6	662	1	GGT4_MOUSE	Q99jp7 mus musculu	344	34	60.7	429	2	Q5KNJ8_CRYNE	Q5knj8 cryptococcu
272	34.5	61.6	662	1	GGT4_RAT	Q99mz4 rattus norv	345	34	60.7	429	2	P91534_CABEL	Q544x5 caenorhabdi
273	34.5	61.6	666	1	GGT4_HUMAN	Q9u1j14 h gamma-glu	346	34	60.7	431	2	Q49566_ARATH	Q49566 arabidopsie
274	34	60.7	64	2	Q8UP09_AGR75	Q8uf09 agrobacteri	347	34	60.7	433	2	Q6Z6F6_CABBR	Q6z6f6 caenorhabdi
275	34	60.7	64	2	Q9PRG9_XYLPF	Q9prg9 xyliella fas	348	34	60.7	434	2	Q4FTV8_9GNMM	Q4ftv8 psychrobact
276	34	60.7	76	2	Q816P7_BACCR	Q816p7 bacillus ce	349	34	60.7	436	1	VE2_HPV22	P50768 human papil
277	34	60.7	107	1	Y149_NPVAC	P41706 autographa	350	34	60.7	439	2	Q6CVH8_KLUJA	Q6cvh8 kluyveromyc
278	34	60.7	107	2	Q8WN55_SHEEP	Q8wny5 ovis aries	351	34	60.7	443	2	Q4KBF4_PSEF5	Q4kbf4 pseudomonas
279	34	60.7	107	2	Q8B9B4_NPVRO	Q8b9b4 rachiplusia	352	34	60.7	453	1	VRK3_MOUSE	Q8k3q5 mus musculu
280	34	60.7	108	1	KV5J_MOUSE	P01643 mus musculu	353	34	60.7	453	2	Q66HG2_RAT	Q66hc2 rattus norv
281	34	60.7	113	2	Q8CB85_MOUSE	Q8cb85 mus musculu	354	34	60.7	471	1	PRAV_CAEEL	Q09448 caenorhabdi
282	34	60.7	121	2	Q8OQU4_9BETA	Q8oqu4 cercopithe	355	34	60.7	473	1	YCLC_BACSU	P94405 bacillus su
283	34	60.7	122	2	Q8U285_PYRPU	Q8u285 pyrococcus	356	34	60.7	473	2	Q65N11_BACLD	Q65n11 bacillus li
284	34	60.7	129	2	Q8LD90_SYNEL	Q8ld90 synecococc	357	34	60.7	477	2	Q9MT81_9CONI	Q9mt81 torreya nuc
285	34	60.7	130	1	KV5G_MOUSE	P01639 mus musculu	358	34	60.7	479	2	Q5SD90_DICTDI	Q5sd90 dictyosteli
286	34	60.7	130	2	Q7O275_ANOGA	Q7o275 anopheles g	359	34	60.7	484	2	Q4PB62_UTDMA	Q4pb62 ustilago ma
287	34	60.7	131	2	Q6R9D0_MAIZE	Q6r9d0 zea mays (m	360	34	60.7	485	2	Q6MRA6_BBEBA	Q6mra6 bdellovibri
288	34	60.7	153	2	Q6ZB61_ORYSA	Q6zb61 oryza sativ	361	34	60.7	491	2	Q4WNU0_ASFFU	Q4wnu0 aspergillus
289	34	60.7	155	2	Q6WZ21_9RHIZ	Q6wz21 methylocyst	362	34	60.7	492	2	Q4AEN7_LEIFXX	Q4aen7 leifsonia x
290	34	60.7	169	2	Q6ZTP2_HUMAN	Q6ztp2 mus sapien	363	34	60.7	495	1	MATK_TORCL	Q9mrv7 torreya cal
291	34	60.7	173	2	Q6ENR2_SACOF	Q6enr2 saccharum o	364	34	60.7	495	2	Q9MSA8_9CONI	Q9msa8 torreya gra
292	34	60.7	173	2	Q6L3F1_9POAL	Q6l3f1 saccharum h	365	34	60.7	495	2	Q9MSA9_9CONI	Q9msa9 torreya far
293	34	60.7	173	2	Q36907_MAIZE	Q36907 zea mays (m	366	34	60.7	495	2	Q9MVV4_9CONI	Q9mvv4 torreya nuc
294	34	60.7	181	2	Q8CAQ3_MOUSE	Q8caq3 mus musculu	367	34	60.7	505	1	MATK_PHYPA	Q6yxn6 physcomitre
295	34	60.7	222	2	Q6EN90_ORYNI	Q6en90 oryza nivar	368	34	60.7	508	2	Q5MDR4_9CONI	Q5mdr4 torreya tax
296	34	60.7	229	2	Q847D1_NODSP	Q847d1 nodularia s	369	34	60.7	512	2	Q59RK0_CANAL	Q59rk0 candida alb
297	34	60.7	232	2	Q7XLA9_ORYSA	Q7xla9 oryza sativ	370	34	60.7	525	1	ALB32_ARATH	Q81718 arabidopsie
298	34	60.7	239	2	Q62513_ORYSA	Q6z513 oryza sativ	371	34	60.7	531	2	Q4SMX3_TRTNG	Q4smx3 tetraodon n
299	34	60.7	249	2	Q8S6H5_ORYSA	Q8s6h5 oryza sativ	372	34	60.7	544	2	Q6CQN3_KLUJA	Q6cqn3 kluyveromyc
300	34	60.7	249	2	Q37066_ORYSA	Q37066 oryza sativ	373	34	60.7	547	1	BUD9_YEAST	P53226 saccharomyc
301	34	60.7	254	2	Q4FWZ5_LEIMA	Q4fwz5 leishmania	374	34	60.7	548	2	Q4WZL8_ASFFU	Q4wzl8 aspergillus
302	34	60.7	259	2	Q6CPJ6_KLUJA	Q6cpj6 kluyveromyc	375	34	60.7	549	2	Q61QG1_CABBR	Q61qg1 caenorhabdi
303	34	60.7	260	2	Q5S1S4_PIG	Q5s1s4 sus scrofa	376	34	60.7	550	2	Q5F1M4_MVTGA	Q5f1m4 mytilus gal
304	34	60.7	260	2	Q6DUZ8_GEGJA	Q6duz8 gekko japon	377	34	60.7	551	1	COX1_MYTEB	P41774 mytilus edu
305	34	60.7	280	2	Q5O2F5_BRARE	Q5o2f5 brachydanio	378	34	60.7	551	1	VND2_MOUSE	Q88870 mus musculu
306	34	60.7	289	2	Q4WUX6_ASFFU	Q4wux6 aspergillus	379	34	60.7	554	2	Q5F0J0_MVTGA	Q5f0j0 mytilus gal
307	34	60.7	290	2	Q55UP2_CRYNE	Q55up2 cryptococcu	380	34	60.7	568	2	Q52AA0_MAGGR	Q52aa0 magnaporthe
308	34	60.7	290	2	Q5XHQ0_CRYNE	Q5xhq0 cryptococcu	381	34	60.7	568	2	Q39078_ARATH	Q39078 arabidopsie
309	34	60.7	307	2	Q6Z3P1_ORYSA	Q6z3p1 oryza sativ	382	34	60.7	572	2	Q8H0B5_RAPSA	Q8h0b5 raphanus sa
310	34	60.7	309	2	O06036_LACLC	Q06036 lactococcus	383	34	60.7	572	2	Q8VYM6_ARATH	Q8vym6 arabidopsie
311	34	60.7	309	2	Q99JA7_MOUSE	Q99ja7 mus musculu	384	34	60.7	573	2	Q7PZS8_ANOGA	Q7pzs8 anopheles g
312	34	60.7	310	2	Q61162_MOUSE	Q61162 mus musculu	385	34	60.7	573	2	Q57VD7_9TRYP	Q57vd7 trypanosoma
313	34	60.7	316	1	COAA_YERPE	Q66frr1 yersinia pe	386	34	60.7	574	2	Q65653_ARATH	Q65653 arabidopsie
314	34	60.7	316	2	Q66FR1_YERPS	Q66frr1 yersinia ps	387	34	60.7	575	2	Q84VQ6_RAPSA	Q84vq6 raphanus sa
315	34	60.7	333	2	Q8QRY0_9BETA	Q8qry0 pongine her	388	34	60.7	577	2	O56552_ARATH	O56552 arabidopsie
316	34	60.7	334	1	ALF1_XANAC	Q8phb5 xanthomonas	389	34	60.7	578	2	Q88015_ARATH	Q88015 arabidopsie
317	34	60.7	334	1	ALF1_XANCP	Q8p5z7 xanthomonas	390	34	60.7	579	2	Q58CR3_BOVIN	Q58cr3 bos taurus
318	34	60.7	334	2	Q4UY20_XANCP	Q4uy20 xanthomonas	391	34	60.7	584	2	Q50VB6_ETHNI	Q50vb6 entamoeba h
319	34	60.7	339	2	Q9YHB1_XENLA	Q9yhb1 xenopus lae	392	34	60.7	584	2	Q7W098_BORPE	Q7w098 bordetella
320	34	60.7	345	2	Q9NZ54_HUMAN	Q9nzs54 homo sapien	393	34	60.7	584	2	Q7W4P3_BORPE	Q7w4p3 bordetella
321	34	60.7	346	1	VGLM_HIV7J	P52372 human herpe	394	34	60.7	584	2	Q7WG69_BORBR	Q7wg69 bordetella
322	34	60.7	346	2	Q7Y52_9BETA	Q7y52 human herpe	395	34	60.7	596	2	Q88H30_PSEPK	Q88h30 pseudomonas
323	34	60.7	355	2	Q4NDF9_9MITC	Q4ndf9 arthrobacte	396	34	60.7	597	2	Q8ZUY6_NITEU	Q8zuy6 nitrosomona

397	34	60.7	602	1	CHLE_PELCA	062760 felis silve	470	33	58.9	134	2	Q7Q6T7	ANOGA	Q7Q6T7 anopheles g
398	34	60.7	602	1	CHLE_PANTT	062761 panthera ti	471	33	58.9	145	2	Q4FXT8	LEISHA	Q4FXT8 leishmania
399	34	60.7	608	2	Q6ATT6_ORYSA	Q6att6 oryza sativ	472	33	58.9	147	2	Q5JNN3	ORYSA	Q5JNN3 oryza sativ
400	34	60.7	622	2	Q5IYI8_MAGGR	Q5iyl8 magnaporthe	473	33	58.9	149	2	Q8JONF2	ANASP	Q8JONF2 anabaena sp
401	34	60.7	627	2	Q6A589_CABEL	Q6a589 caenorhabdi	474	33	58.9	151	2	Q5LYX1	STRIT2	Q5LYX1 streptococc
402	34	60.7	629	2	Q4W9M9_ASPFU	Q4w9m9 aspergillus	475	33	58.9	151	2	Q5M2N6	STRIT2	Q5M2N6 streptococc
403	34	60.7	632	2	Q17370_CABEL	Q17370 caenorhabdi	476	33	58.9	155	2	Q59MA3	CANAL	Q59MA3 candida alb
404	34	60.7	653	1	EXOC7_RAT	Q5a922 ratatus norv	477	33	58.9	159	1	RM23_CABER		Q61da8 caenorhabdi
405	34	60.7	655	2	Q5YNB5_NOCFA	Q5ynb5 nocardia fa	478	33	58.9	159	1	RM23_CABEL		Q9ys9 caenorhabdi
406	34	60.7	660	2	Q72T32_LEPIC	Q72t32 leptospira	479	33	58.9	164	2	Q7N4M6	PHOLL	Q7n4m6 photorhabdu
407	34	60.7	660	2	Q8CXK5_LEPIN	Q8cxk5 leptospira	480	33	58.9	165	2	Q77093	CRIFA	Q77093 crithidia f
408	34	60.7	661	2	Q91K65_ARATH	Q91k65 arabidopsis	481	33	58.9	166	2	Q6LJ07	PHOPR	Q6lj07 photobacter
409	34	60.7	671	2	Q5W253_SERMA	Q5w253 serattia ma	482	33	58.9	169	2	Q8CGR3	RAT	Q8cgr3 rattus norv
410	34	60.7	711	1	MR511_XENLA	Q9w6k1 xenopus lae	483	33	58.9	170	2	Q4X6W0	PLACH	Q4x6w0 plasmodium
411	34	60.7	716	2	Q6AQZ1_DESPS	Q6aqz1 desulfotale	484	33	58.9	176	1	ITRY_ACACO		P24924 acacia conf
412	34	60.7	721	2	Q9V3J6_DROME	Q9v3j6 drosophila	485	33	58.9	185	2	Q9Y0V9	DROME	Q9y0v9 drosophila
413	34	60.7	729	2	Q55545_SYNY3	Q55545 synecocyst	486	33	58.9	185	2	Q9W0S5	DROME	Q9w0s5 drosophila
414	34	60.7	753	2	Q6ARM0_DESPS	Q6arw0 desulfotale	487	33	58.9	197	2	Q8NBT2	HUMAN	Q8nbt2 homo sapien
415	34	60.7	777	2	Q5CUG9_CRYPV	Q5cug9 cryptospori	488	33	58.9	201	2	Q9D083	MOUSE	Q9d083 m mus muscu
416	34	60.7	781	2	Q8QAZ9_9POXV	Q8qaz9 orf virus.	489	33	58.9	208	2	Q5LCH8	BACFN	Q5lch8 bacteroides
417	34	60.7	787	2	Q6TVQ2_9POXV	Q6tvq2 orf virus.	490	33	58.9	208	2	Q64TM5	BACFN	Q64tm5 bacteroides
418	34	60.7	787	2	Q6TW32_9POXV	Q6tw32 orf virus.	491	33	58.9	218	2	Q4V5G9	DROME	Q4v5g9 drosophila
419	34	60.7	820	2	Q520Y8_MAGGR	Q520y8 magnaporthe	492	33	58.9	227	2	Q8CCC2	MOUSE	Q8ccc2 mus musculu
420	34	60.7	838	2	Q6PEZ1_MOUSE	Q6pezi mus musculu	493	33	58.9	234	2	Q8PRW0	METWA	Q8prw0 methanosarc
421	34	60.7	875	2	Q7X8Q2_CHLRE	Q7x8q2 chlamydomon	494	33	58.9	236	2	Q8KOM7	MOUSE	Q8kom7 m riken cdn
422	34	60.7	930	2	Q5BDM1_ARATH	Q5bgi8 arabidopsis	495	33	58.9	247	2	Q526W8	MAGGR	Q526w8 magnaporthe
423	34	60.7	948	2	Q5BDM1_EMENI	Q5bdl1 aspergillus	496	33	58.9	248	2	Q8TW44	METKA	Q8tw44 methanopyru
424	34	60.7	1020	2	Q96IA9_DROME	Q96ia9 drosophila	497	33	58.9	251	1	TFIS_ASPOR		Q8fgy8 aspergillus
425	34	60.7	1128	2	Q6BJI9_DEBHA	Q6bj19 debaryomyce	498	33	58.9	254	2	Q6LXZ5	METMP	Q6lxz5 methanococc
426	34	60.7	1151	2	Q9JI30_RAT	Q9ji30 rattus norv	499	33	58.9	257	2	Q7NJV4	GLOVI	Q7njv4 gloebacter
427	34	60.7	1160	2	Q7QH39_ANOGA	Q7qb39 anopheles g	500	33	58.9	262	2	Q6YK00	9SCAR	Q6yk00 lepidiota n
428	34	60.7	1167	2	Q5ZWR0_9TRYP	Q5zwr0 trypanosoma	501	33	58.9	262	2	Q4S8V3	TETNG	Q4s8v3 tetraodon n
429	34	60.7	1200	2	Q9VCW3_DROME	Q9vcw3 drosophila	502	33	58.9	263	2	Q5BG56	EMENI	Q5bg56 aspergillus
430	34	60.7	1235	2	Q517S3_ENTHI	Q517s3 entamoeba h	503	33	58.9	267	2	Q5ODT4	9DIPT	Q5odt4 chrysomya s
431	34	60.7	1251	2	Q80ZX0_MOUSE	Q80zx0 mus musculu	504	33	58.9	270	2	Q5ODV5	LUCPU	Q5odv5 lucilia cup
432	34	60.7	1289	2	Q4IRB0_GIBZE	Q4irb0 gibberella	505	33	58.9	270	2	Q5ODW3	9DIPT	Q5odw3 calliphora
433	34	60.7	1289	2	Q910I2_REOVD	Q910i2 reovirus ty	506	33	58.9	272	2	Q6XAS9	9NOCA	Q6xas9 rhodococcus
434	34	60.7	1289	2	Q91RA2_REOVD	Q91ra2 reovirus ty	507	33	58.9	273	2	Q5ODT9	CHRRU	Q5odt9 chrysomya r
435	34	60.7	1289	2	Q91RA3_REOVL	Q91ra3 reovirus ty	508	33	58.9	274	2	Q5ODU0	CHRRU	Q5odu0 chrysomya r
436	34	60.7	1289	2	Q91RA6_REOVL	Q91ra6 reovirus ty	509	33	58.9	276	2	Q5YIE1	NOCFA	Q5yiel nocardia fa
437	34	60.7	1300	2	Q8EFO4_SHEON	Q8efo4 shewanella	510	33	58.9	285	2	Q94BD2	9MAGN	Q94bd2 olax bentha
438	34	60.7	1417	2	Q10688_9VIRU	Q10688 cymbidium m	511	33	58.9	289	2	Q8Y2V3	ANASP	Q8y2v3 anabaena sp
439	34	60.7	1417	2	Q37153_9VIRU	Q37153 cymbidium m	512	33	58.9	296	2	Q5F4V2	CABEL	Q5f4v2 caenorhabdi
440	34	60.7	1417	2	Q6PF94_9VIRU	Q6pf94 cymbidium m	513	33	58.9	296	2	Q37TV6	CANFA	Q37tv6 canis famli
441	34	60.7	1417	2	Q4LEP3_9VIRU	Q4lep3 cymbidium m	514	33	58.9	299	2	Q6VVE1	HIRME	Q6vvel hirudo medi
442	34	60.7	1574	2	Q54L62_DICDI	Q54l62 dictyosteli	515	33	58.9	303	2	Q4WSST	ASPFU	Q4wsst aspergillus
443	34	60.7	1587	2	Q7Q5D1_ANOGA	Q7q5d1 anopheles g	516	33	58.9	303	2	Q4TKX0	9SPHN	Q4tkx0 erythrobaet
444	34	60.7	1754	2	Q5CGZ5_CRYHO	Q5cgz5 cryptospori	517	33	58.9	309	2	Q7Q4T6	ANOGA	Q7q4t6 anopheles g
445	34	60.7	1875	2	Q61J79_CABER	Q61j79 caenorhabdi	518	33	58.9	309	2	Q5NMB2	ZYMMO	Q5nmb2 zymomonas m
446	34	60.7	1896	2	Q4N823_THEPA	Q4n823 theileria p	519	33	58.9	311	2	Q6R4V2	9VIRU	Q6r4v2 bacterioph
447	34	60.7	2294	2	Q629G8_CABER	Q629g8 caenorhabdi	520	33	58.9	311	2	Q4YCR7	PLABE	Q4ycr7 plasmodium
448	34	60.7	8147	2	Q52V46_9ACTO	Q52v46 streptomyce	521	33	58.9	318	2	Q4Z2Z0	PSESY	Q4z2z0 pseudomonas
449	33.5	59.8	219	2	Q4KIM5_9MYRI	Q4kim5 pseudomonas	522	33	58.9	318	2	Q87VE9	PSESM	Q87ve9 pseudomonas
450	33.5	59.8	555	2	Q4KIM5_PSEFY	Q4kim5 pseudomonas	523	33	58.9	323	2	Q7RJ87	PLAYO	Q7rj87 plasmodium
451	33.5	59.8	555	2	Q89E09_PSEPK	Q89e09 pseudomonas	524	33	58.9	323	2	Q84HK1	9ACTO	Q84hk1 streptomyce
452	33.5	59.8	578	2	Q9A9J6_CAUCR	Q9a9j6 caulobacter	525	33	58.9	328	2	Q82XA3	BPBCH	Q82xa3 bacterioph
453	33.5	59.8	688	2	Q5U0F4_ANCCA	Q5u0f4 ancylostoma	526	33	58.9	334	2	Q5I152	PSEAE	Q5i152 pseudomonas
454	33.5	59.8	781	2	Q5AL46_CANAL	Q5al46 candida alb	527	33	58.9	337	1	CHLE2	BRALA	Q95003 mus musculu
455	33.5	59.8	797	2	Q4WU38_ASPFU	Q4wu38 aspergillus	528	33	58.9	341	1	PTAFR	MOUSE	Q76001 branchiosco
456	33.5	59.8	824	2	Q4PBA0_USTMA	Q4pba0 ustilago ma	529	33	58.9	341	1	PTAFR	RAT	P46002 rattus norv
457	33.5	59.8	1068	1	CABR_PASMU	Q9cqv0 pasteurella	530	33	58.9	341	2	Q7RSG8	PLAYO	Q7rs88 plasmodium
458	33.5	59.8	1075	1	CABR_HAEDU	Q7vp67 haemophilus	531	33	58.9	341	2	Q4Z4Z9	PLABE	Q4z4z9 plasmodium
459	33.5	59.8	1100	2	Q65OB7_MANSM	Q65ob7 manheimia	532	33	58.9	341	2	Q4M0H3	9BURK	Q4m0h3 burkholderi
460	33	58.9	71	2	Q5P8V7_AZOSE	Q5p8v7 azoarcus sp	533	33	58.9	342	1	PTAFR	BOVIN	Q9cty5 bos taurus
461	33	58.9	77	2	Q92Y33_RHIME	Q92y33 rhizobium m	534	33	58.9	342	1	PTAFR	CAPHI	Q9qk76 capria hircu
462	33	58.9	90	2	Q8YWA1_ANASP	Q8ywal anabaena sp	535	33	58.9	342	1	PTAFR	CAVPO	P21556 cavia porce
463	33	58.9	99	2	Q84J92_ORYSA	Q84j92 oryza sativ	536	33	58.9	342	1	PTAFR	HUMAN	P25105 homo sapien
464	33	58.9	100	2	Q4T824_TETNG	Q4t824 tetraodon n	537	33	58.9	342	1	PTAFR	PIG	Q9xsd4 sus scrofa
465	33	58.9	106	2	Q92501_NPVEM	Q92501 bombyx mori	538	33	58.9	345	2	Q6PH72	BRARE	Q6ph72 brachydanio
466	33	58.9	111	1	RL31_ENCCU	Q8esc8 encephalito	539	33	58.9	346	2	Q82YV4	PIRAE	Q82yv4 pyrobaculum
467	33	58.9	117	2	Q06697_BORBU	Q06697 borrelia bu	540	33	58.9	346	2	P71444	9UACT	P71444 lactococcus
468	33	58.9	119	2	Q9S0J8_BORBU	Q9s0j8 borrelia bu	541	33	58.9	347	2	Q66KX1	XENLA	Q66kx1 xenopus lae
469	33	58.9	129	1	KV3M_HUMAN	P18136 homo sapien	542	33	58.9	357	2	Q7UFQ8	RHOBA	Q7ufq8 rhodopirell

543	33	58.9	360	1	DVR1_XENLA	P09534 xenopus lae	616	33	58.9	566	2	Q59HB7_HUMAN	Q59hb7 homo sapien
544	33	58.9	361	2	Q519F3_XENLA	Q519f3 xenopus lae	617	33	58.9	570	2	Q8C491_MOUSE	Q8c491 mus musculu
545	33	58.9	362	2	Q5EAV2_XENLA	Q5eav2 xenopus lae	618	33	58.9	570	2	Q8R3M5_MOUSE	Q8r3m5 m lgn prot
546	33	58.9	364	2	Q5OUT8_ENTHI	Q5out8 entamoeba h	619	33	58.9	572	2	Q9WJP3_BLV	Q9wj3 bovine leuk
547	33	58.9	371	2	Q5BGG6_EMENI	Q5bgg6 aspergillus	620	33	58.9	573	2	Q4WBC9_ASPFU	Q4wbc9 aspergillus
548	33	58.9	371	1	SPL9_ARATH	Q5b9g6 arabidopsis	621	33	58.9	575	2	P91178_CABEL	P91178 caenorhabdi
549	33	58.9	377	1	CDG37_TETFL	Q70dg7 tetraodon f	622	33	58.9	578	2	Q8XSG4_RALSO	Q8xsg4 ralatonia e
550	33	58.9	379	1	PANE_YEAST	P38787 saccharomyc	623	33	58.9	584	2	Q6Z953_ORISA	Q6z953 oryza sativ
551	33	58.9	381	2	Q59NM5_CANAL	Q59nm5 candida alb	624	33	58.9	587	2	Q8CBF1_MOUSE	Q8cbf1 mus musculu
552	33	58.9	384	2	Q560F4_CRYNE	Q560f4 cryptococcu	625	33	58.9	632	2	Q4RJQ8_TETNG	Q4rjq8 tetraodon n
553	33	58.9	384	2	Q5KPF6_CRYNE	Q5kpf6 cryptococcu	626	33	58.9	646	2	Q61SW6_CAEBR	Q61sw6 caenorhabdi
554	33	58.9	387	2	Q6CPZ9_KLULA	Q6cpz9 kluyveromyc	627	33	58.9	666	2	Q5LSA8_BACFN	Q5lsa8 bacteroides
555	33	58.9	388	1	SMK1_YEAST	P41808 saccharomyc	628	33	58.9	666	2	Q6AR76_BACFR	Q6ar76 bacteroides
556	33	58.9	388	2	Q63NZ7_BURPS	Q63nz7 burkholderi	629	33	58.9	682	2	Q6M930_NEUCR	Q6m930 neurospora
557	33	58.9	391	1	GAG_BLVAV	P25058 bovine leuk	630	33	58.9	682	2	Q8BI15_MOUSE	Q8bi15 mus musculu
558	33	58.9	391	1	GAG_BLVJ	P03344 bovine leuk	631	33	58.9	686	2	Q86VL6_HUMAN	Q86vl6 homo sapien
559	33	58.9	391	2	Q5DGM0_SCHJA	Q5dgm0 schistosoma	632	33	58.9	698	2	Q605T6_METCA	Q605t6 methylococc
560	33	58.9	392	2	Q8E9V2_SHEON	Q8e9v2 shewanella	633	33	58.9	699	2	Q6YVV8_ORISA	Q6yvv8 oryza sativ
561	33	58.9	393	2	Q85490_BLV	Q85490 bovine leuk	634	33	58.9	700	2	Q54PC3_DICDI	Q54pc3 dictyosteli
562	33	58.9	395	2	Q5L1W7_GEOKA	Q5l1w7 geobacillus	635	33	58.9	712	2	Q21593_CABEL	Q21593 caenorhabdi
563	33	58.9	395	2	Q8RL19_MOUSE	Q8rl19 mus musculu	636	33	58.9	743	1	TPE3_HUMAN	Tpe3 magnaporthe
564	33	58.9	405	2	Q4SKM8_TETNG	Q4skm8 tetraodon n	637	33	58.9	747	2	Q51254_MAGGR	Q51254 magnaporthe
565	33	58.9	408	2	Q17129_9APIC	Q17129 babesia div	638	33	58.9	767	2	Q4Y6N7_PLACH	Q4y6n7 plasmodium
566	33	58.9	410	1	FBXW4_MOUSE	Q9jnj2 mus musculu	639	33	58.9	779	2	Q8YX39_ANASP	Q8yx39 anabaena sp
567	33	58.9	411	2	Q8UB97_AGR75	Q8ub97 agrobacteri	640	33	58.9	781	2	Q8YK17_ANASP	Q8yk17 anabaena sp
568	33	58.9	414	2	Q9J028_9PAPI	Q9j028 rabbit oral	641	33	58.9	816	2	Q5ZD54_MAGGR	Q5zd54 magnaporthe
569	33	58.9	415	1	Y1242_PHOHL	Q7n7b3 photorhabd	642	33	58.9	821	2	Q61229_LYTVA	Q61229 lytechninus
570	33	58.9	420	1	CCNA_CHLVR	P51986 chlomydrha	643	33	58.9	826	2	Q8H06_ORISA	Q8h06 oryza sativ
571	33	58.9	421	2	Q98BU4_CHLSW	Q98bu4 chlamydomon	644	33	58.9	832	2	Q89H12_BRAJA	Q89h12 bradyrhizob
572	33	58.9	422	2	Q97YU1_SULSO	Q97yu1 sulfolobus	645	33	58.9	832	2	Q6PF52_XENLA	Q6pf52 xenopus lae
573	33	58.9	422	2	Q97261_SULSO	Q97261 sulfolobus	646	33	58.9	853	2	Q6LPC7_PLAF7	Q6lpc7 plasmodium
574	33	58.9	427	2	Q9G5M9_9ORTH	Q9g5m9 melanopius	647	33	58.9	862	2	Q8H858_ORISA	Q8h858 oryza sativ
575	33	58.9	428	2	Q872K3_NEUCR	Q872k3 neurospora	648	33	58.9	877	1	YBGG_ECOLI	Ybgg eccherichia
576	33	58.9	428	2	Q5L796_CHLAB	Q5l796 chlamydophi	649	33	58.9	877	1	Q83LZ9_SHIFL	Q83l29 shigella fl
577	33	58.9	430	2	Q411C6_GIBZE	Q411c6 gibberella	650	33	58.9	892	2	Q8R291_ORISA	Q8r291 oryza sativ
578	33	58.9	435	1	EF1A_SULAC	P17196 sulfolobus	651	33	58.9	998	2	Q8GEG6_ERWPY	Q8geg6 erwinia pyr
579	33	58.9	444	2	Q6R975_MAIZE	Q6r975 zea mays (m	652	33	58.9	1039	2	Q7PX58_ANOGA	Q7px58 anopheles g
580	33	58.9	446	2	Q4WUUI_ASPFU	Q4wuui aspergillus	653	33	58.9	1047	2	Q8CJQ0_STRCO	Q8cjq0 streptomyce
581	33	58.9	447	2	Q90705_9VIRU	Q90705 chelonius in	654	33	58.9	1058	2	Q4HWT5_GIBZE	Q4hwt5 gibberella
582	33	58.9	448	2	Q5GXA5_XANOR	Q5gxa5 xanthomonas	655	33	58.9	1073	2	Q53RX7_HUMAN	Q53rx7 homo sapien
583	33	58.9	449	2	Q7S4R6_NEUCR	Q7s4r6 neurospora	656	33	58.9	1087	2	Q91778_XENLA	Q91778 xenopus lae
584	33	58.9	453	2	Q8CB13_MOUSE	Q8cb13 mus musculu	657	33	58.9	1102	2	Q4WSG6_ASPFU	Q4wsg6 aspergillus
585	33	58.9	456	2	Q4WGR1_ASPFU	Q4wgr1 aspergillus	658	33	58.9	1102	2	Q8TFY5_ASPFU	Q8tfy5 aspergillus
586	33	58.9	458	2	Q8HEV8_HAPAU	Q8hev8 hapalemur a	659	33	58.9	1104	1	NIR_EMENI	Nir emeniciella
587	33	58.9	458	2	Q8SDC6_HAPGR	Q8sdc6 hapalemur g	660	33	58.9	1104	2	Q5BEM3_EMENI	Q5bem3 aspergillus
588	33	58.9	458	2	Q8SDC7_HAPGR	Q8sdc7 hapalemur g	661	33	58.9	1110	2	Q92198_ASPFU	Q92198 aspergillus
589	33	58.9	458	2	Q8SDC8_HAPGR	Q8sdc8 hapalemur g	662	33	58.9	1130	1	ITA6_HUMAN	Ita6 homo sapien
590	33	58.9	458	2	Q8SDC9_HAPGR	Q8sdc9 hapalemur g	663	33	58.9	1135	1	VGLM_TSWV1	Vglm tomato spot
591	33	58.9	458	2	Q8SDD0_HAPGR	Q8sdd0 hapalemur g	664	33	58.9	1135	1	VGLM_TSWVD	Vglm tomato spot
592	33	58.9	458	2	Q8SDD1_HAPGR	Q8sdd1 hapalemur g	665	33	58.9	1135	2	Q5XPI4_TSWV	Q5xpi4 tomato spot
593	33	58.9	458	2	Q8HQA3_HAPGR	Q8hqa3 hapalemur g	666	33	58.9	1135	2	Q5XPI5_TSWV	Q5xpi5 tomato spot
594	33	58.9	458	2	Q8HQA7_HAPGR	Q8hqa7 hapalemur g	667	33	58.9	1135	2	Q5XPI6_TSWV	Q5xpi6 tomato spot
595	33	58.9	460	2	Q82181_ARATH	Q82181 arabidopsis	668	33	58.9	1135	2	Q5XPI8_TSWV	Q5xpi8 tomato spot
596	33	58.9	475	2	Q9FWN3_ORISA	Q9fwn3 oryza sativ	669	33	58.9	1135	2	Q5XP20_TSWV	Q5xp20 tomato spot
597	33	58.9	476	1	ACOL_AUECA	Q12618 ajellomyces	670	33	58.9	1135	2	Q5XP22_TSWV	Q5xp22 tomato spot
598	33	58.9	481	1	ATGL1_SCHPO	Q42651 schizosacch	671	33	58.9	1135	2	Q5XP24_TSWV	Q5xp24 tomato spot
599	33	58.9	488	1	NMR_NEUCR	P23762 neurospora	672	33	58.9	1135	2	Q5XP26_TSWV	Q5xp26 tomato spot
600	33	58.9	494	2	Q7NOR2_CHRVO	Q7nqr2 chromobacte	673	33	58.9	1135	2	Q5XP28_TSWV	Q5xp28 tomato spot
601	33	58.9	495	2	Q5BDE2_EMENI	Q5bde2 aspergillus	674	33	58.9	1135	2	Q5XP30_TSWV	Q5xp30 tomato spot
602	33	58.9	501	2	Q59UG7_CANAL	Q59ug7 candida alb	675	33	58.9	1189	2	Q7UT81_RHOBA	Q7ut81 rhodospirell
603	33	58.9	505	2	Q5J2X5_9CARY	Q5j2x5 bieneria c	676	33	58.9	1254	2	Q7SID5_BRARE	Q7sid5 brachydanio
604	33	58.9	505	2	Q89R36_BRAJA	Q89r36 bradyrhizob	677	33	58.9	1311	2	Q4S249_TETNG	Q4s249 tetraodon n
605	33	58.9	520	2	Q786A5_NEUCR	Q786a5 neurospora	678	33	58.9	1313	2	Q9H8C8_HUMAN	Q9h8c8 homo sapien
606	33	58.9	522	2	Q6N7Q0_RHOCA	Q6n7q0 rhodospseudo	679	33	58.9	1349	2	Q7X7K3_ORISA	Q7x7k3 oryza sativ
607	33	58.9	528	2	Q54VX8_DICDI	Q54vx8 dictyosteli	680	33	58.9	1380	2	Q8NE38_HUMAN	Q8ne38 homo sapien
608	33	58.9	532	2	Q5ALL5_CANAL	Q5all5 candida alb	681	33	58.9	1382	2	Q5JYPO_HUMAN	Q5jypo homo sapien
609	33	58.9	533	2	Q7TIF0_MYCHO	Q7tyf0 mycobacteri	682	33	58.9	1386	2	Q5DKR3_9VIRU	Q5dkr3 hydrangea r
610	33	58.9	533	2	Q06173_MYCBO	Q06173 mycobacteri	683	33	58.9	1406	2	Q9Y21C_HUMAN	Q9y21c bovine leuk
611	33	58.9	544	2	Q6GWS5_BRARE	Q6gws5 brachydanio	684	33	58.9	1417	2	Q92812_BLV	Q92812 bovine leuk
612	33	58.9	550	1	LIGA_MOUSE	Q61211 mus musculu	685	33	58.9	1469	2	Q9U190_LEIMA	Q9u190 leishmania
613	33	58.9	552	2	Q8CC17_MOUSE	Q8cc17 mus musculu	686	33	58.9	1580	1	ABCC8_HUMAN	Q9a428 homo sapien
614	33	58.9	559	2	Q97SA8_STRPN	Q97sa8 streptococc	687	33	58.9	2023	2	Q7RG71_PLAYO	Q7rg71 plasmodium
615	33	58.9	563	2	Q50FX9_ENTHI	Q50fx9 entamoeba h	688	33	58.9	2538	2	Q6RKK2_GIBMO	Q6rkk2 gibberella

689	33	58.9	2565	2	Q41HG8_GIRZE	Q41hg8 gibberella	762	32	57.1	149	2	Q5YV47_NOCFA	Q5YV47 nocardia fa
690	33	58.9	2581	2	Q6FKES_CANGA	Q6fke5 candida gla	763	32	57.1	150	2	Q6CL54_KULJA	Q6cle4 kluyveromyc
691	33	58.9	3129	2	Q61TY2_CABER	Q61ty2 caenorhabdi	764	32	57.1	150	2	Q8K637_STRP3	Q8k637 streptococc
692	33	58.9	3175	2	Q7JKT8_CABEL	Q7jkt8 caenorhabdi	765	32	57.1	150	2	Q90XN4_9ACTI	Q90xn4 acipenser s
693	33	58.9	3184	2	Q9XV66_CABEL	Q9xv66 caenorhabdi	766	32	57.1	150	2	Q90XN5_9ACTI	Q90xn5 polypterus
694	33	58.9	4360	2	Q9UVN5_ALTAL	Q9uvn5 alternaria	767	32	57.1	158	2	Q41929_GIBZE	Q41929 gibberella
695	33	58.9	5541	2	Q6W5P9_9ACTO	Q6w5p9 streptomyc	768	32	57.1	162	1	PHEA_ANASP	P35796 anabaena sp
696	33	58.9	7191	2	Q6XA09_9PLEO	Q6xa09 streptomyc	769	32	57.1	162	1	PHEA_WASIA	P35796 anabaena sp
697	32.5	58.0	213	2	Q6MPP5_BDEBA	Q6mpp5 bdellovibri	770	32	57.1	163	2	Q819U1_9ACAR	Q819u1 ornithodora
698	32.5	58.0	297	2	Q6E5A3_ZEA	Q6e5a3 zea mays (m	771	32	57.1	167	2	Q8G5T9_COFA	Q8gst9 coffea cane
699	32.5	58.0	298	2	Q67XN1_ARATH	Q67xn1 arabidopsis	772	32	57.1	167	2	Q8EN55_OCEIH	Q8en5 oceanobacil
700	32.5	58.0	298	2	Q680J5_ARATH	Q680j5 arabidopsis	773	32	57.1	170	2	Q7N1P8_PHOLL	Q7n1p8 photorhabd
701	32.5	58.0	298	2	Q68XV5_ARATH	Q68xv5 arabidopsis	774	32	57.1	172	2	Q4F9N1_LBPDE	Q4f9n1 leptinotars
702	32.5	58.0	568	2	Q51013_XENLA	Q51013 xenopus lae	775	32	57.1	174	2	Q8TQ21_METAC	Q8tq21 methanosarc
703	32.5	58.0	583	2	Q9ABW6_CAUCR	Q9abw6 caulobacter	776	32	57.1	175	2	Q9U455_ANOGA	Q9u455 anophles g
704	32.5	58.0	594	2	Q9EA17_9POTV	Q9ea17 carnation v	777	32	57.1	175	2	Q4F9M8_9EUC	Q4f9m8 orconectes
705	32.5	58.0	743	2	Q6C909_YARLI	Q6c909 yarrowia li	778	32	57.1	176	2	Q52G70_MAGGR	Q52g70 magnaporthe
706	32.5	58.0	780	2	Q6BPD5_DBEHA	Q6bpd5 debaryomyce	779	32	57.1	176	2	Q6XNA6_RHOER	Q6xna6 rhodococcus
707	32.5	58.0	847	2	Q8YRN6_PSEPU	Q8yrn6 pseudomonas	780	32	57.1	178	2	Q4HCA5_9PEIO	Q4hca5 deinococcus
708	32.5	58.0	847	2	Q88HJ2_PSEPK	Q88hj2 pseudomonas	781	32	57.1	182	2	Q8R703_THETN	Q8r703 thermoaer
709	32.5	58.0	905	2	Q9S6N0_BORPE	Q9s6n0 bordetella	782	32	57.1	187	2	Q6Y010_9CAEN	Q6y010 buyecon per
710	32.5	58.0	905	2	Q9S3M8_BORPE	Q9s3m8 bordetella	783	32	57.1	188	2	Q5U9Q6_9VIRU	Q5u9q6 beet necrot
711	32.5	58.0	905	2	Q9S6M9_BORPE	Q9s6m9 bordetella	784	32	57.1	188	2	Q5U9Q7_9VIRU	Q5u9q7 beet necrot
712	32.5	58.0	907	2	Q69257_BORPE	Q69257 bordetella	785	32	57.1	188	2	Q5U9Q8_9VIRU	Q5u9q8 beet necrot
713	32.5	58.0	909	2	Q6U896_BORBR	Q6u896 bordetella	786	32	57.1	188	2	Q65668_9VIRU	Q65668 beet necrot
714	32.5	58.0	910	1	PERT_BORPE	P14283 bordetella	787	32	57.1	188	2	Q8H905_9VIRU	Q8h905 beet necrot
715	32.5	58.0	910	2	Q9S6N1_BORPE	Q9s6n1 bordetella	788	32	57.1	188	2	Q6H917_9VIRU	Q6h917 beet necrot
716	32.5	58.0	910	2	Q69259_BORPE	Q69259 bordetella	789	32	57.1	188	2	Q6H919_9VIRU	Q6h919 beet necrot
717	32.5	58.0	910	2	Q546U4_BORBR	Q546u4 bordetella	790	32	57.1	188	2	Q88620_9VIRU	Q88620 beet necrot
718	32.5	58.0	911	2	Q9L4E2_BORBR	Q9l4e2 bordetella	791	32	57.1	188	2	Q8JPY2_9VIRU	Q8jpy2 beet necrot
719	32.5	58.0	912	2	Q8RSU0_BORPE	Q8rsu0 bordetella	792	32	57.1	188	2	Q9YIY8_9VIRU	Q9yiy8 beet necrot
720	32.5	58.0	915	2	Q8GJ68_BORPE	Q8gj68 bordetella	793	32	57.1	188	2	Q9YZK2_9VIRU	Q9yzk2 beet necrot
721	32.5	58.0	915	2	Q88143_BORPE	Q88143 bordetella	794	32	57.1	188	2	Q9YZK3_9VIRU	Q9yzk3 beet necrot
722	32.5	58.0	916	1	PERT_BORBR	Q03035 bordetella	795	32	57.1	188	2	Q86757_9VIRU	Q86757 beet necrot
723	32.5	58.0	920	2	Q93L98_BORPE	Q93l98 bordetella	796	32	57.1	188	2	Q4ZE95_9VIRU	Q4ze95 beet necrot
724	32.5	58.0	922	1	PERT_BORPA	P24328 bordetella	797	32	57.1	188	2	Q6H913_9VIRU	Q6h913 beet necrot
725	32	57.1	51	2	Q8KZ18_9PROT	Q8kz18 uncultured	798	32	57.1	188	2	Q9YI11_9VIRU	Q9yil1 beet necrot
726	32	57.1	53	2	Q52IK2_PODSI	Q52ik2 podarcis si	799	32	57.1	192	2	Q8Z6T0_SALTI	Q8z6t0 salmonella
727	32	57.1	55	2	Q8QGR9_CHICK	Q8qgr9 gallus gall	800	32	57.1	192	2	Q8Z6T0_SALTI	Q8z6t0 salmonella
728	32	57.1	57	2	Q7UH73_RHOBA	Q7uh73 rhodopirell	801	32	57.1	197	2	Q6CXB3_KULJA	Q6cxb3 kluyveromyc
729	32	57.1	80	2	Q4RB66_TETNG	Q4rb66 tetraodon n	802	32	57.1	203	2	Q21766_CABEL	Q21766 caenorhabdi
730	32	57.1	81	2	Q5JDM0_PYRKO	Q5jdm0 pyrococcus	803	32	57.1	207	2	Q4TJ63_TETNG	Q4tj63 tetraodon n
731	32	57.1	85	2	Q4JL84_ARATH	Q4jl84 arabidopsis	804	32	57.1	208	2	Q9JK12_MOUSE	Q9jk12 mus musculus
732	32	57.1	85	2	Q8A289_BACTN	Q8a289 bacteroides	805	32	57.1	210	2	Q33553_STRIN	Q33553 streptococc
733	32	57.1	87	2	Q93DP9_9BACT	Q93dp9 uncultured	806	32	57.1	216	2	Q8LPA0_ARATH	Q8lpa0 arabidopsis
734	32	57.1	89	2	Q93DQ2_9BACT	Q93dq2 uncultured	807	32	57.1	216	2	Q94K63_ARATH	Q94k63 arabidopsis
735	32	57.1	89	2	Q84798_CHLTR	Q84798 chlamydia t	808	32	57.1	216	2	Q8Z6V5_SALTI	Q8z6v5 salmonella
736	32	57.1	96	2	Q4MNA6_BACCE	Q4mna6 bacillus ce	809	32	57.1	219	2	Q4JUJ1_CORJK	Q4juj1 corynebacte
737	32	57.1	96	2	Q81KA3_BACAN	Q81ka3 bacillus an	810	32	57.1	220	2	Q5H9P6_HUMAN	Q5h9p6 homo sapien
738	32	57.1	98	2	Q61214_PICTO	Q61214 picophilus	811	32	57.1	221	2	Q8JTM1_9CORO	Q8jtm1 avian infec
739	32	57.1	105	2	Q695R1_9ADEN	Q695r1 simian aden	812	32	57.1	223	1	CAS2_CAPHI	P33049 capra hircu
740	32	57.1	113	2	Q50VES_ENTHI	Q50ves entamoeba h	813	32	57.1	223	1	CAS2_SHEEP	P04654 ovis aries
741	32	57.1	119	2	Q5XAF2_STRP6	Q5xaf2 streptococc	814	32	57.1	223	2	Q9MYU6_CAPHI	Q9myu6 capra hircu
742	32	57.1	119	2	Q9YVE3_STRPY	Q9yve3 streptococc	815	32	57.1	228	2	Q6L1A2_PICTO	Q6l1a2 picophilus
743	32	57.1	119	2	Q7CMV8_STRP8	Q7cmv8 streptococc	816	32	57.1	228	2	Q6LFS1_PHOPR	Q6lfs1 photobacter
744	32	57.1	120	2	Q4MNC5_ASPFU	Q4mnc5 aspergillus	817	32	57.1	232	2	Q7MUVO_PORGI	Q7muvo porphyrom
745	32	57.1	120	2	Q8E1J6_ASPFU	Q8e1j6 streptococc	818	32	57.1	232	2	Q50069_ARATH	Q50069 arabidopsis
746	32	57.1	120	2	Q8E1J6_ASPFU	Q8e1j6 streptococc	819	32	57.1	234	2	Q9CV76_MOUSE	Q9cv76 mus musculus
747	32	57.1	124	2	Q8C713_STRP3	Q8c713 streptococc	820	32	57.1	235	2	Q9FN86_ARATH	Q9fn86 arabidopsis
748	32	57.1	131	2	Q9MBH4_ARATH	Q9mbh4 arabidopsis	821	32	57.1	235	2	Q9YPT2_ANASP	Q9ypt2 anabaena sp
749	32	57.1	132	2	Q4INJ5_GIBZE	Q4inj5 gibberella	822	32	57.1	240	2	Q86714_STRCP	Q86714 streptomyc
750	32	57.1	134	2	Q9SV91_ARATH	Q9sv91 arabidopsis	823	32	57.1	240	2	Q5TI56_MOUSE	Q5ti56 mus musculus
751	32	57.1	136	2	Q8LEK1_ARATH	Q8lek1 arabidopsis	824	32	57.1	241	2	Q89TT6_BRAJA	Q89tk6 bradyrhizob
752	32	57.1	137	2	Q4ZCE4_9VIRU	Q4zce4 bacterioph	825	32	57.1	243	2	Q86K17_DICDI	Q86k17 dictyostell
753	32	57.1	143	1	CASE_MOUSE	P02664 mus muscu	826	32	57.1	243	2	Q79UY2_BRAJA	Q79uy2 bradyrhizob
754	32	57.1	143	2	Q542L5_MOUSE	Q542l5 m 10 days 1	827	32	57.1	245	2	Q9SEGH_CAPAN	Q9segh capsicum an
755	32	57.1	144	1	TYPEX_TRYBB	Q77404 trypanosoma	828	32	57.1	248	1	SFSA_PROMP	SF7331 prochloroco
756	32	57.1	144	2	Q57WB2_9TRYP	Q57wb2 trypanosoma	829	32	57.1	250	2	Q11TG2_BBP1	Q11tg2 bacterioph
757	32	57.1	144	2	Q57WB4_9TRYP	Q57wb4 trypanosoma	830	32	57.1	251	2	Q556F1_DICDI	Q556f1 dictyostell
758	32	57.1	145	2	Q510B8_GEOKA	Q510b8 geobacillus	831	32	57.1	258	1	MYPR_ONCMY	P79826 oncorhynch
759	32	57.1	148	2	Q7XUW6_ORYSA	Q7xuw6 oryza sativ	832	32	57.1	258	1	Q9CX27_MOUSE	Q9cx27 mus musculus
760	32	57.1	149	2	Q6RYT2_LEIIN	Q6ryt2 leishmania	833	32	57.1	259	2	Q8BT82_MOUSE	Q8bt82 mus musculus
761	32	57.1	149	2	Q4FXT9_LEIMA	Q4fxt9 leishmania	834	32	57.1	259	2	Q8C645_MOUSE	Q8c645 mus musculus



835	32	57.1	259	2	Q9SEJ7_MOUSE	Q9sej7 m plk inter	908	32	57.1	387	2	Q6FL99_CANGA	Q6fl99 candida gla
836	32	57.1	260	1	COBS_SVNY3	Q55714 synechocyst	909	32	57.1	388	1	VE2_HPV29	VE20772 human papil
837	32	57.1	261	2	Q7RUF4_ANOGA	Q7rip4 anopheles g	910	32	57.1	391	2	Q89LI2_ORISA	Q89li2 oryza sativ
838	32	57.1	262	2	Q8FAX6_PROTNA	Q8fx62 methanosarc	911	32	57.1	393	1	BUP1_MOUSE	B09c97 mus musculus
839	32	57.1	263	2	Q9DGD6_PROTNA	Q9dgd6 protopteris	912	32	57.1	393	1	BUP1_MOUSE	Q03248 rattus norv
840	32	57.1	267	2	Q7WC18_BORPA	Q7wc18 bordetella	913	32	57.1	394	2	Q6LPM7_PHOPR	Q6lpm7 photobacter
841	32	57.1	268	2	Q8TUK4_METAC	Q8tuk4 methanosarc	914	32	57.1	395	2	Q5TSK2_ANOGA	Q5tsk2 anopheles g
842	32	57.1	272	2	Q4SJS1_TETNG	Q4sjs1 tetraodon n	915	32	57.1	398	1	VE2_HPV42	VE22223 human papil
843	32	57.1	273	2	Q4UHY7_THEAN	Q4uhy7 theileria a	916	32	57.1	399	2	Q7SAJ5_ASHGO	Q7saj5 ashbya goss
844	32	57.1	273	2	Q4RIU0_TETNG	Q4riu0 tetraodon n	917	32	57.1	400	2	Q4IAT0_GIBZE	Q4iat0 gibberella
845	32	57.1	274	2	Q5BPI8_ARATH	Q5bpi8 arabidopsis	918	32	57.1	403	2	Q6FDH5_ACIAD	Q6fdh5 acinetobact
846	32	57.1	278	2	Q9I5H1_PSEAE	Q9i5h1 pseudomonas	919	32	57.1	408	2	Q4RW04_TETNG	Q4rw04 tetraodon n
847	32	57.1	279	2	Q8BSS2_PSESM	Q8bss2 pseudomonas	920	32	57.1	410	2	Q6E8G2_9HEMI	Q6e8g2 notocera ap
848	32	57.1	285	2	Q6LPS1_PHOPR	Q6lps1 photobacter	921	32	57.1	410	2	Q6E8G4_9HEMI	Q6e8g4 notocera ap
849	32	57.1	286	2	Q6J9V2_MAIZE	Q6j9v2 zea mays (m	922	32	57.1	410	2	Q6E8G8_9HEMI	Q6e8g8 notocera ap
850	32	57.1	288	2	Q6MEU7_PARUW	Q6meu7 parachlamyd	923	32	57.1	416	1	PUR2_STRCO	Q8rk14 streptomyce
851	32	57.1	291	2	Q5GIV5_POTVY	Q5giv5 sweet potat	924	32	57.1	417	2	Q82FV3_STRAW	Q82fv3 streptomyce
852	32	57.1	294	2	Q89QD8_BRAJA	Q89qd8 bradyrhizob	925	32	57.1	420	1	CSK2A_THGPA	P28547 theileria p
853	32	57.1	306	1	CSK1_SCHPO	P36615 schizosacch	926	32	57.1	420	2	Q965E5_DROME	Q965e5 drosophila
854	32	57.1	307	2	Q8CUW0_OCEIH	Q8cuw0 oceanobacil	927	32	57.1	420	2	Q9VYV4_DROME	Q9vvy4 drosophila
855	32	57.1	307	2	Q5UPD5_MINIV	Q5upd5 minivirius.	928	32	57.1	420	2	Q4N1S0_THEAN	Q4n1s0 theileria p
856	32	57.1	309	2	Q5B4H6_EMENI	Q5b4h6 aspergillus	929	32	57.1	420	2	Q4U925_THEAN	Q4u925 theileria p
857	32	57.1	315	2	Q64471_ARATH	Q64471 arabidopsis	930	32	57.1	421	2	Q8A1N5_BACTN	Q8a1n5 bacteroides
858	32	57.1	317	2	Q5LPZ1_SILPO	Q5lpz1 silicibacte	931	32	57.1	425	2	Q8PVY9_METMA	Q8pvy9 methanosarc
859	32	57.1	319	2	Q5IT34_MAGGR	Q5it34 magnaporthe	932	32	57.1	427	1	CAD_DROME	P03085 drosophila
860	32	57.1	320	2	Q6ASJ7_BACGR	Q6asj7 bacteroides	933	32	57.1	431	2	Q7S922_XENLA	Q7s922 xenopus lae
861	32	57.1	321	2	Q88R32_PSEPK	Q88r32 pseudomonas	934	32	57.1	432	2	Q7F9S9_ORISA	Q7f9s9 oryza sativ
862	32	57.1	326	2	Q652P2_ORISA	Q652p2 oryza sativ	935	32	57.1	432	2	Q8GGR5_STRAZ	Q8ggr5 streptomyce
863	32	57.1	326	2	Q4V182_BACYZ	Q4v182 bacillus ce	936	32	57.1	433	2	Q4J988_SULAC	Q4j988 sulfolobus
864	32	57.1	329	1	DHOA_EMENI	P25415 emerigella	937	32	57.1	433	2	Q8FNK9_COREF	Q8fnk9 corynebacte
865	32	57.1	329	2	Q5BE93_EMENI	Q5be93 aspergillus	938	32	57.1	435	1	Y5714_ARATH	Y04656 arabidopsis
866	32	57.1	330	2	Q60S22_CABBR	Q60s22 caenorhabdi	939	32	57.1	436	2	Q5DGI1_SCHJA	Q5dgi1 schistosoma
867	32	57.1	330	2	Q9DAY1_MOUSE	Q9day1 mus musculu	940	32	57.1	438	2	Q4W906_ASFFU	Q4w906 aspergillus
868	32	57.1	332	2	Q88GX6_PSEPK	Q88gx6 pseudomonas	941	32	57.1	438	2	Q8RAL1_THETN	Q8ral1 thermoaer
869	32	57.1	337	2	Q9KUG9_VIBCH	Q9kug9 vibrio chol	942	32	57.1	440	2	Q6ZP26_HUMAN	Q6zpz6 homo sapien
870	32	57.1	341	2	Q5F8J3_PSEPU	Q5f8j3 pseudomonas	943	32	57.1	440	2	Q7PZ86_ANOGA	Q7pzb6 anopheles g
871	32	57.1	341	2	Q53EE2_9NEOB	Q53ee2 eleutheroda	944	32	57.1	441	2	Q989K1_RHILO	Q989k1 rhizobium l
872	32	57.1	343	2	Q5DH72_SCHJA	Q5dh72 schistosoma	945	32	57.1	442	2	Q23503_ARATH	Q23503 arabidopsis
873	32	57.1	343	2	Q9V9P3_DROME	Q9v9p3 drosophila	946	32	57.1	443	1	DGTL2_PSEAE	Q23503 pseudomonas
874	32	57.1	343	2	Q4QPP6_DROME	Q4qp6 drosophila	947	32	57.1	443	2	Q4ZUL3_PSESY	Q4zul3 pseudomonas
875	32	57.1	343	2	Q7UP82_RHOBA	Q7up82 rhodopirell	948	32	57.1	443	2	Q4K8V6_PSEFS	Q4k8v6 pseudomonas
876	32	57.1	343	2	Q53EG2_9NEOB	Q53eg2 eleutheroda	949	32	57.1	443	2	Q883M5_PSESM	Q883m5 pseudomonas
877	32	57.1	344	2	Q7UDM0_RHOBA	Q7udm0 rhodopirell	950	32	57.1	445	2	Q65TL7_MANSM	Q65tl7 manheimia
878	32	57.1	345	2	Q4KCM2_PSEFS	Q4kcm2 pseudomonas	951	32	57.1	450	2	Q4WIR9_ASFFU	Q4wir9 aspergillus
879	32	57.1	348	2	Q8WPV4_THEAN	Q8wpv4 theileria a	952	32	57.1	450	2	Q95BV6_ADAAL	Q95bv6 ada allenii
880	32	57.1	353	2	Q8GAP9_9CYAN	Q8gap9 lyngbya maj	953	32	57.1	452	1	VE2_HPV17	P36785 human papil
881	32	57.1	356	2	Q5ZS90_LEGPH	Q5zs90 legionella	954	32	57.1	459	1	NU4M_LEMCA	Q34878 lemur catia
882	32	57.1	359	2	Q4N7M2_THEPA	Q4n7m2 theileria p	955	32	57.1	459	2	Q63655_LEMCA	Q63655 lemur catia
883	32	57.1	360	2	Q9LU24_ARATH	Q9lu24 arabidopsis	956	32	57.1	459	2	Q70XG3_THYEL	Q70xg3 thylany9 el
884	32	57.1	365	2	Q72MY6_LEPIC	Q72my6 leptospira	957	32	57.1	460	2	Q5S140_HUMAN	Q5sy40 homo sapien
885	32	57.1	365	2	Q8F8Q3_LEPIN	Q8f8q3 leptospira	958	32	57.1	460	2	Q9VUN6_DROME	Q9vum6 drosophila
886	32	57.1	368	1	VE2_HPV6A	P03119 human papil	959	32	57.1	460	2	Q70XH6_CABFU	Q70xh6 caenolestes
887	32	57.1	368	1	VE2_HPV6B	Q84294 human papil	960	32	57.1	460	2	Q5Q505_POTTR	Q5q505 potorous tr
888	32	57.1	368	2	Q9FD67_ENTFA	Q9fd67 enterococcu	961	32	57.1	462	1	CHSA_SULAC	Q54088 arabidobus
889	32	57.1	368	2	Q837E3_ENTFA	Q837e1 enterococcu	962	32	57.1	462	2	Q74231_GIBFU	Q74231 gibberella
890	32	57.1	368	2	Q77UUI_9PAPI	Q77uui human papil	963	32	57.1	464	2	Q4PBM1_USDMA	Q4pbm1 ustilago ma
891	32	57.1	368	2	Q5YYP1_9PAPI	Q5yyp1 human papil	964	32	57.1	465	2	Q416G1_GIBZE	Q416g1 gibberella
892	32	57.1	369	2	Q5SYP0_THET8	Q5syp0 thermus the	965	32	57.1	469	2	Q9BB23_9ASPA	Q9bb23 bifrenaria
893	32	57.1	369	2	Q72KC9_THET2	Q72kc9 thermus the	966	32	57.1	474	2	Q82300_CHLCV	Q823q0 chlamydomo
894	32	57.1	371	2	Q46169_TRICA	Q46169 tribolium c	967	32	57.1	477	2	Q6CUE2_KIULA	Q6cue2 kluyveromyc
895	32	57.1	371	2	Q934U8_SALTI	Q934u8 salmonella	968	32	57.1	478	2	Q7Q683_ANOGA	Q7q683 anopheles g
896	32	57.1	372	2	Q26098_HELPU	Q26098 helicobacte	969	32	57.1	481	2	Q6YT08_ORISA	Q6ytq8 oryza sativ
897	32	57.1	372	2	Q61699_BRAFL	Q61699 brachylosto	970	32	57.1	483	2	Q8AA74_BACTN	Q8aa74 bacteroides
898	32	57.1	378	2	Q6NGS3_CORGL	Q6ngs3 corynebacte	971	32	57.1	486	2	Q5DMW8_CUCME	Q5dmw8 cucumis mel
899	32	57.1	380	2	Q6M3K0_CORDL	Q6m3k0 corynebacte	972	32	57.1	490	2	Q94CW7_ORISA	Q94cw7 oryza sativ
900	32	57.1	380	2	Q8NNG6_CORGL	Q8nng6 corynebacte	973	32	57.1	499	2	Q7FAT8_HUMAN	Q7fat8 oryza sativ
901	32	57.1	382	1	VE2_HPV15	P36784 human papil	974	32	57.1	501	2	Q6ZMM8_9YNSA	Q6zmm8 homo sapien
902	32	57.1	383	2	Q68F26_XENLA	Q68f26 xenopus lae	975	32	57.1	501	2	Q4Q851_LEIMA	Q4q851 leishmania
903	32	57.1	384	1	BUP1_HUMAN	Q5ubri1 homo sapien	976	32	57.1	502	2	Q72AY0_DESVH	Q72ay0 deaulefovibr
904	32	57.1	384	1	BUP1_PONPY	Q5btm6 pongo pygma	977	32	57.1	506	2	Q4FKR0_9TRYP	Q4fkr0 trypanosoma
905	32	57.1	384	2	Q4P9R2_USTMA	Q4p9r2 ustilago ma	978	32	57.1	509	2	Q4WKN6_ASFFU	Q4wkn6 aspergillus
906	32	57.1	384	2	Q5FTH5_GLUOX	Q5fth5 gluconobact	979	32	57.1	509	2	Q86TJ0_HUMAN	Q86tj0 homo sapien
907	32	57.1	386	2	Q9VRA9_DROME	Q9vra9 drosophila	980	32	57.1	510	2	Q5B3A7_EMENI	Q5b3a7 aspergillus

981 32 57.1 512 2 Q5AV53 EMENI  
 982 32 57.1 516 2 Q7VBH6 PROMA  
 983 32 57.1 517 2 Q5Q0A5 ARATH  
 984 32 57.1 517 2 Q9FK83 ARATH  
 985 32 57.1 518 2 Q6S600 oikopleura  
 986 32 57.1 518 2 Q8SC58 SHEON  
 987 32 57.1 523 2 Q8THZ6 METAC  
 988 32 57.1 523 2 Q7Q982 ANOGA  
 989 32 57.1 523 2 Q95U04 DROME  
 990 32 57.1 523 2 Q9VP67 DROME  
 991 32 57.1 523 2 Q51F34 ENTHI  
 992 32 57.1 525 2 Q609X2 METCA  
 993 32 57.1 533 1 GALTGT HUMAN  
 994 32 57.1 533 1 GALTGT MOUSE  
 995 32 57.1 533 1 GALTGT RAT  
 996 32 57.1 533 2 Q5SD12 BOVIN  
 997 32 57.1 537 2 Q5P527 AZOSE  
 998 32 57.1 541 2 Q9A4N7 CAUCR  
 999 32 57.1 546 2 Q6AJX4 DESPS  
 1000 32 57.1 548 2 Q517H5 ENTHI

## ALIGNMENTS

RESULT 1  
 Q5JL84 MOUSE PRELIMINARY; PRT; 107 AA.  
 AC Q5JL84;  
 DT 01-OCT-2000 (TRENBLrel. 15, Created)  
 DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)  
 DE Anti-myosin immunoglobulin light chain variable region  
 DE (Fragment).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=BALB/c;  
 RX MEDLINE=20448942; PubMed=10992488;  
 RX DOI=10.1128/IAI.68.10.5803-5808.2000;  
 RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;  
 RT "T-Cell-dependent antibody response to the dominant epitope of  
 RT streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive  
 RT with cardiac myosin".  
 RL Infect Immun. 68:5803-5808(2000).  
 DR EMBL; AF206022; AAF69320.1; -; mRNA.  
 DR HSSP; P01594; IJLV5.  
 DR Ensembl; ENSMUSG00000058965; Mus musculus.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003596; IG\_v.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PSS08335; IG\_LIKE; 1.  
 FT NON\_TER 1  
 FT NON\_TER 107 107  
 SQ SEQUENCE 107 AA; 11648 MW; ACF9B1253ACA1E5D CRC64;

Query Match 78.6%; Score 44; DB 2; Length 107;  
 Best Local Similarity 87.5%; Pred. No. 5;  
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QYSLPWT 9  
 |||||  
 Db 90 QYSLPWT 97

RESULT 2  
 Q5C491 SCHJA PRELIMINARY; PRT; 229 AA.  
 ID Q5C491\_SCHJA  
 AC Q5C491;

DT 10-MAY-2005 (TRENBLrel. 30, Created)  
 DT 10-MAY-2005 (TRENBLrel. 30, Last sequence update)  
 DE Hypothetical protein.  
 OS Schistosoma japonica (Blood fluke).  
 OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;  
 OC Schistosomatidae; Schistosomatidae; Schistosoma.  
 OX NCBI\_TaxID=6182;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC Han Z.;  
 RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY809645; AAX25534.1; -; mRNA.  
 DR InterPro; IPR012282; Cytochrome c R.  
 DR InterPro; IPR002563; Flv\_red\_FMN\_Bind.  
 DR InterPro; IPR012287; Homeodomain-rel.  
 KW Hypothetical protein.  
 SQ SEQUENCE 229 AA; 25604 MW; A03FDEE19D62FDE2 CRC64;

Query Match 76.8%; Score 43; DB 2; Length 229;  
 Best Local Similarity 77.8%; Pred. No. 16;  
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HOYSLPWT 9  
 |||||  
 Db 104 HOYSLPWT 112

RESULT 3  
 Q9TOV1\_9CAUD PRELIMINARY; PRT; 770 AA.  
 ID Q9TOV1\_9CAUD PRELIMINARY;  
 AC Q9TOV1;  
 DT 01-MAY-2000 (TRENBLrel. 13, Created)  
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)  
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)  
 DE Putative primase.  
 OS Lactobacillus casei bacteriophage A2.  
 OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.  
 OX NCBI\_TaxID=51369;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=97197195; PubMed=9044284;  
 RA Garcia P., Alonso J.C., Suarez J.E.;  
 RT "Molecular analysis of the cos region of the Lactobacillus casei  
 RT bacteriophage A2. Gene product 3, gp3, specifically binds to its  
 RT downstream cos region".  
 RL Mol. Microbiol. 23:505-514(1997).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=98317291; PubMed=9642205;  
 RA Ladero V., Garcia P., Bascaran V., Herrero M., Alvarez M.,  
 RA Suarez J.E.;  
 RT "Identification of the repressor-encoding gene of the Lactobacillus  
 RT bacteriophage A2".  
 RL J. Bacteriol. 180:3474-3476(1998).  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=98445458; PubMed=9770432; DOI=10.1006/viro.1998.9353;  
 RA Alvarez M.A., Herrero M., Suarez J.E.;  
 RT "The Site-Specific Recombination system of the Lactobacillus spp  
 RT bacteriophage A2 Integrates in Gram Positive and Gram Negative  
 RT Bacteria".  
 RL Virology 250:185-193(1998).  
 RN [4]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=20351728; PubMed=10891412; DOI=10.1006/viro.2000.0382;  
 RA Moscoso M., Suarez J.E.;  
 RT "Characterisation of the DNA replication module of bacteriophage A2  
 RT and use of its origin of replication as a defence against infection  
 RT during milk fermentation by Lactobacillus casei".  
 RL Virology 273:101-111(2000).  
 RN [5]  
 RP NUCLEOTIDE SEQUENCE.

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RX MEDLINE=99214330; PubMed=10196287;
RA Garcia P., Ladero V., Alonso J.C., Suarez J.E.;
RT "Cooperative interaction of Cl protein regulates lysogeny of
RT Lactobacillus casei by Lactobacillio phage A2.";
RL J. Virol. 73:3920-3929(1999).
RN [6]
RP NUCLEOTIDE SEQUENCE.
RA Ladero V., Garcia P., Alonso J.C., Suarez J.E.;
RT "A2 Cro, the lysogenic cycle repressor, specifically binds to the
RT genetic switch region of Lactobacillus casei bacteriophage A2.";
RL Virology 262:222-229(1999).
RN [7]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22262118; PubMed=12374837;
RX DOI=10.1128/JB.184.21.6026-6036.2002;
RA Proux C., van Sinderen D., Suarez J., Garcia P., Ladero V.,
RA Fitzgerald G.F., Desiere F., Brussow H.;
RT "The dilemma of phage taxonomy illustrated by comparative genomics of
RT Sfi21-like Siphoviridae in lactic acid bacteria.";
RL J. Bacteriol. 184:6026-6036(2002).
RN [8]
RP NUCLEOTIDE SEQUENCE.
RA Garcia P., Ladero V., Suarez J.E.;
RT "Complete nucleotide sequence and analysis of the morphogenetic module
RT of the Lactobacillus casei bacteriophage A2.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ251789; CAB63672.1; -; Genomic_DNA.
DR InterPro; IPR004968; Pox D5.
DR InterPro; IPR006500; Primase C.
DR Pfam; PF03288; Pox D5; 1.
DR TIGRFAMs; TIGR01613; primase_Cterm; 1.
KW DNA-binding; Transcription.
SQ SEQUENCE 770 AA; 88233 MW; 382B4F853010D0CB CRC64;

Query Match 76.8%; Score 43; DB 2; Length 770;
Best Local Similarity 55.6%; Pred. No. 56;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 HOYKLPWT 9
|:|:|:|
|:|:|:|
Db 27 HKYTKIPWS 35

RESULT 4
Q5DM7 SCHJA
ID Q5DM7 SCHJA PRELIMINARY; PRT; 275 AA.
AC Q5DM7
DT 10-MAY-2005 (TRENBLrel. 30, Created)
DT 10-MAY-2005 (TRENBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TRENBLrel. 30, Last annotation update)
DE Hypothetical protein.
OS Schistosoma japonicum (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
OC Schistosomatidae; Schistosomatidae; Schistosoma.
OX NCBI_TaxID=6182;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Han Z.;
RT "The full-length cDNA sequences of Schistosoma japonicum genes.";
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY816097; AAW27829.1; -; mRNA.
DR InterPro; IPR001202; WW_Rsp5_WWP.
DR PROSITE; PS01159; WW_DOMAIN_1; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 275 AA; 31773 MW; 5495EF158C4E997P CRC64;

Query Match 75.0%; Score 42; DB 2; Length 275;
Best Local Similarity 87.5%; Pred. No. 30;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYKLPWT 9
|:|:|:|
|:|:|:|

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Db 245 QYKLPWT 252

RESULT 5
Q6BN22 DEBHA
ID Q6BN22 DEBHA PRELIMINARY; PRT; 572 AA.
AC Q6BN22
DT 25-OCT-2004 (TRENBLrel. 28, Created)
DT 25-OCT-2004 (TRENBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TRENBLrel. 28, Last annotation update)
DE Similarities with sp|P47168 Saccharomyces cerevisiae YJR136C.
GN OrderedLocusNames=DEHA0F010459;
OS Debaryomyces hansenii (Yeast) (Torulaspora hansenii).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Debaryomycetes.
OX NCBI_TaxID=4959;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=ATCC 36239 / CBS 767;
RX PubMed=15229592; DOI=10.1038/nature02579;
RA Dujon B., Sherman D., Durrens P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marck C., Neuvéglise C., Talla E.,
RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
RA Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleyskaen C.,
RA Boisarane A., Boyer J., Cattolico L., Confanioli F., de Daruvar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA Nicaut J.-M., Nikolaki M., Oztas S., Ozier-Kalogeropoulos O.,
RA Pellenz S., Potier S., Richard G.-F., Straub M.-L., Suleau A.,
RA Swennen D., Tekala F., Wesolowski-Leuvel M., Westhof E., Wirth B.,
RA Zenlou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,
RA Boucher C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
RA Wincker P., Souciet J.-L.;
RT "Genome evolution in yeasts.";
RL Nature 430:35-44(2004).
DR EMBL; CR382138; CAG88702.1; -; Genomic_DNA.
KW Complete proteome.
SQ SEQUENCE 572 AA; 65217 MW; 73D939503DED2E8D CRC64;

Query Match 73.2%; Score 41; DB 2; Length 572;
Best Local Similarity 66.7%; Pred. No. 94;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HOYKLPWT 9
|:|:|:|
|:|:|:|
Db 155 HMFKLPWT 163

RESULT 6
Q8XVB0 RALSO
ID Q8XVB0 RALSO PRELIMINARY; PRT; 623 AA.
AC Q8XVB0
DT 01-MAR-2002 (TRENBLrel. 20, Created)
DT 01-MAR-2002 (TRENBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE PROBABLE GAMMA-GLUTAMYLTRANSFERASE PROTEIN (EC 2.3.2.2).
GN Name=ggT2; OrderedLocusNames=RSC2921; ORFNames=RS00172;
OS Ralstonia solanacearum (Pseudomonas solanacearum).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Ralstonia.
OX NCBI_TaxID=305;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=GM11000;
RX MEDLINE=21681879; PubMed=11823852; DOI=10.1038/415497a;
RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
RA Ariat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
RA Chandler M., Choise N., Claudel-Renard C., Cunnac S., Demange N.,
RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,
RA Siguier P., Thebault P., Whalen M., Wincker P., Levy M.,
RA Weissenbach J., Boucher C.A.;
RT "Genome sequence of the plant pathogen Ralstonia solanacearum.";

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RL Nature 415:497-502(2002).
DR EMBL; AL646072; CAD16628.1; -, Genomic_DNA.
DR MEROPS; T03.001; -.
DR GO; GO:0003840; F:gamma-glutamyltransferase activity; IEA.
DR InterPro; IPR000101; GGT peptidase.
DR Pfam; PF01019; G_glu_transpept; 1.
DR PRINTS; PR01210; GGTTRANSPTASE.
KW Complete proteome.
SQ SEQUENCE 623 AA; 65009 MW; 2201015F85FEA576 CRC64;

Query Match 71.4%; Score 40; DB 2; Length 623;
Best Local Similarity 75.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QYSKLPWT 9
Db 181 RYGLPWT 188

RESULT 7
KVIR_HUMAN
ID KVIR_HUMAN STANDARD; PRT; 108 AA.
AC P01610;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE IG kappa chain V-I region WEA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=83273707; PubMed=6410398;
RA Goni F., Frangione B.;
RT "Amino acid sequence of the Fv region of a human monoclonal IgM
RT (protein WEA) with antibody activity against 3,4-pyruvylated galactose
RT in Klebsiella polysaccharides K30 and K33."
RL Proc. Natl. Acad. Sci. U.S.A. 80:4837-4841(1983).
CC -1- MISCELLANEOUS: This chain was obtained from a monoclonal antibody
CC against 3,4-pyruvylated galactose and isolated from a patient with
CC Waldenström's macroglobulinemia.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR PIR; A01876; KIHUWE.
DR HSSP; P80362; 1WTL.
DR SMR; P01610; 1-108.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_V.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region; Monoclonal antibody.
FT REGION 1 23
FT REGION 24 34
FT REGION 35 49
FT REGION 50 56
FT REGION 57 88
FT REGION 89 97
FT REGION 98 107
FT DISULFID 23 88
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11840 MW; 9249B61F0945618C CRC64;

Query Match 69.6%; Score 39; DB 1; Length 108;
Best Local Similarity 75.0%; Pred. No. 40;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 QYSKLPWT 9
Db 90 QYSSFPWT 97

RESULT 8
Q8YSA0 ANASP
ID Q8YSA0 ANASP PRELIMINARY; PRT; 258 AA.
AC Q8YSA0;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Beta-carotene ketolase.
GN OrderedLocusNames=alr3189;
OS Anabaena sp. (strain PCC 7120).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
OX NCBI_TaxID=103690;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21595285; PubMed=11759840;
RA Kameko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
RA Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA Nakazaki N., Shimo S., Sugimoto M., Takazawa M., Yamada M.,
RA Yasuda M., Tabata S.;
RT "Complete genomic sequence of the filamentous nitrogen-fixing
RT cyanobacterium Anabaena sp. strain PCC 7120."
RL DNA Res. 8:205-213(2001).
DR EMBL; BA000019; BAB74888.1; -, Genomic_DNA.
DR PIR; AF2204; AF2204.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0016717; F:oxidoreductase activity, acting on paired d. . .; IEA.
DR GO; GO:0016701; F:oxidoreductase activity, acting on single d. . .; IEA.
DR GO; GO:0016119; P:carotene metabolism; IEA.
DR GO; GO:0006636; P:fatty acid desaturation; IEA.
DR InterPro; IPR011393; Carotene ketolase.
DR InterPro; IPR005804; Fa desat.
DR InterPro; IPR010257; FA desat. sub.
DR Pfam; PF00487; FA desaturase; 1.
DR PIRSF; PIRSF027840; Carotene_ketolas; 1.
DR ProDom; PD001081; FA_desat_sub; 1.
KW Complete proteome.
SQ SEQUENCE 258 AA; 30313 MW; 8F8C8E4ECF8EF61B CRC64;

Query Match 69.6%; Score 39; DB 2; Length 258;
Best Local Similarity 62.5%; Pred. No. 96;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HQYSKLPW 8
Db 240 HEYQLPW 247

RESULT 9
Q5E4B3 VIBF1
ID Q5E4B3 VIBF1 PRELIMINARY; PRT; 315 AA.
AC Q5E4B3;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE TRNA-dihydrouridine synthase.
GN OrderedLocusNames=VF1638;
OS Vibrio fischeri (strain ATCC 700601 / ES114).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=312309;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=15703294; DOI=10.1073/pnas.0409900102;
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RA Ruby E.G., Urbanowski M., Campbell J., Dunn A., Faini M., Gunsalus R.,  
 RA Lostroh P., Lupp C., McCann J., Millikan D., Schaefer A., Stabb E.,  
 RA Stevens A., Visick K., Whistler C., Greenberg E.P.;  
 RT "Complete genome sequence of *Vibrio fischeri*: a symbiotic bacterium  
 RT with pathogenic congeners.";  
 RL EMBL: CP000020; AAW86133.1; -; Genomic\_DNA.  
 DR InterPro: IPR001269; Du\_synth.  
 DR Pfam: PF01207; Duf; 1.  
 DR PIRSF: PIRSF006621; Duf; 1.  
 DR PROSITE: PS01136; UPF0034; 1.  
 KW Complete proteome.  
 SQ SEQUENCE 315 AA; 35683 MW; 7341EF8C565117FF CRC64;

Query Match 69.6%; Score 39; DB 2; Length 315;  
 Best Local Similarity 62.5%; Pred. No. 1.2e+02;  
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYSLPW 8  
 | : |||  
 Db 239 HHHSKMPW 246

RESULT 10  
 Q9VST8 DROME  
 ID Q9VST8 DROME PRELIMINARY; PRT; 351 AA.  
 AC Q9VST8;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)  
 DE CG4942-PA (ID38503p).  
 GN ORFNames=CG4942;  
 GN Drosophila melanogaster (Fruit fly).  
 OS Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;  
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers J.H.C., Blazej R.G., Champe M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,  
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Milshina N.V., Mobbart N., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svirekas R., Tector C., Turner R., Venter E.M., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,

RA Ye J., Yeh R.-P., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.-H., Zhong P.N., Zhong W., Zhou X., Zhu S., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of *Drosophila melanogaster*.";  
 RL Science 287:2185-2195(2000).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=22426065; PubMed=12537568;  
 RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,  
 RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,  
 RA George R.A., Hoskins R.A., Lavery T., Muzny D.M., Nelson C.R.,  
 RA Pacle J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,  
 RA Svirekas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,  
 RA Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;  
 RT "Finishing a whole-genome shotgun: release 3 of the *Drosophila*  
 RT melanogaster euchromatic genome sequence.";  
 RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=22426070; PubMed=12537573;  
 RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Svirekas R.,  
 RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,  
 RA Ashburner M., Celniker S.E.;  
 RT "The transposable elements of the *Drosophila melanogaster* euchromatin:  
 RT a genomics perspective.";  
 RL Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).  
 RN [4]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=22426069; PubMed=12537572;  
 RA Miya S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,  
 RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,  
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,  
 RA Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,  
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,  
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,  
 RA Lewis S.E.;  
 RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a  
 RT systematic review.";  
 RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).  
 RN [5]  
 RP NUCLEOTIDE SEQUENCE.  
 RG Berkeley Drosophila Genome Project;  
 RA Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,  
 RA Hoskins R., Scapleton M., Pacle J., Park S., Svirekas R., Smith E.,  
 RA Yu C., Rubin G.;  
 RT "Drosophila melanogaster release 4 sequence.";  
 RN Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 RL [6]  
 RP NUCLEOTIDE SEQUENCE.  
 RG Flybase;  
 RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.  
 RN [7]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=Berkley;  
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,  
 RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,  
 RA Gonzalez M., Guarini H., Li P., Liao G., Miranda A., Mungall C.J.,  
 RA Nuncio J., Pacle J., Paragas V., Park S., Phouanavong S., Wan K.,  
 RA Yu C., Lewis S.E., Rubin G.M., Celniker S.;  
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
 CC -I- INTERACTION:  
 CC Q9V427:inx2; NbExp=1; IntAct=EBI-175436, EBI-103179;  
 CC -I- SUBCELLULAR LOCATION: Integral membrane protein (by similarity).  
 CC -I- SIMILARITY: Belongs to the OXA1/oxa family.  
 CC EMBL: AE003553; AAF50323.1; -; Genomic\_DNA.  
 CC EMBL: AY049618; AAL39763.1; -; mRNA.  
 CC IntAct: Q9VST8; -;  
 CC Ensembl: CG4942; Drosophila melanogaster.  
 CC FlyBase: FBgn0035960; CG4942.  
 CC GO: GO:0016021; C: integral to membrane; IEA.  
 CC GO: GO:0051205; P: protein insertion into membrane; IEA.  
 CC InterPro: IPR001708; Inermemb\_insert.  
 CC Pfam: PF02096; 60KD\_IMP; 1.

```

KW Transmembrane.
SQ SEQUENCE 351 AA; 39295 MW; C9C4469BF750FF1E CRC64;

Query Match 69.6%; Score 39; DB 2; Length 351;
Best Local Similarity 75.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 HQYSLPW 8
DB 79 HDYSLPW 86

RESULT 11
Q5BC20 EMENI PRELIMINARY; PRT; 626 AA.
AC Q5BC20;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Hypothetical protein.
GN ORFNames=AN1590.2;
OS Aspergillus nidulans FGSC A4.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; Emericella.
OX NCBI_TaxID=227321;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FGSC A4;
RA Birren B., Nusbaum C., Abouelleil A., Allen N., Anderson S.,
RA Arachchi H.M., Barna N., Bastien V., Bloom T., Boguslavskiy L.,
RA Bouhgalter B., Butler J., Calvo S.E., Camarata J., Chang J.,
RA Chospel J.S., Collymore A., Cook A., Cooke P., Corum B., Dearellano K.,
RA Diaz J.S., Dodge S., Dooley K., Dorris L., Elkins T., Engels R.,
RA Erickson J., Faro S., Ferreira P., Fitzgerald M., Gage D., Galagan J.,
RA Gardyna S., Gerre S., Graham L., Grand-Pierre N., Hafez N.,
RA Hagopian D., Hagos B., Hall J., Horton L., Hulme W., Iliev I.,
RA Jaffe D., Johnson R., Jones C., Kamal M., Kamat A., Karatas A.,
RA Kells C., Landers T., Levine R., Lindblad-Toh K., Liu G., Lui A.,
RA Ma L.-J., Mabbitt R., MacLean C., MacDonald P., Major J., Manning J.,
RA Matthews C., Mauceli E., McCarthy M., Meldrim J., Meneus L.,
RA Mihova T., Mlenga V., Murphy T., Naylor J., Nguyen C., Nicol R.,
RA Nilsen C.B., Norbu C., O'Connor T., O'Donnell P., O'Neil D.,
RA Oliver J., Peterson K., Phunkhang P., Pierre N., Purcell S.,
RA Rachupka A., Ramasamy U., Raymond C., Retta R., Rise C., Rogov P.,
RA Roman J., Schauer S., Schupbach R., Seaman S., Severy P., Smirnov S.,
RA Smith C., Spencer B., Stange-Thomann N., Stojanovic N., Stubbs M.,
RA Talamas J., Tesfaye S., Theodore J., Topham K., Travers M.,
RA Vassiliev H., Venkataraman V.S., Viel R., Vo A., Wang S., Wilson B.,
RA Wu X., Wyman D., Young G., Zainoun J., Zembek L., Zimmer A., Zody M.,
RA Lander E.;
RT "Genome sequence of Aspergillus nidulans.";
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AACD0100025; EAA64297.1; -; Genomic_DNA.
SQ SEQUENCE 626 AA; 71160 MW; 78A1F884A231851A CRC64;

Query Match 69.6%; Score 39; DB 2; Length 626;
Best Local Similarity 62.5%; Pred. No. 2.4e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 HQYSLPW 8
DB 6 HHFSRLPW 13

RESULT 12
Q4P5B6 USTMA
ID Q4P5B6 USTMA PRELIMINARY; PRT; 1080 AA.
AC Q4P5B6;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)

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DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=UM04697.1;
OS Eukaryota; Fungi; Basidiomycota; Ustilaginomycetes;
OC Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.
OX NCBI_TaxID=237631;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=521;
RA Birren B., Nusbaum C., Abebe A., Abouelleil A., Adekoya E.,
RA Ait-zahra M., Allen N., Allen T., An P., Anderson M., Anderson S.,
RA Arachchi H., Armbruster J., Bachanteang P., Baldwin J., Barry A.,
RA Bayul T., Blitshteyn B., Bloom T., Blye J., Boguslavskiy L., N.,
RA Borowsky M., Bouhgalter B., Brunache A., Butler J., Calixte N.,
RA Calvo S., Camarata J., Campo K., Chang J., Cheshateang Y., Citroen M.,
RA Collymore A., Considine T., Cook A., Cooke P., Corum B., Cuomo C.,
RA David R., Dawoe T., Degray S., Dodge S., Dooley K., Dorje P.,
RA Dorjee K., Dorris L., Duffey N., Dupes A., Elkins T., Engels R.,
RA Erickson J., Farina A., Faro S., Ferreira P., Fischer H.,
RA Fitzgerald M., Foley K., Gage D., Galagan J., Gearin G., Gnerre S.,
RA Gnirke A., Goyette A., Graham J., Grandbois E., Gyaltsen K., Hafez N.,
RA Hagopian D., Hagos B., Hall J., Hatcher B., Heller A., Higgins H.,
RA Honan T., Horn A., Houde N., Hughes L., Hulme W., Huby E., Iliev I.,
RA Jaffe D., Jones C., Kamal M., Kamat A., Kamyselis M., Karlsson E.,
RA Kells C., Kieu A., Kisher P., Kodira C., Kulbokas E., Labutti K.,
RA Lama D., Landers T., Leger J., Levine S., Lewis D., Lewis T.,
RA Lindblad-Toh K., Liu X., Lokytisang T., Lokytisang Y., Lucien O.,
RA Lui A., Ma L.-J., Mabbitt R., MacDonald J., Maclean C., Major J.,
RA Manning J., Marabella R., Maru K., Matthews C., Mauceli E.,
RA McCarthy M., McDonough S., Mcghee T., Meldrim J., Meneus L.,
RA Mesirov J., Mihalov A., Minova T., Mikkelsen T., Mlenga V., Moru K.,
RA Mozes J., Mulrain L., Munson G., Naylor J., Neues C., Nguyen C.,
RA Nguyen N., Nguyen T., Nicol R., Nielsen C., Nizzari M., Norbu C.,
RA Norbu N., O'Donnell P., Okoawo O., O'leary S., Omotosho B.,
RA O'Neill K., Osmen S., Parker S., Perrin D., Phunkhang P., Pignani B.,
RA Purcell S., Rachupka T., Ramasamy U., Rameau R., Ray V., Raymond C.,
RA Retta R., Richardson S., Rise C., Rodriguez J., Rogers J., Rogov P.,
RA Rutnan M., Schupbach R., Seaman C., Settippalli S., Sharpe T.,
RA Sheridan J., Sherpa N., Shi J., Smirnov S., Smith C., Sougnez C.,
RA Spencer B., Stalker J., Stange-thomann N., Stavropoulos S.,
RA Stetson K., Stone C., Stone S., Stubbs M., Talamas J., Tchinga P.,
RA Tensing P., Tesfaye S., Theodore J., Thoultsang Y., Topham K.,
RA Towey S., Tsamila T., Tsomo N., Vallee D., Vassiliev H.,
RA Venkataraman V., Vinson J., Vo A., Wade C., Wang S., Wangchuk T.,
RA Wangdi T., Whittaker C., Wilkinson J., Wu Y., Wyman D., Yadav S.,
RA Yang S., Yang X., Yeager S., Yee E., Young G., Zainoun J., Zembek L.,
RA Zimmer A., Zody M., Lander E.;
RT "The genome sequence of Ustilago maydis.";
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -!- SIMILARITY: Belongs to the ATP-dependent AMP-binding enzyme
CC family.
DR EMBL; AACF01000171; EAX86127.1; -; Genomic_DNA.
DR InterPro; IPR000873; AMP-bind.
DR InterPro; IPR006163; Phosphopanteth_bd.
DR InterPro; IPR006162; Ppantne_S.
DR Pfam; PF00501; AMP-binding; 1.
DR Pfam; PF00550; PP-binding; 1.
DR PRINTS; PR00154; AMPBINDING.
DR PROSITE; PS00075; ACP_DOMAIN; 1.
DR PROSITE; PS00012; PHOSPHOPANTETHINE; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 1080 AA; 118067 MW; 5AC1690E0FF546DF CRC64;

Query Match 69.6%; Score 39; DB 2; Length 1080;
Best Local Similarity 77.8%; Pred. No. 4.1e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 HQYSLPW 9

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Db          487 HQISKLVWT 495
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RESULT 13
ID Q5CUY1 CRYPV PRELIMINARY; PRT; 1376 AA.
AC Q5CUY1;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Hypothetical protein.
GN ORFNames=cg3.1050;
OS Cryptosporidium parvum.
OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
OC Cryptosporidiidae; Cryptosporidium.
OX NCBI_TaxID=5807;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Iowa type II;
RX PubMed=15044751; DOI=10.1126/science.1094786;
RA Abrahamson M.S., Templeton T.J., Enomoto S., Abrahamante J.E., Zhu G.,
RA Lancio C.A., Deng M., Liu C., Widmer G., Tzipori S., Buck G.A., Xu P.,
RA Bankier A.T., Dear P.H., Konfortov B.A., Spriggs H.F., Iyer L.,
RA Anantharaman V., Aravind L., Kapur V.;
RT "Complete genome sequence of the apicomplexan, Cryptosporidium
RT parvum."
RL Science 304:441-445 (2004).
DR EMBL; AAE01000004; BAK89169.1; -; Genomic_DNA.
DR InterPro; IPR001611; LRR.
DR PRINTS; PR00019; LEURICHRPT.
KW Hypothetical protein; Leucine-rich repeat; Repeat.
SQ SEQUENCE 1376 AA; 157717 MW; 85466C98B8A9F57D CRC64;

Query Match 69.6%; Score 39; DB 2; Length 1376;
Best Local Similarity 62.5%; Pred. No. 5.2e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 HOYSKLPW 8
Db 606 VEYAKLPW 613
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RESULT 14
Q4P3G3 USTMA PRELIMINARY; PRT; 157 AA.
AC Q4P3G3;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Predicted protein.
GN ORFNames=UM05350.1;
OS Ustilago maydis 521.
OC Eukaryota; Fungi; Basidiomycota; Ustilaginomycetes;
OC Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.
OX NCBI_TaxID=237631;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=521;
RA Ait-zahra M., Allen T., An P., Anderson M., Anderson S.,
RA Arachi H., Armbruster J., Bachantsang P., Baldwin J., Barry A.,
RA Bayul T., Blitshstein B., Bloom T., Blye J., Boguslavskiy L.,
RA Borowsky M., Boukhgalter B., Brunache A., Butler J., Calixte N.,
RA Calvo S., Camarata J., Campo K., Chang J., Cheshatsang Y., Citroen M.,
RA Collamore A., Considine T., Cook A., Cooke P., Corum B., Cuomo C.,
RA David R., Dawoe T., Degray S., Dodge S., Dooley K., Dorje P.,
RA Dorjee K., Dorris L., Duffey N., Dupes A., Elkins T., Engels R.,
RA Erickson J., Farina A., Faro S., Ferreira P., Fischer H.,
RA Fitzgerald M., Foley K., Gage D., Galagan J., Gearin G., Gnerre S.,
RA Gnikre A., Goyette A., Graham J., Grandbois E., Gyalteen K., Hafez N.,
RA Hagopian D., Hagos B., Hall J., Hatcher B., Heller A., Higgins H.,
RA Honan T., Horn A., Houde N., Hughes L., Hulme W., Husby E., Iliev I.,

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RA Jaffe D., Jones C., Kamal M., Kamat A., Kamyssealis M., Karlsson E.,
RA Kells C., Kieu A., Kisner P., Kodira C., Kulbokas E., Labutti K.,
RA Lama D., Landers T., Leger J., Levine S., Lewis D., Lewis T.,
RA Lindblad-toh K., Liu X., Lokyitsang T., Lokyitsang Y., Lucien O.,
RA Lui A., Ma L.J., Mabbitt R., Macdonald J., Maclean C., Major J.,
RA Manning J., Marabella R., Maru K., Matthews C., Mauceli E.,
RA McCarthy M., McDonough S., Mcghee T., Meldrim J., Menaus L.,
RA Mesirov J., Mihalev A., Mihova T., Mikkelsen T., Mlenga V., Moru K.,
RA Mozes J., Mulrain L., Munson G., Naylor J., News C., Nguyen C.,
RA Nguyen N., Nguyen T., Nicol R., Nielsen C., Nizari M., Norbu C.,
RA Norbu N., O'donnell P., Okoawo O., O'leary S., Omotosho B.,
RA O'Neill K., Osman S., Parker S., Perrin D., Phunkhang P., Pignani B.,
RA Purcell S., Rachupka T., Ramasamy U., Rameau R., Ray V., Raymond C.,
RA Retta R., Richardson S., Rise C., Rodriguez J., Rogers J., Rogov P.,
RA Rutnan M., Schupbach R., Seaman C., Settipalli S., Sharpe T.,
RA Sheridan J., Sherpa N., Shi J., Smirnov S., Smith C., Sougnez C.,
RA Spencer B., Stalker J., Stange-thomann N., Stavropoulos S.,
RA Stetson K., Stone C., Stone S., Stubbs M., Talamas J., Tchuinga P.,
RA Tenzing P., Tesfaye S., Theodore J., Thoulutsang Y., Topham K.,
RA Towey S., Tsamla T., Tsomo N., Vallee D., Vassiliev H.,
RA Venkataraman V., Vinson J., Vo A., Wade C., Wang S., Wangchuk T.,
RA Wangdi T., Whittaker C., Wilkinson J., Wu Y., Wyman D., Yadav S.,
RA Yang S., Yang X., Yeager S., Yee E., Young G., Zainoun J., Zembeck L.,
RA Zimmer A., Zody M., Lander E.;
RT "The genome sequence of Ustilago maydis";
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AACP01000192; EAK86599.1; -; Genomic_DNA.
SQ SEQUENCE 157 AA; 17514 MW; 8233CC43CC8ED3E0 CRC64;

Query Match 67.9%; Score 38; DB 2; Length 157;
Best Local Similarity 62.5%; Pred. No. 88;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYSKLPW 8
Db 128 HKYADLPW 135
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RESULT 15
Q9X8F0 STRCO PRELIMINARY; PRT; 288 AA.
AC Q9X8F0;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Putative phosphotransferase.
GN Ordered locus names=SCO3277; ORFNames=SCE39.27c;
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=A3(2) / M145;
RX MEDLINE=21996410; PubMed=12000953; DOI=10.1038/417141a;
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidaigo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kieser T., Larke L., Murphy L.D., Oliver K., O'Neill S.,
RA Rabinowitsch E., Rajandream M.A., Rutherford K.M., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J.R., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RP "Complete genome sequence of the model actinomycete Streptomyces
RT coelicolor A3(2).";
RL Nature 417:141-147 (2002).
DR EMBL; AL939115; CAB40335.1; -; Genomic_DNA.
DR PIR; T36237; T36237
DR GO; GO:0005524; F:ATP binding; IEA.

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DR GO: GO:0016740; F:transferase activity; IEA.
DR InterPro: IPR002575; APH_Trans.
DR Pfam: PF01636; APH; 1.
KW Complete proteome; Transferase.
SQ SEQUENCE 288 AA; 31415 MW; 40B5B5CB48A42DB5C CRC64;

Query Match 67.9%; Score 38; DB 2; Length 288;
Best Local Similarity 75.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 HOYSKLPW 8
Db 256 HVSYDLPW 263

RESULT 16
Q7NAA3 PHOLL PRELIMINARY; PRT; 336 AA.
AC Q7NAA3_
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Complete genome; segment 1/17.
GN OrderedLocusNames=plu0031;
OS Photorhabdus luminescens (subsp. laumondii).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Photorhabdus.
OX NCBI_TaxID=141679;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=TT01;
RX MEDLINE=22957627; PubMed=14528314; DOI=10.1038/nbt886;
RA Duchaud E., Rusniok C., Frangeul L., Buchrieser C., Givaudan A.,
RA Taourit S., Bocs S., Boursaux-Eude C., Chandler M., Charles J.-F.,
RA Dassa E., Derose R., Derzelle S., Freyssinet G., Gaudriault S.,
RA Medigue C., Lanois A., Powell K., Siguier P., Vincent R., Wingate V.,
RA Zouine M., Glaeser P., Bomare N., Danchin A., Kunst F.,
RA "The genome sequence of the entomopathogenic bacterium Photorhabdus
RT luminescens."
RT Nat. Biotechnol. 21:1307-1313(2003).
RL EMBL; BX571859; CAE12326.1; -; Genomic_DNA.
DR PhotoList; plu0031; -.
DR InterPro: IPR00276; GPCR Rhodopn.
DR PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; UNKNOWN_1.
KW Complete proteome.
SQ SEQUENCE 336 AA; 38412 MW; 7EB8746696E2B8B6 CRC64;

Query Match 67.9%; Score 38; DB 2; Length 336;
Best Local Similarity 75.0%; Pred. No. 1.9e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QYSKLPWT 9
Db 104 QYHNLPT 111

RESULT 17
Q9GKJ6 FIG PRELIMINARY; PRT; 349 AA.
AC Q9GKJ6_
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Butyrylcholinesterase (Fragment).
GN Names=BCHE;
OS Sus scrofa (pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC Sus.
OX NCBI_TaxID=9823;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21419000; PubMed=11528129;

DR GO: GO:0016740; F:transferase activity; IEA.
DR Van Zeveren A., Peelman L.J.,
DR "Integration of porcine chromosome 13 maps.";
RT Cytogenet. Cell Genet. 93:297-303(2001).
CC -|- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
EMBL; AF222914; AAG41127.1; -; Genomic_DNA.
DR HSSP; P06276; 1POP.
DR SMR; Q9GKJ6; 1-349.
DR MEROPS; S09.980; -.
DR GO: GO:0004104; F:cholinesterase activity; IEA.
DR GO: GO:0016787; F:hydrolase activity; IEA.
DR InterPro: IPR002018; CarboxylesteraseB.
DR InterPro: IPR000997; Cholinesterase.
DR InterPro: IPR000379; Ser_estrs.
DR Pfam; PF00135; Coesterase; 1.
DR PRINTS; PR00878; CHOLNESTRASE.
DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
FT NON_TER 1
FT NON_TER 349
SQ SEQUENCE 349 AA; 39061 MW; D66354B14725BE58 CRC64;

Query Match 67.9%; Score 38; DB 2; Length 349;
Best Local Similarity 75.0%; Pred. No. 2e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYSKLPW 8
Db 311 HRSSKLPW 318

RESULT 18
O13629 SCHPO PRELIMINARY; PRT; 363 AA.
AC O13629;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE LIPOATE-PROTEIN LIGASE A (SPBC17A3.09c protein) (P1037 protein).
GN ORFNames=SPBC17A3.09c, pl037;
OS Schizosaccharomyces pombe (fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=972 h-;
RX MEDLINE=20089027; PubMed=10620777;
RX DOI=10.1002/(SICI)1097-0061(20000115)16:1<71::AID-YEA505>3.0.CO;2-5;
RA Machida M., Yamazaki S., Kunihiro S., Tanaka T., Kushida N., Jinno K.,
RA Haikawa Y., Yamazaki J., Yamamoto S., Sekine M., Oguchi A., Nagai Y.,
RA Sakai M., Aoki K., Ogura K., Kudoh Y., Kikuchi H., Zhang M.Q.,
RA Yanagida M.;
RT "A 38 kb segment containing the cdc2 gene from the left arm of fission
RT yeast chromosome II: sequence analysis and characterization of the
RT genomic DNA and cDNAs encoded on the segment.";
RL Yeast 16:71-80(2000).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=972 h-;
RX Director-General of Biotechnology Center, Kushida N., Machida M.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360; DOI=10.1038/nature724;
RA Wood V., Gilliam R., Rajandream M.A., Lyne M.H., Lyne R., Stewart A.,
RA Sgouros J.G., Pest N., Hayles J., Baker S.G., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Fellwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris P., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle B.J., Hunt S., Jagels K.,
RA James K.D., Jones L., Jones M., Leather S., McDonald S., McLean J.,

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RA Mooney P., Moule S., Mungall K.L., Murphy L.D., Niblett D., Odell C.,  
 RA Oliver K., O'Neil S., Pearson D., Quail M.A., Rabinowitsch E.,  
 RA Rutherford K.M., Rutter S., Saunders D., Seeger K., Sharp S.,  
 RA Skelton J., Simmonds M.N., Squares R., Squares S., Stevens K.,  
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,  
 RA Woodward J.R., Volckaert G., Aert R., Robben J., Grymonprez B.,  
 RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,  
 RA Gabel C., Fuchs M., Duesterhoeft A., Fritsch C., Holzer E., Moestl D.,  
 RA Hilbert H., Borzym K., Langer I., Beck A., Lehraich H., Reinhardt R.,  
 RA Pohl T.M., Eger P., Zimmermann W., Wedler H., Wambutt R., Fournelle B.,  
 RA Goffeau A., Cadieu E., Dreano S., Gloux S., Hunt C., Moore K., Mottier S.,  
 RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,  
 RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,  
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,  
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,  
 RA Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,  
 RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.,  
 RT "The genome sequence of Schizosaccharomyces pombe";  
 RL Nature 415:871-880(2002).  
 DR EMBL; AB004537; BRA21417.1; -; Genomic\_DNA.  
 DR EMBL; AL109652; CAB51768.1; -; Genomic\_DNA.  
 DR PIR; T39701.  
 DR GeneDB Spombe; SPBC17A3.09c; -.  
 DR GO; GO:0016874; F:ligase activity; IEA.  
 DR GO; GO:0006464; P:protein modification; IEA.  
 DR InterPro; IPR004143; BPL\_LipA\_LipB.  
 DR InterPro; IPR004562; Lipoyltrans.  
 DR Pfam; PF03099; BPL\_LipA\_LipB; 1.  
 DR TIGRPFAMS; TIGR00545; lipoyltrns; 1.  
 KW Complete proteome; Ligase.  
 SQ SEQUENCE 363 AA; 40651 MW; A6BF82EB7CB8EB13 CRC64;  
 Query Match 67.9%; Score 38; DB 2; Length 363;  
 Best Local Similarity 55.0%; Pred. No. 2.1e+02;  
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 HQYSKLPWT 9  
 DB 322 HELSSIPWT 330  
 RESULT 19  
 Q6FQGO CANGA  
 ID Q6FQGO\_CANGA PRELIMINARY; PRT; 386 AA.  
 AC Q6FQGO;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Candida glabrata strain CBS138 chromosome I complete sequence.  
 GN OrderedLocusNames=CAGL01065349;  
 OS Candida glabrata (Yeast) (Torulopsis glabrata).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; mitosporic Saccharomycetales; Candida.  
 OX NCBI\_TaxID=5478;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RC STRAIN=ATCC 2001 / CBS 138;  
 RX PubMed=15229592; DOI=10.1038/nature02579;  
 RA Lafontaine I., de Montigny J., March C., Neugegola S.,  
 RA Goffard N., Frangeul L., Aigle M., Anthonard V., Babour A., Barbe V.,  
 RA Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,  
 RA Boissrame A., Boyer J., Cattolico L., Confanieri F., de Daruvar A.,  
 RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,  
 RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,  
 RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,  
 RA Nicaud J.-M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,  
 RA Pellenz S., Potier S., Richard G.-F., Straub M.-L., Suleau A.,  
 RA Swennen D., Tekia F., Wesolowski-Louvel M., Westhof E., Wirth B.,  
 RA Zeniou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,  
 RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,  
 RA Wincker P., Souciet J.-L.;  
 RT "Genome evolution in yeasts";

RL Nature 430:35-44(2004).  
 CC -I- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).  
 CC -I- SIMILARITY: Belongs to the OXA1/oxaA family.  
 DR EMBL; CR380955; CAG60471.1; -; Genomic\_DNA.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0051205; P:protein insertion into membrane; IEA.  
 DR InterPro; IPR001708; Innermemb\_insert.  
 DR Pfam; PF02096; 60KD\_Imp; 1.  
 KW Complete proteome; Transmembrane.  
 SQ SEQUENCE 386 AA; 43188 MW; 55DBD0BC41423962 CRC64;  
 Query Match 67.9%; Score 38; DB 2; Length 386;  
 Best Local Similarity 75.0%; Pred. No. 2.2e+02;  
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 HQYSKLPW 8  
 DB 110 HAYSGLPW 117  
 RESULT 20  
 Q89UG7 BRAJA  
 ID Q89UG7 BRAJA PRELIMINARY; PRT; 389 AA.  
 AC Q89UG7;  
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE ABC transporter permease protein.  
 GN OrderedLocusNames=blr1450;  
 OS Bradyrhizobium japonicum.  
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
 OC Bradyrhizobiaceae; Bradyrhizobium.  
 OX NCBI\_TaxID=375;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=USDA 110;  
 RX MEDLINE=22484998; PubMed=12597275;  
 RA Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiuni T.,  
 RA Sasamoto S., Watanabe A., Ideawa K., Iriguchi M., Kawashima K.,  
 RA Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,  
 RA Tabata S.;  
 RT "Complete genomic sequence of nitrogen-fixing symbiotic bacterium  
 RT Bradyrhizobium japonicum USDA110.";  
 RL DNA Res. 9:189-197(2002).  
 DR EMBL; BA000040; BAC46715.1; -; Genomic\_DNA.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0005215; P:transporter activity; IEA.  
 DR GO; GO:0006810; P:transport; IEA.  
 DR InterPro; IPR001851; Bac\_inmem\_transp.  
 DR Pfam; PF02653; BPD\_transp\_2; 1.  
 KW Complete proteome.  
 SQ SEQUENCE 389 AA; 42197 MW; 2C7D90C36B8E1B26 CRC64;  
 Query Match 67.9%; Score 38; DB 2; Length 389;  
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 YSKLPW 8  
 DB 117 YSKLPW 122  
 RESULT 21  
 Q6SV30 MANSF  
 ID Q6SV30 MANSF PRELIMINARY; PRT; 433 AA.  
 AC Q6SV30;  
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
 DE Hypothetical protein.  
 GN OrderedLocusNames=MS0573;  
 OS Mannheimia succiniciproducens (strain MBEL55E).  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;

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OC Pasteurellaceae; Mannheimia.
OX NCBI_TaxID=221988;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15378067; DOI=10.1038/nbt1010;
RA Hong S.H., Kim J.S., Lee S.Y., In Y.H., Choi S.S., Rih J.-K.,
RA Kim C.H., Jeong H., Hur C.G., Kim J.J.;
RT "The genome sequence of the capnophilic rumen bacterium Mannheimia
RT succiniciproducens.";
RL Nat. Biotechnol. 22:1275-1281(2004).
DR EMBL; AS016827; AAU37180.1; -; Genomic DNA.
DR GO; GO:0000287; F:magnesium ion binding; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR000644; CBS.
DR InterPro; IPR005170; CoRC.transpt-asc.
DR InterPro; IPR002550; DUF21.
DR Pfam; PF00571; CBS; 1.
DR Pfam; PF03471; CoRC.HlyC; 1.
DR Pfam; PF01595; DUF21; 1.
SQ Complete proteome; Hypothetical protein.
KW SEQUENCE 433 AA; 48957 MW; 96DD1302D147AF7D CRC64;

Query Match 67.9%; Score 38; DB 2; Length 433;
Best Local Similarity 62.5%; Pred. No. 2.5e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HQYSKLPW 8
|||: ||
DB 91 HQVTNAPW 98

RESULT 22
Q75B85 ASHGO
ID Q75B85 ASHGO PRELIMINARY; PRT; 434 AA.
AC Q75B85;
DT 05-JUL-2004 (T-EMBLrel. 27, Created)
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
DE ADL315CP.
GN Name=ADL315C;
OS Ashbya gossypii (Yeast) (Eremothecium gossypii).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Eremothecium.
OX NCBI_TaxID=33169;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=ATCC 10895;
RX PubMed=15001715; DOI=10.1126/science.1095781;
RA Dietrich F.S., Vogeli S., Brachat S., Lerch A., Gates K., Steiner S.,
RA Mohr C., Boehmann R., Luedi P., Choi S., Wing R.A., Flavier A.,
RA Gaffney T.D., Philippsen P.;
RT "The Ashbya gossypii genome as a tool for mapping the ancient
RT Saccharomyces cerevisiae genome.";
RL Science 304:304-307(2004).
CC -|- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -|- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; AS016817; AAS51605.1; -; Genomic DNA.
DR HSSP; P24941; 1KE8.
DR AGD; ADL315C; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006914; F:autophagy; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR GO; GO:0015031; P:protein transport; IEA.
DR InterPro; IPR000719; Prot.kinase.
DR InterPro; IPR008271; Ser_Thr_pkin_AS.
DR InterPro; IPR002290; Ser_Thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot.kinase; 1.
DR SMART; SN00220; S_TKC; 1.

SMART: SM00219; TyrKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; UNKNOWN 1.
KW ATP-binding; Autophagy; Complete proteome; Kinase; Nucleotide-binding;
KW Protein transport; Serine/threonine-protein kinase; Transferase;
SQ SEQUENCE 434 AA; 49672 MW; E3F62F511479CF1B CRC64;

Query Match 67.9%; Score 38; DB 2; Length 434;
Best Local Similarity 71.4%; Pred. No. 2.5e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 QYSKLPW 8
|||: |||
DB 326 QYAKIPW 332

RESULT 23
CHLE_RABIT
ID CHLE_RABIT STANDARD; PRT; 581 AA.
AC P21927;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Cholinesterase precursor (EC 3.1.1.8) (Acylcholine acylhydrolase)
DE (Choline esterase II) (Butyrylcholine esterase)
DE (Pseudocholinesterase).
GN Name=BCHE;
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;
OC Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=New Zealand;
RX MEDLINE=90326526; PubMed=2374720;
RA Jbilo O., Roudani S., Chatonnet A.;
RT "Complete sequence of rabbit butyrylcholinesterase.";
RL Nucleic Acids Res. 18:3990-3990(1990).
RN [2]
RP NUCLEOTIDE SEQUENCE OF 75-215.
RC TISSUE=Liver;
RX MEDLINE=91201348; PubMed=2016308;
RA Arpagaus M., Chatonnet A., Masson P., Newton M., Vaughan T.A.,
RA Bartels C.F., Nogueira C.P., la Du B.N., Lockridge O.;
RT "Use of the polymerase chain reaction for homology probing of
RT butyrylcholinesterase from several vertebrates.";
RL J. Biol. Chem. 266:6966-6974(1991).
CC -|- CATALYTIC ACTIVITY: An acylcholine + H(2)O = choline + a
CC carboxylate.
CC -|- SUBUNIT: Homotetramer. The tetramer is composed of two dimers. The
CC two subunits in a dimer are linked by a disulfide bond.
CC -|- TISSUE SPECIFICITY: Present in most cells except erythrocytes.
CC -|- MISCELLANEOUS: Cholinesterase is highly reactive with
CC organophosphate esters.
CC -|- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; X52090; CAA36308.1; -; Genomic DNA.
DR EMBL; X52091; CAA36308.1; JOINED; Genomic DNA.
DR EMBL; X52092; CAA36308.1; JOINED; Genomic DNA.
DR EMBL; M62779; AAA31169.1; -; Genomic DNA.
DR PIR; S10255; C39768.
DR HSSP; P22303; 1F8U.
DR SMR; P21927; 11-536.
DR MEROPS; S09.980; -.

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DR InterPro; IPR002018; CarbesteraeB.
DR InterPro; IPR000997; Cholinesterase.
DR InterPro; IPR000379; Ser_estrs.
DR PANTHER; PTHR11559; CarbesteraeB; 1.
DR Pfam; PF00135; Coesterase; 1.
DR PRINTS; PR00878; CHOLNESTRASE.
DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
KW Glycoprotein; Hydrolase; Serine esterase; Signal.
FT SIGNAL 1 8 Potential.
FT CHAIN 9 581 Cholinesterase.
FT ACT_SITE 205 205 Acyl-ester intermediate (By similarity).
FT ACT_SITE 332 332 Charge relay system (By similarity).
FT ACT_SITE 445 445 Charge relay system (By similarity).
FT CARBOHYD 64 64 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 113 113 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 248 248 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 263 263 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 348 348 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 462 462 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 488 488 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 492 492 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 493 493 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 72 99 By similarity.
FT DISULFID 259 270 By similarity.
FT DISULFID 407 526 By similarity.
FT DISULFID 578 578 Interchain (By similarity).
SQ SEQUENCE 581 AA; 66156 MW; FE8B199E7B32EB0A CRC64;

Query Match 67.9%; Score 38; DB 1; Length 581;
Best Local Similarity 75.0%; Pred. No. 3.3e+02;
Matches 6; Conservative 1; Mismatches 0; Gaps 0;

QY 1 HOYSKLPW 8
DB 430 HRSSKLPW 437

RESULT 24
QJUKC1 RAT PRELIMINARY; PRT; 597 AA.
AC QJUKC1
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Butyrylcholinesterase.
GN Name=Bche;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC Tissue=Heart;
RA Li B., Stribley J., Ticu A., Xie W., Schopfer L.M., Hammond P.,
RA Brinjoian S., Hinrichs S.H., Lockridge O.;
RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
[2]
RP NUCLEOTIDE SEQUENCE.
RC Tissue=Heart;
RA Ticu A.M., Lockridge O., Bartels C.F.;
RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
DR EMBL; AF244349; AAF44713.1; -; mRNA.
DR HSP; P06276; 1P01.
DR SMR; Q9UKC1; 27-552.
DR MEROPS; S09.980; -.
DR Ensembl; ENSRNOG00000009826; Rattus norvegicus.
DR RGD; 619996; Bche.
DR GO; GO:0004104; F:cholinesterase activity; IEA.
DR GO; GO:0016789; F:hydrolase activity; IEA.
DR GO; GO:0004759; F:serine esterase activity; IEA.

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DR InterPro; IPR002018; CarbesteraeB.
DR InterPro; IPR000997; Cholinesterase.
DR InterPro; IPR000379; Ser_estrs.
DR Pfam; PF00135; Coesterase; 1.
DR PRINTS; PR00878; CHOLNESTRASE.
DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
KW Hydrolase; Serine esterase.
SQ SEQUENCE 597 AA; 67777 MW; 771204D166C7BEAC CRC64;

Query Match 67.9%; Score 38; DB 2; Length 597;
Best Local Similarity 75.0%; Pred. No. 3.4e+02;
Matches 6; Conservative 1; Mismatches 0; Gaps 0;

QY 1 HOYSKLPW 8
DB 446 HRSSKLPW 453

RESULT 25
CHLE_HUMAN
ID CHLE_HUMAN STANDARD; PRT; 602 AA.
AC P06276;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Cholinesterase precursor (EC 3.1.1.8) (Acylcholine acylhydrolase)
DE (Choline esterase II) (Butyrylcholine esterase)
DE (Pseudocholinesterase).
GN Name=BChE; Synonyms=CHE1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA MEDLINE=90212557; PubMed=2322535;
RA Arpagaus M., Kott M., Vatsis K.P., Bartels C.F., la Du B.N.,
RA Lockridge O.;
RA "Structure of the gene for human butyrylcholinesterase. Evidence for a
RA single copy."
RL Biochemistry 29:124-131(1990).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC Tissue=Fetal;
RX MEDLINE=87231856; PubMed=3035536;
RX Prody C.A., Zevin-Sonkin D., Gnatt A., Goldberg O., Soreg H.;
RA "Isolation and characterization of full-length cDNA clones coding for
RA cholinesterase from fetal human tissues."
RL Proc. Natl. Acad. Sci. U.S.A. 84:3555-3559(1987).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC Tissue=Brain;
RX MEDLINE=88016155; PubMed=3477799;
RX McTierman C., Adkins S., Chatonnet A., Vaughan T.A., Bartels C.F.,
RA Kott M., Rosenberry T.L., la Du B.N., Lockridge O.;
RT "Brain cDNA clone for human cholinesterase."
RL Proc. Natl. Acad. Sci. U.S.A. 84:6682-6686(1987).
RN [4]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC Tissue=Skin;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

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RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahay J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [5]  
RP PROTEIN SEQUENCE OF 29-602.  
RC TISSUE=Plasma;  
RX MEDLINE=87109144; PubMed=3542989;  
RA Lockridge O., Bartels C.F., Vaughan T.A., Wong C.K., Norton S.E.,  
RA Johnson L.L.;  
RT "Complete amino acid sequence of human serum cholinesterase.";  
RL J. Biol. Chem. 262:549-557 (1987).  
RN [6]  
RP DISULFIDE BONDS.  
RX MEDLINE=88007487; PubMed=3115973;  
RA Lockridge O., Adkins S., la Du B.N.;  
RT "Location of disulfide bonds within the sequence of human serum  
RT cholinesterase.";  
RL J. Biol. Chem. 262:12945-12952 (1987).  
RN [7]  
RP REVIEW.  
RX MEDLINE=89149758; PubMed=3067729;  
RA Lockridge O.;  
RT "Structure of human serum cholinesterase.";  
RL Bioessays 9:125-128 (1988).  
RN [8]  
RP VARIANT ATYPICAL GLY-98.  
RX MEDLINE=89128896; PubMed=2915989;  
RA McGuire M.C., Nogueira C.P., Bartels C.F., Lightstone H., Hajra A.,  
RA van der Spek A.F.L., Lockridge O., la Du B.N.;  
RT "Identification of the structural mutation responsible for the  
RT dibucaine-resistant (atypical) variant form of human serum  
RT cholinesterase.";  
RL Proc. Natl. Acad. Sci. U.S.A. 86:953-957 (1989).  
RN [9]  
RP VARIANT ILE-358.  
RX MEDLINE=96287386; PubMed=8680411;  
RA Iida S., Kinoshita M., Fujii H., Moriyama Y., Nakamura Y., Yura N.,  
RA Moriaki K.;  
RT "Mutations of human butyrylcholinesterase gene in a family with  
RT hypocholinesterasemia.";  
RL Hum. Mutat. 6:349-351 (1995).  
CC -|- CATALYTIC ACTIVITY: An acylcholine + H(2)O = choline + a  
CC carboxylate.  
CC -|- SUBUNIT: Homotetramer. The tetramer is composed of two dimers. The  
CC two subunits in a dimer are linked by a disulfide bond.  
CC -|- TISSUE SPECIFICITY: Present in most cells except erythrocytes.  
CC -|- DISEASE: Mutant alleles of CHE1 are responsible for  
CC hypocholinesterasemia resulting in suxamethonium sensitivity.  
CC Homozygous persons resulting in prolonged apnea after administration of  
CC the muscle relaxant suxamethonium in connection with surgical  
CC anaesthesia.  
CC -|- MISCELLANEOUS: Cholinesterase is highly reactive with  
CC organophosphate esters.  
CC -|- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.  
CC -----  
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CC use as long as its content is in no way modified and this statement is not  
CC removed.  
CC -----  
DR EMBL; M32391; AAA92926.1; -; Genomic\_DNA.  
DR EMBL; M32389; AAA92926.1; JOINED; Genomic\_DNA.  
DR EMBL; M32390; AAA92926.1; JOINED; Genomic\_DNA.  
DR EMBL; M16541; AAA98113.1; -; mRNA.  
DR EMBL; M16474; AAA52015.1; -; mRNA.

DR EMBL; BC018141; AAH18141.1; -; mRNA.  
DR PIR; A33769; ACNU.  
DR PDB; 1EHO; Model; A=30-560.  
DR PDB; 1EHQ; Model; A=30-560.  
DR PDB; 1KQJ; Model; A=30-560.  
DR PDB; 1PO1; X-ray; A=29-557.  
DR PDB; 1POM; X-ray; A=29-557.  
DR PDB; 1POP; X-ray; A=29-557.  
DR PDB; 1POQ; X-ray; A=29-557.  
DR PDB; 1XLU; X-ray; A=29-557.  
DR PDB; 1XLV; X-ray; A=29-557.  
DR PDB; 1XLW; X-ray; A=29-557.  
DR MEROPS; S09.980; -.  
DR Ensembl; ENSG00000114200; Homo sapiens.  
DR HGNC; HGNC:1983; SCHE.  
DR H-invDB; HIX0003828; -.  
DR MIM; 177400; -.  
DR GO; GO:0005576; C:extracellular region; NAS.  
DR GO; GO:0001540; F:beta-amyloid binding; NAS.  
DR GO; GO:0003824; E:catalytic activity; NAS.  
DR GO; GO:0004104; F:cholinesterase activity; NAS.  
DR GO; GO:0019899; F:enzyme binding; NAS.  
DR GO; GO:0050783; P:cocaine metabolism; TAS.  
DR InterPro; IPR002018; CarbesteraseB.  
DR InterPro; IPR000997; Cholinesterase.  
DR InterPro; IPR000379; Ser\_estrs.  
DR PANTHER; PTHR11559; CarbesteraseB; 1.  
DR Pfam; PF00135; Coesterase; 1.  
DR PRINTS; PR00878; CHOLINESTRASE.  
DR PROSITE; PS00122; CARBOXYLESTERASE B\_1; 1.  
DR PROSITE; PS00941; CARBOXYLESTERASE B\_2; 1.  
KW 3D-structure; Direct protein sequencing; Disease mutation;  
KW Glycoprotein; Hydrolase; Polymorphism; Serine esterase; Signal.  
FT SIGNAL 1 28  
FT CHAIN 29 602 Cholinesterase.  
FT ACT\_SITE 226 226 Acyl-ester intermediate (By similarity).  
FT ACT\_SITE 353 353 Charge relay system (By similarity).  
FT ACT\_SITE 466 466 Charge relay system (By similarity).  
FT CARBOHYD 45 45 N-linked (GlcNAc...).  
FT CARBOHYD 85 85 N-linked (GlcNAc...).  
FT CARBOHYD 134 134 N-linked (GlcNAc...).  
FT CARBOHYD 269 269 N-linked (GlcNAc...).  
FT CARBOHYD 284 284 N-linked (GlcNAc...).  
FT CARBOHYD 369 369 N-linked (GlcNAc...).  
FT CARBOHYD 483 483 N-linked (GlcNAc...).  
FT CARBOHYD 509 509 N-linked (GlcNAc...).  
FT CARBOHYD 514 514 N-linked (GlcNAc...).  
FT DISULFID 93 120 Interchain.  
FT DISULFID 280 291 D -> G (in atypical form, dibucaine-  
FT DISULFID 428 547 resistant; dbSNP:1799807).  
FT DISULFID 599 599 /FTID=VAR\_002360.  
FT VARIANT 271 271 T -> M (in fluoride-1).  
FT VARIANT 358 358 L -> I (in hypocholinesterasemia).  
FT VARIANT 418 418 G -> V (in fluoride-2).  
FT VARIANT 567 567 A -> T (in K variant; with reduced enzyme  
FT activity; dbSNP:1803274).  
FT /FTID=VAR\_002364.  
SQ SEQUENCE 602 AA; 68418 MW; C9836409D9057F27 CRC64;  
Query Match 67.9%; Score 38; DB 1; Length 602;  
Best Local Similarity 75.0%; Pred. No. 3.4e+02;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 1 HOYSKLPW 8  
|: |||||  
DB 451 HRSSKLPW 458

```

RESULT 26
QSR7Z4_PONPY PRELIMINARY; PRT; 602 AA.
AC QSR7Z4;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Hypothetical protein DKFZp469L1320.
GN Name=DKFZp469L1320;
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Pongo.
OX NCBI_TaxID=9600;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Kidney;
RG The German cDNA Consortium;
RA Bloeker H., Boecher M., Brandt P., Mewes H.W., Weil B., Amid C.,
OR Oanger A., Fobo G., Han M., Wiemann S.;
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
DR EMBL; CR859963; CAH92116.1; -; mRNA.
DR SMR; QSR7Z4; 32-557.
DR GO; GO:0004104; F:cholinesterase activity; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0004759; F:serine esterase activity; IEA.
DR InterPro; IPR002018; CarboxylesteraseB.
DR InterPro; IPR000997; Cholinesterase.
DR InterPro; IPR000379; Ser esters.
DR Pfam; PF00135; Coesterase; 1.
DR PRINTS; PR00878; CHOLNESTRASE.
DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
KW Hydrolase; Hypothetical protein; Serine esterase.
SQ SEQUENCE 602 AA; 68511 MW; 83BF0EA76E52A8BC CRC64;

Query Match 67.9%; Score 38; DB 2; Length 602;
Best Local Similarity 75.0%; Pred. No. 3.4e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HQYSKLPW 8
DB 451 HRSSKLPW 458

RESULT 27
CHLE_MOUSE
ID CHLE_MOUSE STANDARD; PRT; 603 AA.
AC Q03311;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Cholinesterase precursor (EC 3.1.1.8) (Acylcholine acylhydrolase)
DE (Choline esterase II) (Butyrylcholine esterase)
DE (PseudoCholinesterase).
DE Name=Bche;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC MEDLINE=90380429; PubMed=2400605; DOI=10.1016/0896-6273(90)90168-F;
RA Rachinsky T.L., Camp S., Li Y., Ekstrom T.J., Newton M., Taylor P.;
RT "Molecular cloning of mouse acetylcholinesterase: tissue distribution
of alternatively spliced mRNA species.";
RL Neuron 5:317-327(1990).
RN [2]
RP NUCLEOTIDE SEQUENCE OF 97-237.
RC TISSUE=Liver;

RX MEDLINE=91201348; PubMed=2016308;
RA Arpagaus M., Chatonnet A., Masson P., Newton M., Vaughan T.A.,
RA Bartels C.F., Nogueira C.P., la Du B.N., Lockridge O.;
RT "Use of the polymerase chain reaction for homology probing of
butyrylcholinesterase from several vertebrates.";
J. Biol. Chem. 266:6966-6974(1991).
CC -1- CATALYTIC ACTIVITY: An acylcholine + H(2)O = choline + a
carboxylate.
CC -1- SUBUNIT: Homotetramer. The tetramer is composed of two dimers. The
two subunits in a dimer are linked by a disulfide bond.
CC -1- TISSUE SPECIFICITY: Present in most cells except erythrocytes.
CC -1- MISCELLANEOUS: Cholinesterase is highly reactive with
organophosphate esters.
CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.
CC
DR EMBL; M99492; AAA37328.1; -; mRNA.
DR PIR; S70849; S70849.
DR HSP; P22303; 1F8U.
DR SMR; Q03311; 34-558.
DR MEROPS; S09.980; . . . 00027792; Mus musculus.
DR Ensembl; ENSMUSG00000027792; Mus musculus.
DR MGI; MGI:894278; Bche.
DR InterPro; IPR002018; CarboxylesteraseB.
DR InterPro; IPR000997; Cholinesterase.
DR InterPro; IPR000379; Ser esters.
DR PANTHER; PTHR11559; CarboxylesteraseB; 1.
DR Pfam; PF00135; Coesterase; 1.
DR PRINTS; PR00878; CHOLNESTRASE.
DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
KW Glycoprotein; Hydrolase; Serine esterase; Signal.
FT SIGNAL 1 29
FT CHAIN 30 603 Cholinesterase.
FT ACT_SITE 227 227 Acyl-ester intermediate (By similarity).
FT ACT_SITE 354 354 Charge relay system (By similarity).
FT ACT_SITE 467 467 Charge relay system (By similarity).
FT CARBOHYD 86 86 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 135 135 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 270 270 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 370 370 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 484 484 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 510 510 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 515 515 N-linked (GlcNAc...) (Potential).
FT DISULFID 94 121 By similarity.
FT DISULFID 281 292 By similarity.
FT DISULFID 429 548 By similarity.
FT DISULFID 600 600 Interchain (By similarity).
FT CONFLICT 129 129 R -> P (in Ref. 2).
SQ SEQUENCE 603 AA; 68521 MW; 719B1B220D1E5367 CRC64;

Query Match 67.9%; Score 38; DB 1; Length 603;
Best Local Similarity 75.0%; Pred. No. 3.4e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HQYSKLPW 8
DB 452 HRSSKLPW 459

RESULT 28
Q543J3_MOUSE PRELIMINARY; PRT; 603 AA.
ID Q543J3_MOUSE PRELIMINARY;
AC Q543J3;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Adult male liver tumor cDNA, RIKEN full-length enriched library,

```

DE clone:C730038620 product:butyrylcholinesterase.  
GN Name=Bche;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN (1)  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Liver;  
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;  
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,  
RA Nikaide I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,  
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojibori T.,  
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,  
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,  
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,  
RA Dalia E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,  
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,  
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,  
RA Kanai A., Kawaji H., Kawasaki I.V., Lee Y., Lenhard R.M., Lyons P.A.,  
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard R.M., Lyons P.A.,  
RA Maglott D.R., Malcais L., Marchionni L., McKenzie L., Miki H.,  
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,  
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,  
RA Ravasi T., Reed J.C., Reed D.J., Ring B.Z., Ringwald M.,  
RA Sandelin A., Schneider C., Sempile C.A., Setou M., Shimada K.,  
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,  
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,  
RA Wilming L.G., Wyszewski-Boris A., Yanagisawa M., Yang I., Yang L.,  
RA Yuan Z., Zavalon M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,  
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,  
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,  
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,  
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,  
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,  
RA Birney E., Hayashizaki Y.;  
RT "Analysis of the mouse transcriptome based on functional annotation of  
RT 60,770 full-length cDNAs.";  
RL Nature 420:563-573(2002).  
RN (4)  
RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Liver;  
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;  
RA Carninci P., Shibata Y., Muramatsu M., Sugahara Y., Itoh M.,  
RA Konno H., Okazaki Y., Muramatsu N., Hayashizaki Y.;  
RT "Normalization and subtraction of cap-trapper-selected cDNAs to  
RT prepare full-length cDNA libraries for rapid discovery of new genes.";  
RL Genome Res. 10:1617-1630(2000).  
RN (5)  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Liver;  
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;  
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,  
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,  
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,  
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,  
RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,  
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,  
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;  
RT "RIKEN integrated sequence analysis (RISA) system-384-format  
RT sequencing pipeline with 384 multiplexed sequencer.";  
RL Genome Res. 10:1757-1771(2000).  
RN (16)  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Liver;  
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,  
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,  
RA Hayashida K., Hayatsu N., Hiramoto K., Hirakawa T., Kikawa T.,  
RA Hori F., Imotani K., Ishii Y., Itoh M., Kikawa I., Kasukawa T.,  
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,  
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,  
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,  
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,  
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,  
RA Tagawa A., Takahashi F., Takaku-Akaiura S., Takeda Y., Tanaka T.,  
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;  
RT Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
RC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.  
DR EMBL; AK050337; BAC34196.1; -; mRNA.  
DR SMR; Q543J3; 34-558.  
DR MGI; MGI:894278; Bche.  
DR GO; GO:0003824; F:catalytic activity; IEA.  
DR GO; GO:0004104; F:cholinesterase activity; IEA.  
DR InterPro; IPR002018; Carboxylesterase.  
DR InterPro; IPR000397; Cholinesterase.  
DR InterPro; IPR000379; Serine.  
DR Pfam; PF00135; Coesterase; 1.  
DR PRINTS; PR00878; CHOLINESTRASE.  
DR PROSITE; PS00122; CARBOXYLESTERASE\_B\_1; 1.  
DR PROSITE; PS00941; CARBOXYLESTERASE\_B\_2; 1.  
KW Hydrolase; Serine esterase.  
SQ SEQUENCE 603 AA; 68462 MW; 2CB79C4679B3713 CRC64;

Query Match 67.9%; Score 38; DB 2; Length 603;  
Best Local Similarity 75.0%; Pred. No. 3.4e+02;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYSKLPW 8  
DB 452 HRSKLPW 459

RESULT 29  
Q90ZK8 CHICK PRELIMINARY; PRT; 603 AA.  
ID Q90ZK8; AC Q90ZK8;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Butyrylcholinesterase precursor (EC 3.1.1.8).  
GN Name=BChE;  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC

OC Gallus.  
 RN NCBI\_TaxID=9031;  
 [1] :|||||  
 RP NUCLEOTIDE SEQUENCE.  
 RA Geissler K., Chatonnet A., Layer P.G.;  
 RT "Chicken Butyrylcholinesterase."  
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
 CC -|- FUNCTION: Rapidly hydrolyzes choline released into the synapse (By similarity).  
 CC -|- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.  
 DR EMBL; AJ306928; CAC37792.1; -; mRNA.  
 DR HSSP; P06276; 1P01.  
 DR SMR; Q90ZK8; 33-557.  
 DR MEROPS; S09\_980; -.  
 DR Ensembl; ENSGALG0000009478; Gallus gallus.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0045202; C:synapse; IEA.  
 DR GO; GO:0004104; F:cholinesterase activity; IEA.  
 DR GO; GO:0016787; F:hydrolase activity; IEA.  
 DR GO; GO:0042135; P:neurotransmitter catabolism; IEA.  
 DR InterPro; IPR020218; CarboxesteraseB.  
 DR InterPro; IPR000997; Cholinesterase.  
 DR InterPro; IPR000379; Ser\_estr.  
 DR Pfam; PF00135; Coesterase; 1.  
 DR PRINTS; PR00878; CHOLNESTRASE.  
 DR PROSITE; PS00122; CARBOXYLESTERASE\_B\_1; 1.  
 DR PROSITE; PS00941; CARBOXYLESTERASE\_B\_2; 1.  
 KW Hydrolase; Membrane; Serine esterase; Signal.  
 FT SIGNAL 1 29 Potential.  
 FT CHAIN 30 603 butyrylcholinesterase.  
 SQ SEQUENCE 603 AA; 68481 MW; A350FDDF68574ADF CRC64;  
 Query Match 67.9%; Score 38; DB 2; Length 603;  
 Best Local Similarity 75.0%; Pred. No. 3.4e+02;  
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 HQYSKLPW 8  
 Db 451 HRSSKLPW 458  
 ||:|||||  
 RESULT 30  
 Q6MI24\_BDEBA PRELIMINARY; PRT; 657 AA.  
 ID Q6MI24\_BDEBA  
 AC Q6MI24;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Hypothetical protein precursor (EC 3.6.3.14).  
 GN OrderedLocustNames=Bd3355;  
 OS Bdellovibrio bacteriovorus.  
 OC Bacteria; Proteobacteria; Deltaproteobacteria; Bdellovibrionales;  
 OC Bdellovibrionaceae; Bdellovibrio.  
 OX NCBI\_TaxID=959;  
 RN [1] :|||||  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=HD100 / DSM 50701 / ATCC 15356 / NCIB 9529;  
 RX PubMed=14752164; DOI=10.1126/science.1093027;  
 RA Rendulic S., Jagtap P., Rosinus A., Eppinger M., Baar C., Lanz C.,  
 RA Keller H., Lambert C., Evans K.J., Goessmann A., Meyer F.,  
 RA Sockett R.E., Schuster S.C.;  
 RT "A predator unmasked: life cycle of Bdellovibrio bacteriovorus from a genomic perspective."  
 RL Science 303:689-692(2004).  
 DR EMBL; BX842655; CAE78158.1; -; Genomic DNA.  
 KW Complete proteome; Hydrolase; Hypothetical protein; Signal.  
 FT SIGNAL 1 9  
 SQ SEQUENCE 657 AA; 74124 MW; B3CBFA18D745419C CRC64;  
 Query Match 67.9%; Score 38; DB 2; Length 657;  
 Best Local Similarity 71.4%; Pred. No. 3.7e+02;  
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 QYSKLPW 8  
 Db 455 EYSKLPW 461  
 ||:|||||  
 RESULT 31  
 Q8MY38\_9NEOP PRELIMINARY; PRT; 698 AA.  
 ID Q8MY38\_9NEOP  
 AC Q8MY38;  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Gag-like protein.  
 GN Name=ORP1;  
 OS Papilio xuthus.  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditryaia;  
 OC Papilionoidea; Papilionidae; Papilioninae; Papilio.  
 OX NCBI\_TaxID=66420;  
 RN [1] :|||||  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=22531580; PubMed=12644555; DOI=10.1093/molbev/meg031;  
 RA Kojima K.K., Fujiwara H.;  
 RT "Evolution of target specificity in R1 clade non-LTR retrotransposons."  
 RL Mol. Biol. Evol. 20:351-361(2003).  
 DR EMBL; AB078928; BAC06449.1; -; Genomic DNA.  
 DR GO; GO:0003676; F:nucleic acid binding; IEA.  
 DR InterPro; IPR001878; Znf CCHC.  
 DR Pfam; PF00098; zf-CCHC; 2.  
 DR PRINTS; PR00939; C2HCZNFINGER.  
 DR SMART; SM00343; Znf C2HC; 2.  
 DR PROSITE; PS50158; ZF\_CCHC; 2.  
 SQ SEQUENCE 698 AA; 75954 MW; E10A654A5A6F90A5 CRC64;  
 Query Match 67.9%; Score 38; DB 2; Length 698;  
 Best Local Similarity 66.7%; Pred. No. 4e+02;  
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 HQYSKLPW 9  
 Db 375 HQKLPW 383  
 ||:|||||  
 RESULT 32  
 Q6CJY8\_KLUJA PRELIMINARY; PRT; 1036 AA.  
 ID Q6CJY8\_KLUJA  
 AC Q6CJY8;  
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
 DE Kluyveromyces lactis strain NRRL Y-1140 chromosome F of strain NRRL Y-1140 of Kluyveromyces lactis.  
 GN OrderedLocustNames=KLLA0F14927g;  
 OS Kluyveromyces lactis (Yeast).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.  
 OX NCBI\_TaxID=28985;  
 RN [1] :|||||  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RC STRAIN=CBS 2359 / IFO 1267 / NRRL Y-1140 / WM37;  
 RX PubMed=15229592; DOI=10.1038/nature02579;  
 RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,  
 RA Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,  
 RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,  
 RA Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykaeten C.,  
 RA Boissane A., Boyer J., Cattolico L., Confanieri F., de Daruvar A.,  
 RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,  
 RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,  
 RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,  
 RA Nicaud J.-M., Nikoleki M., Oztas S., Ozier-Kalogeropoulos O.,  
 RA Pellenz S., Potier S., Richard G.-F., Straub M.-L., Suleau A.,  
 RA Swennen D., Tekaia F., Wesolowski-Louvel M., Westhof E., Wirth B.,



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RA Zeniou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,
RA Bouchier C., Caudron B., Scarpellini C., Gaillardin C., Weissenbach J.,
RA Winkler P., Souciet J.-L.;
RT "Genome evolution in yeasts.";
RL Nature 430:35-44(2004).
CC -1- SIMILARITY: Contains 2 C2 domains.
DR EMBL; CR382126; CAG98459.1; -; Genomic_DNA.
DR GO; GO:0004609; P:phosphatidylserine decarboxylase activity; IEA.
DR GO; GO:0008654; P:phospholipid biosynthesis; IEA.
DR InterPro; IPR000008; C2.
DR InterPro; IPR003817; PS_Dcarboxylase.
DR InterPro; IPR005221; PS_decarb.
DR Pfam; PF0168; C2; 2.
DR Pfam; PF02666; PS_Dcarboxylase; 1.
DR PRINTS; PR00360; C2DOMAIN.
DR SMART; SM00239; C2; 2.
DR TIGRFAMs; TIGR00163; PS_decarb; 1.
DR PROSITE; PS50004; C2_DOMAIN_2; 1.
KW Complete proteome.
SQ SEQUENCE 1036 AA; 118499 MW; 22DF98B5DBF3705C CRC64;

Query Match 67.9%; Score 38; DB 2; Length 1036;
Best Local Similarity 55.6%; Pred. No. 5.9e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYSLKPWT 9
|:|:|:|:
Db 571 HFYKVPWS 579

RESULT 33
Q4P862 USTMA PRELIMINARY; PRT; 1069 AA.
AC Q4P862;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=UM03701.1;
OS Ustilago maydis 521.
OC Eukaryota; Fungi; Basidiomycota; Ustilaginomycetes;
OC Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.
OX NCBI_TaxID=237631;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=521;
RA Birren B., Nusbaum C., Abebe A., Abouelleil A., Adekoya E.,
RA Ait-zahra M., Allen N., Allen T., An P., Anderson M., Anderson S.,
RA Arachchi H., Armbruster J., Bachantsang P., Baldwin J., Barry A.,
RA Bayul T., Blitshteyn B., Bloom T., Blye J., Boguslavskiy L.,
RA Borowsky M., Boukhgalter B., Brunache A., Butler J., Calixte N.,
RA Calvo S., Camarata J., Campo K., Chang J., Cheshatsang Y., Citroen M.,
RA Collymore A., Considine T., Cook A., Cooke P., Corum B., Cuomo C.,
RA David R., Dawoe T., Degray S., Dodge S., Dooley K., Dorje P.,
RA Dorjee K., Dorris L., Duffey N., Dupes A., Elkins T., Engels R.,
RA Erickson J., Farina A., Faro S., Ferreira P., Fischer H.,
RA Fitzgerald M., Foley K., Gage D., Galagan J., Galtsova K., Gnerre S.,
RA Gnirke A., Goyette A., Graham J., Grandbois E., Gyaltsen K., Hafez N.,
RA Hagopian D., Hagos B., Hall J., Hatcher B., Heller A., Higgins H.,
RA Hogan T., Horn A., Houde N., Hughes L., Hulme W., Huseby E., Iliev I.,
RA Jaffe D., Jones C., Kamal M., Kamat A., Kamysseleis M., Karlsson E.,
RA Kellis C., Kieu A., Kienner P., Kodira C., Kulbokas E., Labutti K.,
RA Lama D., Landers T., Leger J., Levine S., Lewis D., Lewis T.,
RA Lindblad-toh K., Liu X., Lokvitsang T., Lokvitsang Y., Lucien O.,
RA Lui A., Ma L.J., Mabbitt R., Macdonald J., Maclean C., Major J.,
RA Manning J., Marabella R., Maru K., Matthews C., Mauceli E.,
RA McCarthy M., McDonough S., Mcghee T., Meldrim J., Meneus L.,
RA Mesirov J., Mihalev A., Mihova T., Mikkelsen T., Mienga V., Moru K.,
RA Mozes J., Mullrain L., Munson G., Naylor J., News C., Nguyen C.,
RA Nguyen N., Nguyen T., Nicol R., Nielsen C., Nizzari M., Norbu C.,
RA Norbu N., O'donnell P., Okoro O., O'leary S., Omotosho B.,
RA O'Neill K., Osman S., Parker S., Perrin D., Phunkhang P., Picani B.,
RA Purcell S., Rachupka T., Ramasamy U., Rameau R., Ray V., Raymond C.,
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RA Retta R., Richardson S., Rise C., Rodriguez J., Rogers J., Rogov P.,
RA Rutnan M., Schubach R., Seaman C., Settipalli S., Sharpe T.,
RA Sheridan J., Sherpa N., Shi J., Smirnov S., Smith C., Sougnez C.,
RA Spencer B., Stalker J., Stange-thomann N., Stavropoulos S.,
RA Stetson K., Stone C., Stone S., Stubbs M., Talamas J., Tchuinga P.,
RA Tenzing P., Testaye S., Theodore J., Thoulutsang Y., Topham K.,
RA Towey S., Tsamla T., Tsomo N., Vallee D., Vassiliev H.,
RA Venkataran V., Vinson J., Vo A., Wade C., Wang S., Wangchuk T.,
RA Wangdi T., Whittaker C., Wilkinson J., Wu Y., Wyman D., Yadvav S.,
RA Yang S., Yang X., Yeager S., Yee E., Young G., Zainoun J., Zembeck L.,
RA Zimmer A., Zody M., Lander E.;
RT "The genome sequence of Ustilago maydis.";
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AACP01000124; EAK84879.1; -; Genomic_DNA.
DR InterPro; IPR000340; DS_phosphatase.
DR InterPro; IPR000387; TYR_phosphatase.
DR Pfam; PF00782; DSPC; 1.
DR SMART; SM00195; DSPC; 1.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS00056; TYR_PHOSPHATASE_2; 1.
DR PROSITE; PS00054; TYR_PHOSPHATASE_DUAL; 1.
KW Hydrolase; Hypothetical protein.
SQ SEQUENCE 1069 AA; 113198 MW; D113B6B440E26D32 CRC64;

Query Match 67.9%; Score 38; DB 2; Length 1069;
Best Local Similarity 75.0%; Pred. No. 6.1e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYSLKPWT 9
|:|:|:|:
Db 507 RYVKLPWT 514

RESULT 34
MCE_RECVD STANDARD; PRT; 1289 AA.
ID MCE_RECVD
AC P11079;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE mRNA capping enzyme (mRNA guanylyltransferase) (EC 2.7.7.50) (GTP--RNA
DE guanylyltransferase).
DE Name=L2;
OS Reovirus type 3 (strain Dearing) (T3D) (Mammalian orthoreovirus 3).
OC Viruses; dsRNA viruses; Reoviridae; Orthoreovirus;
OC Mammalian orthoreoviruses.
OX NCBI_TaxID=10886;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC RNA].
RX MEDLINE=88058999; PubMed=2824487;
RA Seliger L.S., Zheng K., Shatkin A.J.;
RT "Complete nucleotide sequence of reovirus L2 gene and deduced amino
RT acid sequence of viral mRNA guanylyltransferase.";
RL J. Biol. Chem. 262:16289-16293(1987).
CC -1- FUNCTION: mRNA capping.
CC -1- CATALYTIC ACTIVITY: GTP + (5')pp-Pur-mRNA = diphosphate +
CC G(5')ppp-Pur-mRNA.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; J03488; AAA47253.1; -; Genomic_RNA.
DR PIR; A28471; RMXRR3.
DR PDB; 1EJ6; X-ray; A=1-1289.
DR SMR; P11079; 3-1289.
DR InterPro; IPR010311; Reovirus_L2.
DR Pfam; PF06016; Reovirus_L2; 1.
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```

KW 3D-structure; mRNA capping; mRNA processing; Nucleotidyltransferase;
KW Transferase..
FT REGION 941 968 Hydrophilic.
SQ SEQUENCE 1289 AA; 144067 MW; 8C497F0B6937018B CRC64;

Query Match 67.9%; Score 38; DB 1; Length 1289;
Best Local Similarity 66.7%; Pred. No. 7.4e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HOYSKLPWT 9
||:|:|
Db 659 HQHSSLTWT 667

RESULT 35
Q91RA1 REOVD
ID Q91RA1 REOVD PRELIMINARY; PRT; 1289 AA.
AC Q91RA1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE Core-spike protein lambda-2.
OS Reovirus type 3 (strain Dearing) (T3D) (Mammalian orthoreovirus 3).
OC Viruses; dsRNA viruses; Reoviridae; Orthoreovirus;
OC Mammalian orthoreoviruses.
OX NCBI_TaxID=10886;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Hall;
RX MEDLINE=21425393; PubMed=11531411; DOI=10.1006/viro.2001.1052;
RA Breun L.A., Broering T.J., McCutcheon A.M., Harrison S.J.,
Luongo C.L., Nibert M.L.;
" Mammalian reovirus L2 gene and lambda2 core spike protein sequences
RT and whole-genome comparisons of reoviruses type 1 Lang, type 2 Jones,
RT and type 3 Dearing.";
RL Virology 287:333-348(2001).
DR EMBL; AF378010; AKS7514.1; -; mRNA.
DR SMR; Q91RA1; 3-1289.
DR InterPro; IPR010311; Reovirus_L2.
DR Pfam; PF06016; Reovirus_L2; 1.
SQ SEQUENCE 1289 AA; 143843 MW; E41D982522E2B8F4 CRC64;

Query Match 67.9%; Score 38; DB 2; Length 1289;
Best Local Similarity 66.7%; Pred. No. 7.4e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HOYSKLPWT 9
||:|:|
Db 659 HQHSSLTWT 667

RESULT 36
Q5CJX7 CRYHO
ID Q5CJX7 CRYHO PRELIMINARY; PRT; 1326 AA.
AC Q5CJX7;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE Hypothetical protein.
GN ORFNames=Chro.40385;
OS Cryptosporidium hominis.
OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
OC Cryptosporidiidae; Cryptosporidium.
OX NCBI_TaxID=237895;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=TU502;
RA Xu P., Widmer G., Wang Y., Ozaki L.S., Alves J.M., Serrano M.G.,
Puiu D., Manque P., Akiyoshi D., Mackey A.J., Pearson W.R., Dear P.H.,
Bankier A.T., Peterson D.L., Abrahamsen M.S., Kapur V., Tripori S.,
Buck G.A.;
" The genome of Cryptosporidium hominis.";
RT Nature 431:1107-1112(2004).

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DR EMBL; AAELO1000107; EAL36906.1; -; Genomic_DNA.
DR InterPro; IPR000409; Beige_BEACH.
DR Pfam; PF02138; Beach; 1.
DR PROSITE; PS50197; BEACH; 1.
KW Hypothetical protein.
SQ SEQUENCE 1326 AA; 152792 MW; E8C033C2777306F2 CRC64;

Query Match 67.9%; Score 38; DB 2; Length 1326;
Best Local Similarity 50.0%; Pred. No. 7.6e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYSKLPW 8
||:|:|
Db 690 HEYANPW 697

RESULT 37
KV1B HUMAN
ID KV1B HUMAN STANDARD; PRT; 108 AA.
AC P01594;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-I region AU.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=72189444; PubMed=5028201;
RA Schleich H., Hilschmann N.;
" Rule of antibody structure. The primary structure of a monoclonal
RT immunoglobulin L-chain of the kappa-type, subgroup I (Bence-Jones
RT protein Au).";
RL Hoppe-Seyler's Z. Physiol. Chem. 353:345-370(1972).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RX MEDLINE=77022433; PubMed=1234024;
RA Fehlgammer H., Schiffer M., Epp O., Colman P.M., Lattman E.E.,
Schwager P., Steigemann W., Schramm H.J.;
" The structure determination of the variable portion of the Bence-
RT Jones protein Au.";
RL Biophys. Struct. Mech. 1:139-146(1975).
CC -!- MISCELLANEOUS: The structure of the V region was determined by
CC molecular replacement methods using the known structure of the V
CC region of the kappa chain REI.
CC -!- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC -!- MISCELLANEOUS: This is a Bence-Jones protein.
CC -----
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC PIR; A91653; K1HUAU.
CC PDB; 1JVS; X-ray; A=1-107.
CC Ensembl; ENSG00000173782; Homo sapiens.
CC GO; GO:0005576; Extracellular region; NAS.
CC GO; GO:0003823; P:antigen binding; NAS.
CC GO; GO:0006955; P:immune response; NAS.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003596; Ig_v.
CC SMART; SM00406; IGV; 1.
CC PROSITE; PS50835; IG_LIKE; 1.
KW 3D-structure; Bence-Jones protein; Direct protein sequencing;
KW Immunoglobulin domain; Immunoglobulin V region.
FT REGION 1 23 Framework-1.
FT REGION 24 34 Complementarity-determining-1.
FT REGION 35 49 Framework-2.
FT REGION 50 56 Complementarity-determining-2.

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FT REGION 57 88 Framework-3.
FT REGION 89 97 Complementarity-determining-3.
FT REGION 98 107 Framework-4.
FT DISULFID 23 88 By similarity.
FT NON_TER 108 108
FT STRAND 4 5
FT STRAND 10 13
FT TURN 15 16
FT TURN 19 25
FT TURN 30 31
FT TURN 33 38
FT TURN 40 41
FT TURN 44 49
FT TURN 50 52
FT STRAND 53 54
FT TURN 56 57
FT TURN 60 61
FT TURN 62 67
FT TURN 68 69
FT STRAND 70 75
FT HELIX 80 82
FT STRAND 85 90
FT STRAND 97 98
FT STRAND 102 106
SQ SEQUENCE 108 AA; 11939 MW; E8011187E56F6FB9 CRC64;

Query Match 66.1%; Score 37; DB 1; Length 108;
Best Local Similarity 75.0%; Pred. No. 91;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QYSLPWT 9
DB 90 QYDYLFWT 97

RESULT 38
Q9CTV5_MOUSE PRELIMINARY; PRT; 108 AA.
AC Q9CTV5;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE Mus musculus 6 days neonate head cDNA, RIKEN full-length enriched
DE library, clone:5430437C04Rik; product:hypothetical protein, full insert
DE sequence. (Fragment).
GN Name=5430437C04Rik; Synonyms=5830416P10Rik;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Head;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Head;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

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RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., King B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-Oka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Head;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Head;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Head;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitzunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Head;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK019949; BAB31930.1; -; mRNA.
DR Ensembl; ENSMUSG00000025023; Mus musculus.
DR MGI; MGI:1925346; 5430437C04Rik.
DR MGI; MGI:1922001; 5830416P10Rik.
KW Hypothetical protein.
FT NON_TER 1 108
FT NON_TER 1
SQ SEQUENCE 108 AA; 11561 MW; 8BDBBF861623608F CRC64;

Query Match 66.1%; Score 37; DB 2; Length 108;
Best Local Similarity 75.0%; Pred. No. 91;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYSLPWT 9
DB 17 QISRLPWT 24

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RESULT 39
KV4C_HUMAN STANDARD; PRT; 134 AA.
ID P06314;
AC P06314;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-IV region B17 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=86041854; PubMed=2997713;
RA Marsh P., Mills F., Gould H.;
RT "Detection of a unique human V kappa IV germline gene by a cloned cDNA
RT probe."
RL Nucleic Acids Res. 13:6531-6544 (1985).
RN [2]
RP SEQUENCE REVISION TO 76.
RA Marsh P.;
RL Submitted (OCT-1986) to the EMBL/GenBank/DBJ databases.
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; X02990; CAA26733.1; -; mRNA.
CC HSSP; P01625; ILVE.
CC SMR; P06314; 21-134.
CC GO; GO:0005576; C:extracellular region; NAS.
CC GO; GO:0003823; F:antigen binding; NAS.
CC GO; GO:0008955; P:immune response; NAS.
CC InterPro; IPR007110; Ig-like.
CC SMART; SM00406; IGV; 1.
CC PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin domain; Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 134 Ig kappa chain V-IV region B17.
FT REGION 21 43 Framework-1.
FT REGION 44 60 Complementarity-determining-1.
FT REGION 61 75 Framework-2.
FT REGION 76 82 Complementarity-determining-2.
FT REGION 83 114 Framework-3.
FT REGION 115 121 Complementarity-determining-3.
FT REGION 122 133 Framework-4.
FT DISULFID 43 114 By similarity.
FT NON_TER 134 134
SQ SEQUENCE 134 AA; 14966 MW; 6413A22FD0738B32 CRC64;

Query Match 66.1%; Score 37; DB 1; Length 134;
Best Local Similarity 75.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 HOYKLPWT 9
DB 116 QYTNLPWT 123

RESULT 40
Q8VDD0_MOUSE PRELIMINARY; PRT; 134 AA.
ID Q8VDD0;
AC Q8VDD0;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Anti-MOG Z12 variable light chain (Fragment).
GN Name=Gm1502; Synonym=anti-MOG kappa;

Query Match 66.1%; Score 37; DB 1; Length 134;
Best Local Similarity 75.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QYKLPWT 9
DB 116 QYTNLPWT 123

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OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BALB/c;
RA Semb P.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BALB/c;
RA Chernajovsky Y.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=2427335;
RA Caton A.J., Browlee G.G., Staudt L.M., Gerhard W.;
RT "Structural and functional implications of a restricted antibody
RT response to a defined antigenic region on the influenza virus
RT hemagglutinin."
RL EMBO J. 5:1577-1587(1986).
DR EMBL; AJ416331; CAC94866.1; -; mRNA.
DR PIR; G27887; G27887.
DR HSSP; P01834; IMIM.
DR SMR; Q8VDD0; 23-134.
DR Ensembl; ENSMUSG0000062047; Mus musculus.
DR MGI; MGI:2686348; Gm1502.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; IGV.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
FT NON_TER 134 134
SQ SEQUENCE 134 AA; 14525 MW; CDF8E2236E2D0CF CRC64;

Query Match 66.1%; Score 37; DB 2; Length 134;
Best Local Similarity 66.7%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 HOYKLPWT 9
DB 110 HQSSYPWT 118

RESULT 41
O85999_SPHAR PRELIMINARY; PRT; 190 AA.
ID O85999;
AC O85999;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein orf1251 precursor.
GN Name=orf1251;
OS Sphingomonas aromaticivorans.
OG Plasmid pNLI.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Sphingomonadales;
OC Sphingomonadaceae; Novosphingobium.
OX NCBI_TaxID=48935;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=F199;
RX MEDLINE=99175459; PubMed=10049392;
RA Romine M.F., Stillwell L.C., Wong K.-K., Thurston S.J., Sisek E.C.,
RA Sensen C., Gaasterland T., Fredrickson J.K., Saffer J.D.;
RT "Complete sequence of a 184-kilobase catabolic plasmid from
RT Sphingomonas aromaticivorans F199."
RL J. Bacteriol. 181:1585-1602(1999).
DR EMBL; AF079317; AAD04015.1; -; Genomic DNA.
DR PIR; T31291; T31291.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR006311; Tat.
DR TIGRFAMs; TIGR01409; Tat_signal_seq; 1.

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DR PROSITE: PS50835; IG-LIKE; 1.  
 KW Hypothetical protein; Immunoglobulin domain; Plasmid; Signal.  
 FT SIGNAL 1 31 Potential.  
 SQ SEQUENCE 190 AA; 2FA2EF9E979F9822 CRC64;

Query Match 66.1%; Score 37; DB 2; Length 190;  
 Best Local Similarity 75.0%; Pred. No. 1.6e+02; Indels 0; Gaps 0;  
 Matches 6; Conservative 0; Mismatches 2;

QY 1 HQYSLPWP 8  
 |||||  
 Db 114 HQYKLRW 121

## RESULT 42

Q9PU09 LATCH PRELIMINARY; PRT; 242 AA.  
 AC Q9PU09  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
 DE DM20 (Fragment).  
 GN Name=DM20;  
 OS Latimeria chalumnae (Latimeria) (Coelacanth).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Coelacanthiformes; Coelacanthidae; Latimeria.  
 OX NCBI\_TaxID=7897;  
 RN [1]

RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=99330421; PubMed=10403627; DOI=10.1023/A:1020958014398;  
 RA Tohyama Y., Kasama-Yoshida H., Sakuma M., Kobayashi Y., Cao Y.,  
 RA Hasegawa M., Kojima H., Tamai Y., Tanokura M., Kurihara T.;  
 RT "Gene structure and amino acid sequence of Latimeria chalumnae  
 (coelacanth) myelin DM20: phylogenetic relation of the fish.";  
 RL Neurochem. Res. 24:867-873(1999).  
 DR EMBL; AB025938; BAA84207.1; -; Genomic\_DNA.  
 DR InterPro; IPR001614; Myelin\_PLP.  
 DR Pfam; PF01275; Myelin\_PLP; 1.  
 DR PRINTS; PR00214; MYELINPLP.  
 DR SMART; SM00002; PLP; 1.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 242 AA; 26991 MW; 9BE3556B38E25DE2 CRC64;

Query Match 66.1%; Score 37; DB 2; Length 242;  
 Best Local Similarity 75.0%; Pred. No. 2.1e+02;  
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QYSLPWP 9  
 |||||  
 Db 168 QYGLPWP 175

## RESULT 43

Q8UT6 BRARE PRELIMINARY; PRT; 245 AA.  
 ID Q8UT6  
 AC Q8UT6  
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
 DE Dmalphal (Proteolipid protein 1a).  
 GN Name=plp1a;  
 OS Brachydanio rerio (Zebrafish) (Danio rerio).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
 OC Cyprinidae; Danio.  
 OX NCBI\_TaxID=7955;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Werner H., Schweitzer J., Schachner M., Nave K.-A.;  
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=singapore local strain; TISSUE=Embryo;

RX MEDLINE=23388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altshuler S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,  
 RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [3]

RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=singapore local strain; TISSUE=Embryo;  
 RG NIH MGC Project;  
 RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY070259; AAL59885.1; -; mRNA.  
 DR EMBL; BC095297; AAH95297.1; -; mRNA.  
 DR Ensembl; ENSDARG0000005669; Danio rerio.  
 DR ZFIN; ZDB-GENE-001202-1; plp1a.  
 DR GO; GO:0042552; P:myelination; IEP.  
 DR InterPro; IPR001614; Myelin\_PLP.  
 DR Pfam; PF01275; Myelin\_PLP; 1.  
 DR PRINTS; PR00214; MYELINPLP.  
 DR SMART; SM00002; PLP; 1.  
 DR PROSITE; PS01004; MYELIN\_PLP 2; 1.  
 SQ SEQUENCE 245 AA; 27510 MW; 764B19BF8B949C9A CRC64;

Query Match 66.1%; Score 37; DB 2; Length 245;  
 Best Local Similarity 75.0%; Pred. No. 2.1e+02;  
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QYSLPWP 9  
 |||||  
 Db 171 QYGLPWP 178

## RESULT 44

Q6MQC7 BDEBA PRELIMINARY; PRT; 330 AA.  
 ID Q6MQC7  
 AC Q6MQC7  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Hypothetical protein.  
 GN OrderedLocusNames=BQ0547;  
 OS Bdellovibrio bacteriovorus.  
 OC Bacteria; Proteobacteria; Deltaproteobacteria; Bdellovibrionales;  
 OC Bdellovibrionaceae; Bdellovibrio.  
 OX NCBI\_TaxID=959;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=HD100 / DSM 50701 / ATCC 15356 / NCIB 9529;  
 RX PubMed=14752164; DOI=10.1126/science.1093027;  
 RA Rendulic S., Jagtap P., Rosinus A., Eppinger M., Baar C., Lanz C.,  
 RA Keller H., Lambert C., Evans K.J., Gessmann A., Meyer F.,  
 RA Sockett R.E., Schuster S.C.;  
 RT "A predator unmasked: life cycle of Bdellovibrio bacteriovorus from a  
 genomic perspective.";  
 RL Science 303:689-692(2004).  
 DR EMBL; BX842647; CAE78520.1; -; Genomic DNA.  
 KW Complete proteome; Hypothetical protein.  
 SQ SEQUENCE 330 AA; 37401 MW; E67D64135E164929 CRC64;

```

Query Match      66.1%; Score 37; DB 2; Length 330;
Best Local Similarity 62.5%; Pred. No. 2.8e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYSKLPW 8
DB 207 NQYDKVPW 214

RESULT 45
QSAK74 CANAL
ID QSAK74 CANAL PRELIMINARY; PRT; 331 AA.
AC QSAK74;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Hypothetical protein COX18.
GN Names=COX18; ORFNames=CaO19.11428, CaO19.3946;
OS Candida albicans SC5314.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Mitosporic Saccharomycetales; Candida.
OX NCBI_TaxID=237561;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=SC5314;
RX PubMed=15123810; DOI=10.1073/pnas.0401648101;
RA Jones T., Federspiel N.A., Chibana H., Dungan J., Kalman S.,
RA Magee B.B., Newport G., Thorstenson Y.R., Agabian N., Magee P.T.,
RA Davis R.W., Scherer S.;
RT "The diploid genome sequence of Candida albicans.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:7329-7334(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=SC5314;
RA Dungan J., Kuo A., Newport G., Lan C.-Y., Iijima C., Adegbola O.,
RA Roberts J., Persson K., Donnelly S., Favoreto S., Truong K.-W.,
RA Jones T., Scherer S., Agabian N.;
RT "Annotation of the Genome of Candida albicans.";
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to the OXA1/OXA family.
DR EMBL; AACQ01000012; EAL03076.1; -; Genomic DNA.
DR EMBL; AACQ01000011; EAL03240.1; -; Genomic DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0051205; P:protein insertion into membrane; IEA.
KW Hypothetical protein; Transmembrane.
SQ SEQUENCE 331 AA; 38050 MW; B319C02DEBE3644C CRC64;

Query Match      66.1%; Score 37; DB 2; Length 331;
Best Local Similarity 62.5%; Pred. No. 2.8e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYSKLPW 8
DB 46 HEFSGLPW 53

RESULT 46
Q9FLA1 ARATH
ID Q9FLA1 ARATH PRELIMINARY; PRT; 388 AA.
AC Q9FLA1;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Similarity to heat shock transcription factor.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RP NUCLEOTIDE SEQUENCE.

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RX MEDLINE=98344145; PubMed=9679202;
RA Kaneko T., Kotani H., Nakamura Y., Sato S., Asamizu E., Miyajima N.,
RA Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. V. Sequence
RT features of the regions of 1,381,565 bp covered by twenty one
RT physically assigned P1 and TAC clones.";
RL DNA Res. 5:131-145(1998).
DR EMBL; AB010693; BAB10879.1; -; Genomic DNA.
DR GO; GO:0006457; P:protein folding; IEA.
DR GO; GO:0006986; P:response to unfolded protein; IEA.
DR GO; GO:0006512; P:ubiquitin cycle; IEA.
DR InterPro; IPR001810; F-box.
DR InterPro; IPR006566; FBD.
DR Pfam; PF00846; F-box; 1.
DR SMART; SM00579; FBD; 1.
DR PROSITE; PS0181; FBOX; 1.
KW Heat shock.
SQ SEQUENCE 388 AA; 45144 MW; 3117852CD27D24F5 CRC64;

Query Match      66.1%; Score 37; DB 2; Length 388;
Best Local Similarity 75.0%; Pred. No. 3.3e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 HOYSKLPW 8
DB 256 HSYSKLW 263

RESULT 47
OXA1 YEAST
ID OXA1 YEAST STANDARD; PRT; 402 AA.
AC P39952;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Inner membrane protein OXA1, mitochondrial precursor (Oxidase assembly
DE protein 1) (Cytochrome oxidase biogenesis protein OXA1).
GN Name=OXA1; Synonyms=PET1402; OrderedLocusNames=YER154W;
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC 28383 / FL100;
RX MEDLINE=94254098; PubMed=8196054;
RA Bonnefoy N., Chalvet F., Hamel P., Slonimski P.P., Dujardin G.;
RT "OXA1, a Saccharomyces cerevisiae nuclear gene whose sequence is
RT conserved from prokaryotes to eukaryotes controls cytochrome oxidase
RT biogenesis.";
RL J. Mol. Biol. 239:201-212(1994).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=95115877; PubMed=7816036; DOI=10.1007/BF00290106;
RA Bauer M., Behrens M., Esser K., Michaelis G., Pratje E.;
RT "PET1402, a nuclear gene required for proteolytic processing of
RT cytochrome oxidase subunit 2 in yeast.";
RL Mol. Genet. 245:272-278(1994).
RN [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=S288c / AB972;
RX MEDLINE=97313264; PubMed=9169868;
RA Dietrich F.S., Mulligan J.T., Hennessy K.M., Yelton M.A., Allen E.,
RA Araujo R., Aviles E., Berno A., Brennan T., Carpenter J., Chen E.,
RA Cherry J.M., Chung E., Duncan M., Guzman E., Hartzell G.,
RA Hunnicke-Smith S., Hyman R.W., Kayser A., Komp C., Lashkari D., Lew H.,
RA Lin D., Mosedale D., Nakahara K., Namath A., Norgren R., Oefner P.,
RA Olin C., Petel F.X., Roberts D., Sehl P., Schramm S., Shogren T.,
RA Smith V., Taylor P., Wei Y., Botstein D., Davis R.W.;
RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome V.";
RL Nature 387:78-81(1997).
RN [4]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].

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RC STRAIN=5288c;  
RA Mareschky G., Rolfs A., Richardson A., Kane M., Baqui M., Tavcher E.,  
RA Hu Y., Vanberg F., Meger J., Kramer J., Moreira D., Kelley F.,  
RA Zuo D., Raphael J., Hogle C., Jepson D., Williamson J., Camargo A.,  
RA Gonzaga L., Vasconcelos A.T., Simpson A., Kolodner R., Harlow E.,  
RA LaBaer J.;  
RT "Creation of the YFLEX clone resource: cloning of Saccharomyces  
RT cerevisiae ORFs in the Gateway recombinational cloning system.";  
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.  
RN [15]  
RP TOPOLOGY.  
RX MEDLINE=97315163; PubMed=9171337; DOI=10.1093/emboj/16.9.2217;  
RA Herrmann J.M., Neupert W., Stuart R.A.;  
RT "Insertion into the mitochondrial inner membrane of a polytopic  
RT protein, the nuclear-encoded Oxa1p.";  
RL EMBO J. 16:2217-2226(1997).  
RN [16]  
RP FUNCTION.  
RX MEDLINE=98151498; PubMed=9482871; DOI=10.1073/pnas.95.5.2250;  
RA Hell K., Herrmann J.M., Prast E., Neupert W., Stuart R.A.;  
RT "Oxa1p, an essential component of the N-tail protein export machinery  
RT in mitochondria.";  
RL Proc. Natl. Acad. Sci. U.S.A. 95:2250-2255(1998).  
RN [17]  
RP INTERACTION WITH MRP20.  
RX PubMed=14657017; DOI=10.1093/emboj/cdg624;  
RA Jia L., Dienhart M., Schramm M., McCauley M., Hell K., Stuart R.A.;  
RT "Yeast Oxa1 interacts with mitochondrial ribosomes: the importance of  
RT the C-terminal region of Oxa1.";  
RL EMBO J. 22:6438-6447(2003).  
RN [18]  
RP REVIEW.  
RX MEDLINE=22178284; PubMed=12191770; DOI=10.1016/S0167-4889(02)00266-5;  
RA Stuart R.A.;  
RT "Insertion of proteins into the inner membrane of mitochondria: the  
RT role of the Oxa1 complex.";  
RL Biochim. Biophys. Acta 1592:79-87(2002).  
CC -I- FUNCTION: Required for the insertion of integral membrane proteins  
CC into the mitochondrial inner membrane. Essential for the activity  
CC and assembly of cytochrome c oxidase. Plays a central role in the  
CC translocation and export of the N-terminal part of the COX2  
CC protein into the mitochondrial intermembrane space.  
CC -I- SUBUNIT: Interacts with the large ribosome subunit of  
CC mitochondrial ribosome. Interacts directly with MRP20.  
CC -I- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondria;  
CC inner membrane.  
CC -I- SIMILARITY: Belongs to the OXA1/oxaA family.  
CC -----  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.  
CC -----  
CC EMBL; X77558; CAAS4675.1; -; Genomic DNA.  
CC EMBL; X74456; CAAS2465.1; -; Genomic DNA.  
CC EMBL; U18917; AAB64681.1; -; Genomic DNA.  
CC EMBL; AY693132; AAT93151.1; -; Genomic DNA.  
CC F1R; S47329; S47329.  
CC GenOnline; 139232; -;  
CC Ensembl; YER154W; Saccharomyces cerevisiae.  
CC SGD; S00000956; OXA1.  
CC GO; GO:0005743; C:mitochondrial inner membrane; IDA.  
CC GO; GO:0008565; F:protein transporter activity; IMP.  
CC GO; GO:0045039; P:mitochondrial inner membrane protein import; IMP.  
CC InterPro; IPR001708; Innermemb\_insert.  
CC Pfam; PF02096; 60KD\_IMP; 1.  
CC Complete proteome; Innermemb\_insert.  
CC TransIt peptide; Transmembrane.  
CC TRANSIT 1 42 Mitochondrion (Potential).  
CC CHAIN 43 402 Inner membrane protein OXA1.  
CC TOPO\_DOM 43 118 Mitochondrial intermembrane (Potential).  
CC TRANSMEM 119 139 Potential.

FT TOPO\_DOM 140 199 Mitochondrial matrix (Potential).  
FT TRANSMEM 200 220 Potential.  
FT TOPO\_DOM 221 239 Mitochondrial intermembrane (Potential).  
FT TRANSMEM 240 260 Potential.  
FT TOPO\_DOM 261 281 Mitochondrial matrix (Potential).  
FT TRANSMEM 282 302 Potential.  
FT TOPO\_DOM 303 402 Mitochondrial intermembrane (Potential).  
FT CONFLICT 108 108 W -> R (in Ref. 1).  
SQ SEQUENCE 402 AA; 44816 MW; 108890B8F2EE67ED CRC64;  
  
Query Match 66.1%; Score 37; DB 1; Length 402;  
Best Local Similarity 75.0%; Pred. NO. 3.4e+02;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 HOYSKLPW 8  
DB 121 HVYGLPW 128  
  
RESULT 48  
Q46434\_CHLTR PRELIMINARY; PRT; 402 AA.  
AC Q46434;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Phosphoprotein.  
OS Chlamydia trachomatis.  
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.  
OX NCBI\_TaxID=813;  
RN [1]\_Nucleotide SEQUENCE.  
RP Kaul R., Meuser R.U., Wenman W.M.;  
RL Submitted (MAR-1994) to the EMBL/GenBank/DBJ databases.  
DR EMBL; L25078; AAA23164.1; -; Genomic DNA.  
DR GO; GO:0005488; F:binding; IEA.  
DR InterPro; IPR011990; TPR-like\_helical.  
SQ SEQUENCE 402 AA; 46367 MW; 5048FB42B203AB3A CRC64;  
  
Query Match 66.1%; Score 37; DB 2; Length 402;  
Best Local Similarity 75.0%; Pred. NO. 3.4e+02;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 HOYSKLPW 8  
DB 168 HALSKLPW 175  
  
RESULT 49  
Q52011\_NOCEFA PRELIMINARY; PRT; 408 AA.  
ID Q52011\_NOCEFA PRELIMINARY;  
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DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
DE Putative ferredoxin reductase.  
GN OrderedLocustNames=nfa12150;  
OS Nocardia farcinica.  
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RX Ishikawa J., Yamashita A., Mikami Y., Hoshino Y., Kurita H., Hotta K.,  
RA Shiba T., Hattori M.;  
RT "The complete genomic sequence of Nocardia farcinica IFM 10152.";  
RL Proc. Natl. Acad. Sci. U.S.A. 101:14925-14930(2004).  
DR EMBL; AP006618; BAD56060.1; -; Genomic DNA.  
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DR GO; GO:0006118; P:electron transport; IEA.  
DR InterPro; IPR001327; FAD\_pyr\_redox.

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RA Deltus H., Saegling B., Bergmann K., Shamanin V., de Villiers E.M.;
RT "The genomes of three of four novel HPV types, defined by differences
RT of their L1 genes, show high conservation of the E7 gene and the
RT URR.";
RL Virology 240:359-365(1998).
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OM protein - protein search, using sw model

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Post-processing: Minimum Match 0%  
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Pred. No. is the number of results predicted by chance to have a  
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SUMMARIES

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399	35	62.5	9	5	US-10-891-658-127	Sequence 127, App	472	34	60.7	107	4	US-10-127-890-123	Sequence 123, App
400	35	62.5	73	4	US-10-425-115-187496	Sequence 187496,	473	34	60.7	107	4	US-10-127-890-123	Sequence 125, App
401	35	62.5	77	4	US-10-424-599-272275	Sequence 272275,	474	34	60.7	107	4	US-10-340-189-26	Sequence 26, Appl
402	35	62.5	78	4	US-10-600-790-2	Sequence 2, Appli	475	34	60.7	107	4	US-10-340-189-27	Sequence 27, Appl
403	35	62.5	78	4	US-10-437-963-125347	Sequence 125347,	476	34	60.7	107	4	US-10-340-189-87	Sequence 87, Appl
404	35	62.5	78	5	US-10-872-859-36	Sequence 36, Appl	477	34	60.7	107	4	US-10-325-696-26	Sequence 26, Appl
405	35	62.5	83	3	US-09-864-408A-3580	Sequence 3580, Ap	478	34	60.7	107	4	US-10-325-696-27	Sequence 27, Appl
406	35	62.5	86	4	US-10-425-115-263567	Sequence 263567,	479	34	60.7	107	4	US-10-325-696-65	Sequence 65, Appl
407	35	62.5	88	4	US-10-425-115-331650	Sequence 331650,	480	34	60.7	107	4	US-10-309-762-53	Sequence 53, Appl
408	35	62.5	94	3	US-09-764-891-3085	Sequence 3085, Ap	481	34	60.7	107	4	US-10-309-762-56	Sequence 56, Appl
409	35	62.5	94	4	US-10-205-428-271	Sequence 271, App	482	34	60.7	107	4	US-10-723-434-15	Sequence 15, Appl
410	35	62.5	106	4	US-10-425-115-355504	Sequence 355504,	483	34	60.7	107	5	US-10-717-243-123	Sequence 123, App
411	35	62.5	107	4	US-10-723-434-17	Sequence 17, Appl	484	34	60.7	107	5	US-10-717-243-125	Sequence 125, App
412	35	62.5	107	4	US-10-723-434-18	Sequence 18, Appl	485	34	60.7	107	6	US-11-133-775-26	Sequence 26, Appl
413	35	62.5	107	4	US-10-723-434-21	Sequence 21, Appl	486	34	60.7	107	6	US-11-133-775-27	Sequence 27, Appl
414	35	62.5	107	4	US-10-723-434-22	Sequence 22, Appl	487	34	60.7	107	6	US-11-133-775-65	Sequence 65, Appl
415	35	62.5	107	4	US-10-723-434-25	Sequence 25, Appl	488	34	60.7	108	4	US-10-683-815-19	Sequence 19, Appl
416	35	62.5	107	4	US-10-723-434-26	Sequence 26, Appl	489	34	60.7	108	4	US-10-803-622-367	Sequence 267, App
417	35	62.5	107	4	US-10-723-434-27	Sequence 27, Appl	490	34	60.7	108	4	US-10-803-653-267	Sequence 267, App
418	35	62.5	107	4	US-10-723-434-28	Sequence 28, Appl	491	34	60.7	109	3	US-09-943-906-74	Sequence 74, Appl
419	35	62.5	107	4	US-10-723-434-31	Sequence 31, Appl	492	34	60.7	109	4	US-10-435-602-74	Sequence 74, Appl
420	35	62.5	107	4	US-10-723-434-32	Sequence 32, Appl	493	34	60.7	109	6	US-11-027-139-74	Sequence 74, Appl
421	35	62.5	107	4	US-10-723-434-34	Sequence 34, Appl	494	34	60.7	110	4	US-10-096-246-13	Sequence 13, Appl
422	35	62.5	107	5	US-10-891-658-88	Sequence 88, Appl	495	34	60.7	114	4	US-10-424-599-170732	Sequence 170732,
423	35	62.5	108	4	US-10-169-351-42	Sequence 42, Appl	496	34	60.7	115	4	US-10-424-599-188067	Sequence 188067,
424	35	62.5	108	5	US-10-891-658-90	Sequence 90, Appl	497	34	60.7	115	4	US-10-437-963-138889	Sequence 138889,
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431	35	62.5	213	4	US-10-379-392-155	Sequence 155, App	504	34	60.7	187	5	US-10-492-032-33	Sequence 33, Appl
432	35	62.5	225	4	US-10-364-907-15	Sequence 15, Appl	505	34	60.7	199	4	US-10-424-599-249172	Sequence 249172,
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437	35	62.5	440	4	US-10-724-972A-6790	Sequence 6790, Ap	510	34	60.7	240	4	US-10-096-246-35	Sequence 35, Appl
438	35	62.5	444	4	US-10-767-701-44294	Sequence 44294, A	511	34	60.7	240	4	US-10-127-890-147	Sequence 147, App
439	35	62.5	480	4	US-10-369-493-9031	Sequence 9031, Ap	512	34	60.7	240	4	US-10-127-890-148	Sequence 148, App
440	35	62.5	493	4	US-10-032-585-7327	Sequence 7327, Ap	513	34	60.7	240	5	US-10-717-243-147	Sequence 147, App
441	35	62.5	521	4	US-10-437-963-164186	Sequence 164186,	514	34	60.7	240	5	US-10-717-243-148	Sequence 148, App
442	35	62.5	529	4	US-10-425-115-240370	Sequence 240370,	515	34	60.7	249	4	US-10-437-963-196747	Sequence 196747,
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444	35	62.5	533	3	US-09-908-805B-63	Sequence 63, Appl	517	34	60.7	310	4	US-10-340-452-3	Sequence 3, Appli
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446	35	62.5	574	3	US-09-748-739A-21	Sequence 21, Appl	519	34	60.7	325	4	US-10-424-599-204586	Sequence 204586,
447	35	62.5	574	4	US-10-032-233-48	Sequence 48, Appl	520	34	60.7	330	4	US-10-437-963-144216	Sequence 144216,
448	35	62.5	574	4	US-10-413-432-48	Sequence 48, Appl	521	34	60.7	334	4	US-10-369-493-15513	Sequence 15513, A
449	35	62.5	574	4	US-10-324-466-48	Sequence 48, Appl	522	34	60.7	334	5	US-10-200-545-85	Sequence 85, Appl
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451	35	62.5	585	5	US-10-756-149-5293	Sequence 5293, Ap	524	34	60.7	339	4	US-10-369-493-16258	Sequence 16258, A
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453	35	62.5	644	4	US-10-087-192-1428	Sequence 1428, Ap	526	34	60.7	349	4	US-10-437-963-161176	Sequence 161176,
454	35	62.5	688	5	US-10-642-642-45	Sequence 45, Appl	527	34	60.7	381	6	US-11-097-143-5118	Sequence 5118, Ap
455	35	62.5	784	5	US-10-488-645-5	Sequence 5, Appli	528	34	60.7	415	4	US-10-437-963-119892	Sequence 119892,
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458	35	62.5	1934	4	US-10-309-290-136	Sequence 136, App	531	34	60.7	426	3	US-09-372-044-4	Sequence 67, Appl
459	35	62.5	5183	4	US-10-107-521-1	Sequence 1, Appli	532	34	60.7	426	3	US-09-924-417-67	Sequence 8, Appli
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461	34.5	61.6	662	3	US-09-924-358-11	Sequence 11, Appl	534	34	60.7	426	4	US-10-067-741-8	Sequence 8, Appli
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543	34	60.7	574	4	US-10-413-432-49	Sequence 49, Appl	616	33	58.9	130	5	US-10-737-290-161	Sequence 161, Appl
544	34	60.7	574	4	US-10-324-466-49	Sequence 49, Appl	617	33	58.9	131	4	US-10-693-629-38	Sequence 38, Appl
545	34	60.7	583	4	US-10-282-122A-67537	Sequence 67537, A	618	33	58.9	131	4	US-10-693-629-42	Sequence 42, Appl
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562	33	58.9	28	4	US-10-269-711-57	Sequence 57, Appl	635	33	58.9	173	4	US-10-461-093-16	Sequence 16, Appl
563	33	58.9	28	4	US-10-684-109-68	Sequence 68, Appl	636	33	58.9	176	4	US-10-461-093-19	Sequence 19, Appl
564	33	58.9	47	4	US-10-461-093-34	Sequence 34, Appl	637	33	58.9	187	6	US-11-097-143-495	Sequence 495, App
565	33	58.9	52	4	US-10-424-599-178572	Sequence 178572,	638	33	58.9	198	4	US-10-461-093-15	Sequence 15, App
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569	33	58.9	63	4	US-10-437-963-153893	Sequence 153893,	642	33	58.9	215	5	US-10-737-290-122	Sequence 122, App
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572	33	58.9	68	4	US-10-424-599-204075	Sequence 204075,	645	33	58.9	241	4	US-10-293-418-1887	Sequence 1887, Ap
573	33	58.9	74	4	US-10-461-093-30	Sequence 30, Appl	646	33	58.9	278	5	US-10-732-923-14923	Sequence 14923, A
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587	33	58.9	107	4	US-10-309-762-49	Sequence 49, Appl	660	33	58.9	375	4	US-10-374-780A-2344	Sequence 2344, App
588	33	58.9	107	4	US-10-309-762-54	Sequence 54, Appl	661	33	58.9	375	5	US-10-225-066A-528	Sequence 528, App
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592	33	58.9	108	4	US-10-307-724-123	Sequence 123, App	665	33	58.9	420	5	US-10-732-923-2574	Sequence 2574, Ap
593	33	58.9	108	4	US-10-338-366-4	Sequence 4, Appl1	666	33	58.9	421	5	US-10-732-923-4868	Sequence 4868, Ap
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597	33	58.9	108	6	US-10-496-869-33	Sequence 33, Appl	670	33	58.9	501	4	US-10-032-585-7852	Sequence 7852, Ap
598	33	58.9	108	6	US-11-040-846-7	Sequence 7, Appl1	671	33	58.9	530	5	US-10-502-282-6316	Sequence 6316, Ap
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601	33	58.9	109	5	US-10-725-963-27	Sequence 27, Appl	674	33	58.9	544	4	US-10-425-114-43526	Sequence 43526, A
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603	33	58.9	109	5	US-10-994-679-70	Sequence 70, Appl	676	33	58.9	553	3	US-09-925-299-964	Sequence 964, App
604	33	58.9	110	4	US-10-001-934-40	Sequence 40, Appl	677	33	58.9	553	4	US-10-106-698-5868	Sequence 5868, Ap
605	33	58.9	110	4	US-10-275-046-69	Sequence 69, Appl	678	33	58.9	553	5	US-10-473-127-934	Sequence 934, App
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608	33	58.9	118	3	US-09-389-705-10	Sequence 10, Appl	681	33	58.9	559	5	US-10-472-928-814	Sequence 814, App
609	33	58.9	118	3	US-10-115-406-8	Sequence 8, Appl1	682	33	58.9	567	4	US-10-369-493-7364	Sequence 7364, Ap
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696	33	58.9	1073	4	US-10-392-113-2	Sequence 1, Appli	769	32	57.1	114	5	US-10-483-994-8	Sequence 8, Appli
697	33	58.9	1073	4	US-10-383-183-1	Sequence 1, Appli	770	32	57.1	114	5	US-10-483-993-8	Sequence 8, Appli
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851	32	57.1	293	4	US-10-410-764-41	Sequence 41, Appl	924	643	4	US-10-405-877-71	Sequence 71, Appl
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871	32	57.1	365	5	US-10-732-923-4740	Sequence 4740, Appl	944	1131	3	US-09-892-635A-19	Sequence 19, Appl
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874	32	57.1	368	3	US-09-939-471-7	Sequence 7, Appl	947	1181	5	US-10-281-436A-630	Sequence 630, Appl
875	32	57.1	368	3	US-09-939-471-9	Sequence 9, Appl	948	1220	5	US-10-168-659-13	Sequence 13, Appl
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879	32	57.1	368	5	US-10-630-880-7	Sequence 7, Appl	952	1424	6	US-11-097-143-9364	Sequence 9364, Appl
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888	32	57.1	427	5	US-10-745-237-84	Sequence 84, Appl	961	56.2	31.5	US-09-995-529-137	Sequence 137, Appl
889	32	57.1	427	6	US-11-097-143-2175	Sequence 2175, Appl	962	55.4	9	US-09-995-529-137	Sequence 137, Appl
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891	32	57.1	432	5	US-10-473-193-23	Sequence 23, Appl	964	55.4	9	US-10-461-878-3	Sequence 3, Appl
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893	32	57.1	442	4	US-10-385-136-4	Sequence 4, Appl	966	55.4	9	US-10-723-962-135	Sequence 135, Appl
894	32	57.1	442	4	US-10-385-136-6	Sequence 6, Appl	967	55.4	9	US-10-461-885-3	Sequence 3, Appl
895	32	57.1	442	4	US-10-385-136-8	Sequence 8, Appl	968	55.4	9	US-10-843-011-26	Sequence 26, Appl
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897	32	57.1	493	5	US-10-485-466-29	Sequence 29, Appl	970	55.4	9	US-10-993-395-7	Sequence 7, Appl
898	32	57.1	493	5	US-10-437-963-189709	Sequence 189709, A	971	55.4	9	US-11-015-558-6	Sequence 6, Appl
899	32	57.1	523	6	US-11-097-143-22104	Sequence 22104, A	972	55.4	12	US-09-325-542A-10	Sequence 10, Appl
900	32	57.1	525	4	US-10-101-464A-613	Sequence 613, Appl	973	55.4	12	US-10-717-615-10	Sequence 10, Appl
901	32	57.1	525	5	US-10-864-252-613	Sequence 613, Appl	974	55.4	13	US-10-834-666-44	Sequence 44, Appl
902	32	57.1	533	5	US-10-287-436A-539	Sequence 539, Appl	975	55.4	14	US-10-834-666-17	Sequence 17, Appl
903	32	57.1	533	5	US-10-287-436A-1230	Sequence 1230, Appl	976	55.4	15	US-10-834-666-16	Sequence 16, Appl

977 31 55.4 15 5 US-10-808-187-838 Sequence 838, App  
978 31 55.4 15 5 US-10-807-807-838 Sequence 838, App  
979 31 55.4 20 5 US-10-834-666-15 Sequence 15, Appl  
980 31 55.4 21 5 US-10-450-763-58966 Sequence 58966, A  
981 31 55.4 27 3 US-09-864-761-37865 Sequence 37865, A  
982 31 55.4 28 5 US-10-834-666-14 Sequence 14, Appl  
983 31 55.4 36 5 US-10-834-666-12 Sequence 12, Appl  
984 31 55.4 40 4 US-10-424-599-161238 Sequence 161238, A  
985 31 55.4 46 5 US-10-450-763-31858 Sequence 31858, A  
986 31 55.4 48 4 US-10-425-115-239586 Sequence 239586, A  
987 31 55.4 52 4 US-10-437-963-171069 Sequence 171069, A  
988 31 55.4 53 4 US-10-767-701-46266 Sequence 46266, A  
989 31 55.4 60 4 US-10-424-599-179034 Sequence 179034, A  
990 31 55.4 61 4 US-10-425-115-271200 Sequence 271200, A  
991 31 55.4 62 4 US-10-425-115-25818 Sequence 25818, A  
992 31 55.4 68 4 US-10-437-963-1132017 Sequence 132017, A  
993 31 55.4 71 4 US-10-369-294-32 Sequence 32, Appl  
994 31 55.4 71 4 US-10-437-963-155241 Sequence 155241, A  
995 31 55.4 73 4 US-10-424-599-174016 Sequence 174016, A  
996 31 55.4 76 4 US-10-425-115-336092 Sequence 336092, A  
997 31 55.4 78 4 US-10-424-599-215130 Sequence 215130, A  
998 31 55.4 78 5 US-10-834-666-2 Sequence 2, Appl  
999 31 55.4 79 4 US-10-083-357-752 Sequence 752, App  
1000 31 55.4 79 4 US-10-425-115-342947 Sequence 342947, A

## ALIGNMENTS

RESULT 1  
US-09-764-304-10  
; Sequence 10, Application US/09764304  
; Patent No. US20020026036A1  
; GENERAL INFORMATION:  
; APPLICANT: SHITARA, KENYA  
; APPLICANT: HANAI, NOBUO  
; APPLICANT: HASEGAWA, MAMORU  
; APPLICANT: MIYAJI, HIROMASA  
; APPLICANT: KIWANA, YOSHIHISA  
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY  
; FILE REFERENCE: 249-101  
; CURRENT APPLICATION NUMBER: US/09/764,304  
; EARLIER FILING DATE: 2001-01-19  
; EARLIER APPLICATION NUMBER: 09/225,322  
; EARLIER FILING DATE: 1999-01-05  
; EARLIER APPLICATION NUMBER: US 08/454,680  
; EARLIER FILING DATE: 1995-05-31  
; EARLIER APPLICATION NUMBER: US 08/408,133  
; EARLIER FILING DATE: 1995-03-21  
; EARLIER APPLICATION NUMBER: US 08/292,178  
; EARLIER FILING DATE: 1994-08-17  
; EARLIER APPLICATION NUMBER: US07/947,674  
; EARLIER FILING DATE: 1992-09-17  
; EARLIER APPLICATION NUMBER: JP 3-238375  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 10  
; LENGTH: 128  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: light chain  
; OTHER INFORMATION: variable region  
US-09-764-304-19

Query Match 100.0%; Score 56; DB 3; Length 128;  
Best Local Similarity 100.0%; Pred. No. 0.082;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HOYSKLPWT 9  
Db 109 HOYSKLPWT 117

RESULT 3  
US-10-265-713-10  
; Sequence 10, Application US/10265713  
; Publication No. US20030095964A1  
; GENERAL INFORMATION:  
; APPLICANT: SHITARA, KENYA  
; APPLICANT: HANAI, NOBUO  
; APPLICANT: HASEGAWA, MAMORU  
; APPLICANT: MIYAJI, HIROMASA  
; APPLICANT: KIWANA, YOSHIHISA  
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY  
; FILE REFERENCE: 249-101  
; CURRENT APPLICATION NUMBER: US/10/265,713  
; EARLIER FILING DATE: 2002-10-08  
; EARLIER APPLICATION NUMBER: US/09/225,322  
; EARLIER FILING DATE: 1999-01-05  
; EARLIER APPLICATION NUMBER: US 08/454,680  
; EARLIER FILING DATE: 1995-05-31  
; EARLIER APPLICATION NUMBER: US 08/408,133  
; EARLIER FILING DATE: 1995-03-21  
; EARLIER APPLICATION NUMBER: US 08/292,178  
; EARLIER FILING DATE: 1994-08-17  
; EARLIER APPLICATION NUMBER: US07/947,674  
; EARLIER FILING DATE: 1992-09-17  
; EARLIER APPLICATION NUMBER: JP 3-238375  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 10  
; LENGTH: 128  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: cdna KM-641  
US-09-764-304-10

Query Match 100.0%; Score 56; DB 3; Length 128;  
Best Local Similarity 100.0%; Pred. No. 0.082;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HOYSKLPWT 9  
Db 109 HOYSKLPWT 117



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; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: cDNA KM-641
US-10-265-713-10

Query Match      100.0%; Score 56; DB 4; Length 128;
Best Local Similarity 100.0%; Pred. No. 0.082;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 HOYSKLPWT 9
Db      109 HOYSKLPWT 117

RESULT 4
US-10-265-713-19
; Sequence 19, Application US/10265713
; Publication No. US20030095964A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUWANA, YOSHIHISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/10/265,713
; CURRENT FILING DATE: 2002-10-08
; PRIOR APPLICATION NUMBER: US/09/225,322
; PRIOR FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: US 08/454,680
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
; PRIOR APPLICATION NUMBER: US07/947,674
; PRIOR FILING DATE: 1992-09-17
; PRIOR APPLICATION NUMBER: JP 3-238375
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:light chain
US-10-265-713-19

Query Match      100.0%; Score 56; DB 4; Length 128;
Best Local Similarity 100.0%; Pred. No. 0.082;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 HOYSKLPWT 9
Db      109 HOYSKLPWT 117

RESULT 5
US-10-166-626-10
; Sequence 10, Application US/10166626
; Publication No. US20030166876A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU

```

```

; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUWANA, YOSHIHISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/10/166,626
; CURRENT FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: US/09/225,322B
; PRIOR FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: US 08/454,680
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
; PRIOR APPLICATION NUMBER: US07/947,674
; PRIOR FILING DATE: 1992-09-17
; PRIOR APPLICATION NUMBER: JP 3-238375
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: cDNA KM-641
US-10-166-626-10

Query Match      100.0%; Score 56; DB 4; Length 128;
Best Local Similarity 100.0%; Pred. No. 0.082;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 HOYSKLPWT 9
Db      109 HOYSKLPWT 117

RESULT 6
US-10-166-626-19
; Sequence 19, Application US/10166626
; Publication No. US20030166876A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUWANA, YOSHIHISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/10/166,626
; CURRENT FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: US/09/225,322B
; PRIOR FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: US 08/454,680
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
; PRIOR APPLICATION NUMBER: US07/947,674
; PRIOR FILING DATE: 1992-09-17
; PRIOR APPLICATION NUMBER: JP 3-238375
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:variable region
US-10-166-626-19

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Query Match      100.0%; Score 56; DB 4; Length 128;
Best Local Similarity 100.0%; Pred. No. 0.082; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

QY      1 HOYSKLPWT 9
Db      109 HOYSKLPWT 117
|||||

RESULT 7
US-10-938-992-13
; Sequence 13, Application US/10938992
; Publication No. US20050152903A1
; GENERAL INFORMATION:
; APPLICANT: Newman, Walter
; APPLICANT: Qin, Shixin
; APPLICANT: O'Keefe, Theresa
; APPLICANT: Obar, Robert
; TITLE OF INVENTION: Monoclonal Antibodies Against HMGB1
; FILE REFERENCE: 3258.1033-001
; CURRENT APPLICATION NUMBER: US/10/938,992
; CURRENT FILING DATE: 2004-09-10
; PRIOR APPLICATION NUMBER: 60/502,568
; PRIOR FILING DATE: 2003-09-11
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-938-992-13

Query Match      85.7%; Score 48; DB 5; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 QYSKLPWT 9
Db      90 QYSKLPWT 97
|||||

RESULT 8
US-10-697-399-6
; Sequence 6, Application US/10697399
; Publication No. US20040162413A1
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffrey D.
; APPLICANT: Huse, William D.
; APPLICANT: Vasserot, Alain P.
; APPLICANT: Marquis, David P.
; APPLICANT: Smith, Eric P.
; TITLE OF INVENTION: Methods of Optimizing Antibody Variable Region Binding Affinity
; FILE REFERENCE: AME-08122
; CURRENT APPLICATION NUMBER: US/10/697,399
; CURRENT FILING DATE: 2003-10-30
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-697-399-6

Query Match      78.6%; Score 44; DB 4; Length 99;
Best Local Similarity 87.5%; Pred. No. 7.4;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 QYSKLPWT 9
Db      82 QYKLPWT 89
|||
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```
RESULT 9
US-10-371-942-32
; Sequence 32, Application US/10371942
; Publication No. US20030223994A1
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Henricus Renerus Jacobus Mattheus
; APPLICANT: Reiter, Yoram
; TITLE OF INVENTION: MHC-PEPTIDE COMPLEX BINDING LIGANDS
; FILE REFERENCE: 10280-034001
; CURRENT APPLICATION NUMBER: US/10/371,942
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/358,994
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-371-942-32

Query Match      78.6%; Score 44; DB 4; Length 109;
Best Local Similarity 77.8%; Pred. No. 8.1;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 HOYSKLPWT 9
Db      90 HOYGFPLWT 98
|||||

RESULT 10
US-10-988-617A-14
; Sequence 14, Application US/10988617A
; Publication No. US20050124041A1
; GENERAL INFORMATION:
; APPLICANT: KANG, HEUI IL
; APPLICANT: KO, IN YOUNG
; APPLICANT: SONG, MOO YOUNG
; APPLICANT: KIM, CHANG SEOK
; APPLICANT: PARK, SANG KOO
; APPLICANT: LEE, JAE SUN
; APPLICANT: YOO, TAE HYOUNG
; APPLICANT: NA, KANG IN
; TITLE OF INVENTION: AN ANTIBODY VARIABLE REGION OF A MONOCLONAL ANTIBODY AGAINST
; TITLE OF INVENTION: HUMAN TUMOR NECROSIS FACTOR ALPHA AND A GENE ENCODING THE SAME
; FILE REFERENCE: Q84798
; CURRENT APPLICATION NUMBER: US/10/988,617A
; CURRENT FILING DATE: 2004-11-16
; PRIOR APPLICATION NUMBER: KR 10-2003-0080950
; PRIOR FILING DATE: 2003-11-17
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 14
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: light chain CDR3
US-10-988-617A-14

Query Match      76.8%; Score 43; DB 5; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.7e+06;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 HOYSKLPWT 9
Db      1 HOYERSPWT 9
|||||

RESULT 11
US-10-988-617A-8
; Sequence 8, Application US/10988617A
; Publication No. US20050124041A1
```

```
; GENERAL INFORMATION:
; APPLICANT: KANG, HEUI IL
; APPLICANT: KO, IN YOUNG
; APPLICANT: SONG, MOO YOUNG
; APPLICANT: KIM, CHANG SEOK
; APPLICANT: PARK, SANG KOO
; APPLICANT: LEE, JAE SUN
; APPLICANT: YOO, TAE HYOUNG
; APPLICANT: NA, KANG IN
; TITLE OF INVENTION: AN ANTIBODY VARIABLE REGION OF A MONOCLONAL ANTIBODY AGAINST
; TITLE OF INVENTION: HUMAN TUMOR NECROSIS FACTOR ALPHA AND A GENE ENCODING THE SAME
; FILE REFERENCE: Q84798
; CURRENT APPLICATION NUMBER: US/10/988,617A
; PRIOR FILING DATE: 2004-11-16
; PRIOR APPLICATION NUMBER: KR 10-2003-0080950
; PRIOR FILING DATE: 2003-11-17
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 8
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: amino acid sequence of cdna molecule encoding light chain
; OTHER INFORMATION: variable region
US-10-988-617A-8

Query Match          76.8%; Score 43; DB 5; Length 109;
Best Local Similarity 66.7%; Pred. No. 12;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HOYSKLPWT 9
   ||||: |||
Db 90 HOYERSPWT 98

RESULT 12
US-10-264-049-4290
; Sequence 4290, Application US/10264049
; Publication No. US20040005579A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA133PI
; CURRENT APPLICATION NUMBER: US/10/264,049
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/18569
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: US 60/209,467
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 4360
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 4290
; LENGTH: 215
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1168)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
US-10-264-049-4290

Query Match          76.8%; Score 43; DB 4; Length 215;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 YSKLPWT 9
   |||||
Db 196 YSKLPWT 202

RESULT 13
US-10-776-521B-203
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; Sequence 203, Application US/10776521B
; Publication No. US2005020203A1
; GENERAL INFORMATION:
; APPLICANT: Fletcher, Jessica
; APPLICANT: Prince-Cohane, Kenya
; APPLICANT: Mehta, Sunil
; APPLICANT: Slusarewicz, Paul
; APPLICANT: Andjelic, Sofija
; APPLICANT: Barber, Brian
; TITLE OF INVENTION: IMPROVED HEAT SHOCK PROTEIN-BASED VACCINES AND
; TITLE OF INVENTION: IMMUNOTHERAPIES
; FILE REFERENCE: 8449-405-999
; CURRENT APPLICATION NUMBER: US/10/776,521B
; CURRENT FILING DATE: 2004-02-12
; PRIOR APPLICATION NUMBER: 60/503,417
; PRIOR FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: 60/463,746
; PRIOR FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: 60/462,469
; PRIOR FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: 60/447,142
; PRIOR FILING DATE: 2003-02-13
; NUMBER OF SEQ ID NOS: 419
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 203
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Heat shock protein binding domain with a terminal
; OTHER INFORMATION: Trp residue
US-10-776-521B-203

Query Match          71.4%; Score 40; DB 5; Length 8;
Best Local Similarity 62.5%; Pred. No. 1.7e+06;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYSKLPW 8
   ||::|||
Db 1 HSYNRLPW 8

RESULT 14
US-10-820-067A-713
; Sequence 713, Application US/10820067A
; Publication No. US20050214312A1
; GENERAL INFORMATION:
; APPLICANT: Fletcher, J.
; APPLICANT: Prince-Cohane, K.
; APPLICANT: Mehta, S.
; APPLICANT: Slusarewicz, P.
; APPLICANT: Andjelic, S.
; APPLICANT: Barber, B.
; TITLE OF INVENTION: IMPROVED HEAT SHOCK PROTEIN-BASED
; TITLE OF INVENTION: VACCINES AND IMMUNOTHERAPIES
; FILE REFERENCE: 8449-406-999
; CURRENT APPLICATION NUMBER: US/10/820,067A
; CURRENT FILING DATE: 2004-04-08
; PRIOR APPLICATION NUMBER: 60/462,469
; PRIOR FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: 60/463,746
; PRIOR FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: 60/503,417
; PRIOR FILING DATE: 2003-09-16
; NUMBER OF SEQ ID NOS: 926
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 713
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Heat shock protein binding domain with terminal
; OTHER INFORMATION: "trp" residue
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US-10-820-067A-713

Query Match 71.4%; Score 40; DB 5; Length 8;  
Best Local Similarity 62.5%; Pred. No. 1.7e+06;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYSLPW 8  
|||:||||  
Db 1 HSNRLPW 8

RESULT 15

US-10-624-153-24

; Sequence 24, Application US/10624153

; Publication No. US20040086502A1

; GENERAL INFORMATION:

; APPLICANT: CHEN, YVONNE M.

; APPLICANT: LOWMAN, HENRY B.

; APPLICANT: MULLER, YVES

; TITLE OF INVENTION: ANTIBODY VARIANTS

; FILE REFERENCE: P1469R1C1

; CURRENT APPLICATION NUMBER: US/10/624,153

; CURRENT FILING DATE: 2003-07-21

; PRIOR APPLICATION NUMBER: US 09/440,781

; PRIOR FILING DATE: 1999-11-16

; PRIOR APPLICATION NUMBER: US 60/108,945

; PRIOR FILING DATE: 1998-11-18

; NUMBER OF SEQ ID NOS: 99

; SEQ ID NO 24

; LENGTH: 9

; TYPE: PRT

; ORGANISM: artificial sequence

; FEATURE: OTHER INFORMATION: sequence is synthesized

; NAME/KEY: artificial

; LOCATION: 1-9

; OTHER INFORMATION: variant CDR sequence

US-10-624-153-24

Query Match 71.4%; Score 40; DB 4; Length 9;  
Best Local Similarity 75.0%; Pred. No. 1.7e+06;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYSLPW 9  
|||:||||  
Db 2 QYSNVPWT 9

RESULT 16

US-10-624-153-26

; Sequence 26, Application US/10624153

; Publication No. US20040086502A1

; GENERAL INFORMATION:

; APPLICANT: CHEN, YVONNE M.

; APPLICANT: LOWMAN, HENRY B.

; APPLICANT: MULLER, YVES

; TITLE OF INVENTION: ANTIBODY VARIANTS

; FILE REFERENCE: P1469R1C1

; CURRENT APPLICATION NUMBER: US/10/624,153

; CURRENT FILING DATE: 2003-07-21

; PRIOR APPLICATION NUMBER: US 09/440,781

; PRIOR FILING DATE: 1999-11-16

; PRIOR APPLICATION NUMBER: US 60/108,945

; PRIOR FILING DATE: 1998-11-18

; NUMBER OF SEQ ID NOS: 99

; SEQ ID NO 26

; LENGTH: 9

; TYPE: PRT

; ORGANISM: artificial sequence

; FEATURE: OTHER INFORMATION: sequence is synthesized

; NAME/KEY: artificial

; LOCATION: 1-9

; OTHER INFORMATION: variant CDR sequence

; NAME/KEY: artificial  
; LOCATION: 1-9  
; OTHER INFORMATION: variant CDR sequence  
US-10-624-153-26

Query Match 71.4%; Score 40; DB 4; Length 9;  
Best Local Similarity 75.0%; Pred. No. 1.7e+06;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYSLPW 9  
|||:||||  
Db 2 QYSNVPWT 9

RESULT 17

US-10-424-599-159861

; Sequence 159861, Application US/10424599

; Publication No. US20040031072A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J

; APPLICANT: Kovalic, David K

; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

; FILE REFERENCE: 38-21(53223)B

; CURRENT APPLICATION NUMBER: US/10/424,599

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 285684

; SEQ ID NO 159861

; LENGTH: 93

; TYPE: PRT

; ORGANISM: Glycine max

; FEATURE: OTHER INFORMATION: Clone ID: PAT\_MRT3847\_115373C.1.pep

US-10-424-599-159861

Query Match 71.4%; Score 40; DB 4; Length 93;  
Best Local Similarity 66.7%; Pred. No. 34;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HOYSLPW 9  
|||:||||  
Db 56 HRLQLPW 64

RESULT 18

US-10-268-501-5

; Sequence 5, Application US/10268501

; Publication No. US20030086924A1

; GENERAL INFORMATION:

; APPLICANT: Sliwkowski, Mark X.

; TITLE OF INVENTION: Treatment with Anti-ErbB2 Antibodies

; FILE REFERENCE: P1467R2P1

; CURRENT APPLICATION NUMBER: US/10/268,501

; CURRENT FILING DATE: 2002-10-10

; PRIOR APPLICATION NUMBER: US 09/602,812

; PRIOR FILING DATE: 2000-06-23

; PRIOR APPLICATION NUMBER: US 60/141,316

; PRIOR FILING DATE: 1999-06-25

; NUMBER OF SEQ ID NOS: 13

; SEQ ID NO 5

; LENGTH: 107

; TYPE: PRT

; ORGANISM: Artificial sequence

; FEATURE: OTHER INFORMATION: light chain consensus sequence

US-10-268-501-5

Query Match 71.4%; Score 40; DB 4; Length 107;  
Best Local Similarity 75.0%; Pred. No. 39;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYSLPWT 9  
||:||||  
Db 90 QYNSLPWT 97

RESULT 19  
US-10-608-626-5  
; Sequence 5, Application US/10608626  
; Publication No. US20040013667A1  
; GENERAL INFORMATION:  
; APPLICANT: Kelsey, Stephen M.  
; APPLICANT: Sliwowski, Mark X.  
; TITLE OF INVENTION: Treatment with Anti-ErbB2 Antibodies  
; FILE REFERENCE: P1467R2P2  
; CURRENT APPLICATION NUMBER: US/10/608,626  
; CURRENT FILING DATE: 2003-06-27  
; PRIOR APPLICATION NUMBER: US 10/268,501  
; PRIOR FILING DATE: 2002-10-10  
; PRIOR APPLICATION NUMBER: US 09/602,812  
; PRIOR FILING DATE: 2000-06-23  
; PRIOR APPLICATION NUMBER: US 60/141,316  
; PRIOR FILING DATE: 1999-06-25  
; NUMBER OF SEQ ID NOS: 13  
; SEQ ID NO 5  
; LENGTH: 107  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: light chain consensus sequence  
US-10-608-626-5

Query Match 71.4%; Score 40; DB 4; Length 107;  
Best Local Similarity 75.0%; Pred. No. 39;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYSLPWT 9  
||:||||  
Db 90 QYNSLPWT 97

RESULT 20  
US-10-600-152-14  
; Sequence 14, Application US/10600152  
; Publication No. US20040037824A1  
; GENERAL INFORMATION:  
; APPLICANT: Baughman, Sharon A.  
; APPLICANT: Shak Steven  
; TITLE OF INVENTION: Dosages for Treatment with Anti-ErbB2 Antibodies  
; FILE REFERENCE: P1775R1  
; CURRENT APPLICATION NUMBER: US/10/600,152  
; CURRENT FILING DATE: 2003-06-20  
; PRIOR APPLICATION NUMBER: 09/648,067  
; PRIOR FILING DATE: 2000-08-25  
; PRIOR APPLICATION NUMBER: US 60/151,018  
; PRIOR FILING DATE: 1999-08-27  
; PRIOR APPLICATION NUMBER: US 60/213,822  
; PRIOR FILING DATE: 2000-06-23  
; NUMBER OF SEQ ID NOS: 15  
; SEQ ID NO 14  
; LENGTH: 107  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: VL consensus sequence  
US-10-600-152-14

Query Match 71.4%; Score 40; DB 4; Length 107;  
Best Local Similarity 75.0%; Pred. No. 39;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYSLPWT 9  
||:||||  
Db 90 QYNSLPWT 97

RESULT 21  
US-10-619-754-5  
; Sequence 5, Application US/10619754  
; Publication No. US20040106161A1  
; GENERAL INFORMATION:  
; APPLICANT: Genentech, Inc.  
; APPLICANT: Koll, Hans  
; APPLICANT: Bossemaier, Birgit  
; APPLICANT: Muller, Hans-Joachim  
; APPLICANT: Sliwowski, Mark  
; APPLICANT: Kelsey, Stephen  
; TITLE OF INVENTION: Methods For Identifying Tumors That Are  
; RESPONSIVE TO TREATMENT WITH ANTI-ERBB2 ANTIBODIES  
; FILE REFERENCE: 39766-0114A  
; CURRENT APPLICATION NUMBER: US/10/619,754  
; CURRENT FILING DATE: 2003-07-14  
; PRIOR APPLICATION NUMBER: US 60/396,290  
; PRIOR FILING DATE: 2002-07-15  
; PRIOR APPLICATION NUMBER: US 60/480,043  
; PRIOR FILING DATE: 2003-06-20  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5  
; LENGTH: 107  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-619-754-5

Query Match 71.4%; Score 40; DB 4; Length 107;  
Best Local Similarity 75.0%; Pred. No. 39;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYSLPWT 9  
||:||||  
Db 90 QYNSLPWT 97

RESULT 22  
US-10-835-641-18  
; Sequence 18, Application US/10835641  
; Publication No. US20040236078A1  
; GENERAL INFORMATION:  
; APPLICANT: Carter, Paul J.  
; APPLICANT: Presta, Leonard G.  
; TITLE OF INVENTION: Method for Making Humanized Antibodies  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/835,641  
; FILING DATE: 30-Apr-2004  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/705,398  
; FILING DATE: 02-Nov-2000  
; APPLICATION NUMBER: 08/146206  
; FILING DATE: 17-NOV-1993  
; APPLICATION NUMBER: 07/715272  
; FILING DATE: 14-JUN-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lee, Wendy M.

```
;
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709PID2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-10-835-641-18

Query Match 71.4%; Score 40; DB 5; Length 107;
Best Local Similarity 75.0%; Pred. No. 39;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYSLPWT 9
Db 90 QYNSLPWT 97

RESULT 23
US-10-719-310-5
; Sequence 5, Application US/10719310
; Publication No. US20040258685A1
; GENERAL INFORMATION:
; APPLICANT: Brunetta, Paul G.
; APPLICANT: Sliwowski, Mark X.
; TITLE OF INVENTION: THERAPY OF NON-MALIGNANT DISEASES OR DISORDERS WITH
; TITLE OF INVENTION: ANTI-ERBB2 ANTIBODIES
; FILE REFERENCE: P1979R1
; CURRENT APPLICATION NUMBER: US/10/719,310
; CURRENT FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: US 60/428,027
; PRIOR FILING DATE: 2002-11-21
; NUMBER OF SEQ ID NOS: 13
; SEQ ID NO 5
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-10-719-310-5

Query Match 71.4%; Score 40; DB 5; Length 107;
Best Local Similarity 75.0%; Pred. No. 39;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYSLPWT 9
Db 90 QYNSLPWT 97

RESULT 24
US-11-044-749-5
; Sequence 5, Application US/11044749
; Publication No. US20050208043A1
; GENERAL INFORMATION:
; APPLICANT: Adams, Camellia W.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Sliwowski, Mark X.
; TITLE OF INVENTION: Humanized Anti-ErbB2 Antibodies and Treatment with
; TITLE OF INVENTION: Anti-ErbB2 Antibodies
; FILE REFERENCE: P1467R2
; CURRENT APPLICATION NUMBER: US/11/044,749
; CURRENT FILING DATE: 2005-01-27
; PRIOR APPLICATION NUMBER: US/09/602,812
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/141,316
; PRIOR FILING DATE: 1999-06-25
; NUMBER OF SEQ ID NOS: 13
; SEQ ID NO 5

; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709PID2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: light chain consensus sequence
US-11-044-749-5

Query Match 71.4%; Score 40; DB 6; Length 107;
Best Local Similarity 75.0%; Pred. No. 39;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYSLPWT 9
Db 90 QYNSLPWT 97

RESULT 25
US-11-154-465-5
; Sequence 5, Application US/11154465
; Publication No. US20050238640A1
; GENERAL INFORMATION:
; APPLICANT: Adams, Camellia W.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Sliwowski, Mark X.
; TITLE OF INVENTION: Humanized Anti-ErbB2 Antibodies and Treatment with
; TITLE OF INVENTION: Anti-ErbB2 Antibodies
; FILE REFERENCE: P1467R2
; CURRENT APPLICATION NUMBER: US/11/154,465
; CURRENT FILING DATE: 2005-06-16
; PRIOR APPLICATION NUMBER: US/09/602,812
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/141,316
; PRIOR FILING DATE: 1999-06-25
; NUMBER OF SEQ ID NOS: 13
; SEQ ID NO 5
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: light chain consensus sequence
US-11-154-465-5

Query Match 71.4%; Score 40; DB 6; Length 107;
Best Local Similarity 75.0%; Pred. No. 39;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYSLPWT 9
Db 90 QYNSLPWT 97

RESULT 26
US-09-056-160B-12
; Sequence 12, Application US/09056160B
; Patent No. US20020032315A1
; GENERAL INFORMATION:
; APPLICANT: Baca, Manuel
; APPLICANT: Wells, James A.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Lowman, Henry B.
; APPLICANT: Chen, Yvonne M.
; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
; NUMBER OF SEQUENCES: 131
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
```

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/056,160B  
FILING DATE: 06-Apr-1998  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/054,856  
FILING DATE: 06-AUG-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Hasak, Janet E.  
REGISTRATION NUMBER: 28,616  
REFERENCE/DOCKET NUMBER: P1093R2  
TELEPHONE: 650/225-1896  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 108 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-09-056-160B-12

Query Match 71.4%; Score 40; DB 3; Length 108;  
Best Local Similarity 75.0%; Pred. No. 39;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYSKLPWT 9  
||:||||  
Db 90 QYNSLPWT 97

## RESULT 27

US-09-795-798-3  
Sequence 3, Application US/09795798  
Publication No. US20030207336A1  
GENERAL INFORMATION:

APPLICANT: Presta, Leonard G.  
Jardieu, Paula M.  
TITLE OF INVENTION: Humanized Anti-CD11a Antibodies  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/795,798  
FILING DATE: 28-Feb-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/974,899  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:

NAME: Lee, Wendy M.  
REGISTRATION NUMBER: 40,378  
REFERENCE/DOCKET NUMBER: P1014R1  
TELEPHONE: 650/225-1994  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 108 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 3:

## US-09-795-798-3

Query Match 71.4%; Score 40; DB 3; Length 108;  
Best Local Similarity 75.0%; Pred. No. 39;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYSKLPWT 9  
||:||||  
Db 90 QYNSLPWT 97

## RESULT 28

US-10-234-671-12  
Sequence 12, Application US/10234671  
Publication No. US20030190317A1  
GENERAL INFORMATION:

APPLICANT: Baca, Manuel  
Wells, James A.  
Presta, Leonard G.  
Lowman, Henry B.  
Chen, Yvonne M.  
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES  
NUMBER OF SEQUENCES: 131  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/234,671  
FILING DATE: 03-Sep-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/056160  
FILING DATE: 06-APR-1998  
APPLICATION NUMBER: 60/126446  
FILING DATE: 07-APR-1997  
APPLICATION NUMBER: 60/054856  
FILING DATE: 06-AUG-1997  
ATTORNEY/AGENT INFORMATION:

NAME: Cui, Steven X.  
REGISTRATION NUMBER: 44,637  
REFERENCE/DOCKET NUMBER: P1093R2C1  
TELEPHONE: 650/225-8674  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 108 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 12:  
US-10-234-671-12

Query Match 71.4%; Score 40; DB 4; Length 108;  
Best Local Similarity 75.0%; Pred. No. 39;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYSKLPWT 9  
||:||||  
Db 90 QYNSLPWT 97

## RESULT 29

US-10-727-737-3  
Sequence 3, Application US/10727737

```
; Publication No. US20040146507A1
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.
; Jardiou, Paula M.
; TITLE OF INVENTION: Antibody Mutants
; NUMBER OF SEQUENCES: 79
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/727,737
; FILING DATE: 03-Dec-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/975,329B
; FILING DATE: 20-Nov-1997
; APPLICATION NUMBER: 60/031945
; FILING DATE: 27-Nov-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P1064R1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-727-737-3
;
; Query Match 71.4%; Score 40; DB 4; Length 108;
; Best Local Similarity 75.0%; Pred. NO. 39;
; Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
;
; QY 2 QYSKLPWT 9
; Db 90 QYNSLPWT 97
;
; RESULT 30
; US-10-861-049-38
; Sequence 38, Application US/10861049
; Publication No. US20050095243A1
; GENERAL INFORMATION:
; APPLICANT: Andrew Chan
; APPLICANT: Qian Gong
; APPLICANT: Flavius Martin
; TITLE OF INVENTION: COMBINATION THERAPY FOR B CELL DISORDERS
; FILE REFERENCE: P2040RUS
; CURRENT APPLICATION NUMBER: US/10/861,049
; CURRENT FILING DATE: 2004-06-04
; PRIOR APPLICATION NUMBER: US 60/476,531
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/476,481
; PRIOR FILING DATE: 2003-06-05
; PRIOR APPLICATION NUMBER: US 60/476,414
; PRIOR FILING DATE: 2003-06-05
; NUMBER OF SEQ ID NOS: 145
; SEQ ID NO 38
; LENGTH: 108
; TYPE: PRT
;
; ORGANISM: Homo sapiens
; US-10-861-049-38
;
; Query Match 71.4%; Score 40; DB 5; Length 108;
; Best Local Similarity 75.0%; Pred. NO. 39;
; Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
;
; QY 2 QYSKLPWT 9
; Db 90 QYNSLPWT 97
;
; RESULT 31
; US-10-974-591-12
; Sequence 12, Application US/10974591
; Publication No. US20050112126A1
; GENERAL INFORMATION:
; APPLICANT: Baca, Manuel
; Wells, James A.
; Presta, Leonard G.
; Lowman, Henry B.
; Chen, Yvonne M.
; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
; NUMBER OF SEQUENCES: 131
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/974,591
; FILING DATE: 26-Oct-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/723752
; FILING DATE: 27-Nov-2000
; APPLICATION NUMBER: 08/908469
; FILING DATE: 06-Aug-1997
; APPLICATION NUMBER: 08/833504
; FILING DATE: 07-Apr-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Cui, Steven X.
; REGISTRATION NUMBER: 44,637
; REFERENCE/DOCKET NUMBER: P1093FID1C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-8674
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-10-974-591-12
;
; Query Match 71.4%; Score 40; DB 5; Length 108;
; Best Local Similarity 75.0%; Pred. NO. 39;
; Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
;
; QY 2 QYSKLPWT 9
; Db 90 QYNSLPWT 97
;
; RESULT 32
; US-11-021-874-38
```



; Sequence 38, Application US/11021874  
; Publication No. US20050163775A1  
; GENERAL INFORMATION:  
; APPLICANT: Andrew Chan  
; APPLICANT: Gnan Gong  
; APPLICANT: Flavius Martin  
; TITLE OF INVENTION: COMBINATION THERAPY FOR B CELL DISORDERS  
; FILE REFERENCE: P2040R1P1  
; CURRENT APPLICATION NUMBER: US/11/021,874  
; CURRENT FILING DATE: 2004-12-22  
; PRIOR APPLICATION NUMBER: US 10/861,049  
; PRIOR FILING DATE: 2004-06-04  
; PRIOR APPLICATION NUMBER: US 60/476,531  
; PRIOR FILING DATE: 2003-06-06  
; PRIOR APPLICATION NUMBER: US 60/476,481  
; PRIOR FILING DATE: 2003-06-05  
; PRIOR APPLICATION NUMBER: US 60/476,414  
; PRIOR FILING DATE: 2003-06-05  
; NUMBER OF SEQ ID NOS: 165  
; SEQ ID NO 38  
; LENGTH: 108  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-021-874-38

Query Match 71.4%; Score 40; DB 6; Length 108;  
Best Local Similarity 75.0%; Pred. No. 39;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYSLPWT 9  
||:||||  
Db 90 QYNSLPWT 97

RESULT 33  
US-09-811-123-6  
; Sequence 6, Application US/09811123  
; Patent No. US20020001587A1  
; GENERAL INFORMATION:  
; APPLICANT: Sharon Erickson  
; APPLICANT: Ralph Schwall  
; APPLICANT: Mark Sliwkowski  
; TITLE OF INVENTION: METHODS OF TREATMENT USING ANTI-BrbB  
; TITLE OF INVENTION: ANTIBODY-MAYTANSINOID CONJUGATES  
; FILE REFERENCE: GENENT.073A2  
; CURRENT APPLICATION NUMBER: US/09/811,123  
; CURRENT FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/238,327  
; PRIOR FILING DATE: 2000-10-05  
; PRIOR APPLICATION NUMBER: 09/602,530  
; PRIOR FILING DATE: 2000-06-23  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 6  
; LENGTH: 109  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Humanized Antibody Sequence  
US-09-811-123-6

Query Match 71.4%; Score 40; DB 3; Length 109;  
Best Local Similarity 75.0%; Pred. No. 39;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYSLPWT 9  
||:||||  
Db 90 QYNSLPWT 97

RESULT 34  
US-10-044-896-4  
; Sequence 4, Application US/10044896

; Publication No. US20030166228A1  
; GENERAL INFORMATION:  
; APPLICANT: Chuncharapai, Anan  
; APPLICANT: Kim, Jin K.  
; APPLICANT: Stewart, Timothy  
; APPLICANT: Presta, Leonard G.  
; TITLE OF INVENTION: ANTI-INTERFERON-ALPHA ANTIBODIES  
; FILE REFERENCE: GENENT.074A  
; CURRENT APPLICATION NUMBER: US/10/044,896  
; CURRENT FILING DATE: 2002-01-09  
; PRIOR APPLICATION NUMBER: 60/270775  
; PRIOR FILING DATE: 2001-02-22  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 110  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-044-896-4

Query Match 71.4%; Score 40; DB 4; Length 110;  
Best Local Similarity 75.0%; Pred. No. 40;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYSLPWT 9  
||:||||  
Db 90 QYNSLPWT 97

RESULT 35  
US-10-469-125-8  
; Sequence 8, Application US/10469125  
; Publication No. US20040143101A1  
; GENERAL INFORMATION:  
; APPLICANT: Soltis, Daniel A.  
; APPLICANT: Burch, Ronald M.  
; APPLICANT: Shukla, Rajiv  
; TITLE OF INVENTION: IMMUNOGLOBULIN CONSTRUCT CONTAINING ANTI-MUCIN VARIABLE DOMAIN S-  
; FILE REFERENCE: 02755/100G273-US1  
; CURRENT APPLICATION NUMBER: US/10/469,125  
; CURRENT FILING DATE: 2003-08-25  
; PRIOR APPLICATION NUMBER: US 60/281,182  
; PRIOR FILING DATE: 2001-04-02  
; PRIOR APPLICATION NUMBER: PCT/US02/10304  
; PRIOR FILING DATE: 2002-04-02  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 8  
; LENGTH: 126  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-469-125-8

Query Match 71.4%; Score 40; DB 4; Length 126;  
Best Local Similarity 75.0%; Pred. No. 45;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYSLPWT 9  
||:||||  
Db 109 QYNSLPWT 116

RESULT 36  
US-09-187-693-62  
; Sequence 62, Application US/09187693  
; Patent No. US20020173629A1  
; GENERAL INFORMATION:  
; APPLICANT: Jakobovits, Aya  
; APPLICANT: Yang, Xiao-Dong  
; APPLICANT: Gallo, Michael  
; APPLICANT: Jia, Xiao-Chi  
; TITLE OF INVENTION: Human Monoclonal Antibodies to Epidermal

; TITLE OF INVENTION: Growth Factor Receptor  
; FILE REFERENCE: Cell 4.20 CIP2  
; CURRENT APPLICATION NUMBER: US/09/187,693  
; CURRENT FILING DATE: 1998-11-05  
; PRIOR APPLICATION NUMBER: 09/162,280  
; PRIOR FILING DATE: 1998-09-29  
; PRIOR APPLICATION NUMBER: 08/851,362  
; PRIOR FILING DATE: 1997-05-05  
; NUMBER OF SEQ ID NOS: 75  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 62  
; LENGTH: 153  
; TYPE: PRT  
; ORGANISM: human  
; FEATURE:  
; NAME/KEY: VARIANT  
; LOCATION: (1)...(153)  
; OTHER INFORMATION: Xaa = Any Amino Acid  
US-09-187-693-62

Query Match 71.4%; Score 40; DB 3; Length 153;  
Best Local Similarity 66.7%; Pred. No. 54;  
Matches 6; Conservative 0; Mismatches 3; Indels 3; Gaps 0;

QY 1 HQYSKLPWT 9  
|||  
DB 91 HQYSTPWT 99

RESULT 37  
US-11-021-795-62  
; Sequence 62, Application US/11021795  
; Publication NO. US20050100546A1  
; GENERAL INFORMATION:  
; APPLICANT: Jakobovits, Ava  
; APPLICANT: Yang, Xiao-Dong  
; APPLICANT: Gallo, Michael  
; APPLICANT: Jia, Xiao-Chi  
; TITLE OF INVENTION: Human Monoclonal Antibodies to Epidermal  
; FILE REFERENCE: Cell 4.20 CIP2  
; CURRENT APPLICATION NUMBER: US/11/021,795  
; CURRENT FILING DATE: 2004-12-22  
; PRIOR APPLICATION NUMBER: US/09/187,693  
; PRIOR FILING DATE: 1998-11-05  
; PRIOR APPLICATION NUMBER: 09/162,280  
; PRIOR FILING DATE: 1998-09-29  
; PRIOR APPLICATION NUMBER: 08/851,362  
; PRIOR FILING DATE: 1997-05-05  
; NUMBER OF SEQ ID NOS: 75  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 62  
; LENGTH: 153  
; TYPE: PRT  
; ORGANISM: human  
; FEATURE:  
; NAME/KEY: VARIANT  
; LOCATION: (1)...(153)  
; OTHER INFORMATION: Xaa = Any Amino Acid  
US-11-021-795-62

Query Match 71.4%; Score 40; DB 6; Length 153;  
Best Local Similarity 66.7%; Pred. No. 54;  
Matches 6; Conservative 0; Mismatches 3; Indels 3; Gaps 0;

QY 1 HQYSKLPWT 9  
|||  
DB 91 HQYSTPWT 99

RESULT 38  
US-09-187-693-66  
; Sequence 66, Application US/09187693

; Patent No. US20020173629A1  
; GENERAL INFORMATION:  
; APPLICANT: Jakobovits, Ava  
; APPLICANT: Yang, Xiao-Dong  
; APPLICANT: Gallo, Michael  
; APPLICANT: Jia, Xiao-Chi  
; TITLE OF INVENTION: Human Monoclonal Antibodies to Epidermal  
; FILE REFERENCE: Cell 4.20 CIP2  
; CURRENT APPLICATION NUMBER: US/09/187,693  
; CURRENT FILING DATE: 1998-11-05  
; PRIOR APPLICATION NUMBER: 09/162,280  
; PRIOR FILING DATE: 1998-09-29  
; PRIOR APPLICATION NUMBER: 08/851,362  
; PRIOR FILING DATE: 1997-05-05  
; NUMBER OF SEQ ID NOS: 75  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 66  
; LENGTH: 159  
; TYPE: PRT  
; ORGANISM: human  
; FEATURE:  
; NAME/KEY: VARIANT  
; LOCATION: (1)...(159)  
; OTHER INFORMATION: Xaa = Any Amino Acid  
US-09-187-693-66

Query Match 71.4%; Score 40; DB 3; Length 159;  
Best Local Similarity 66.7%; Pred. No. 56;  
Matches 6; Conservative 0; Mismatches 3; Indels 3; Gaps 0;

QY 1 HQYSKLPWT 9  
|||  
DB 88 HQYSTPWT 96

RESULT 39  
US-11-021-795-66  
; Sequence 66, Application US/11021795  
; Publication NO. US20050100546A1  
; GENERAL INFORMATION:  
; APPLICANT: Jakobovits, Ava  
; APPLICANT: Yang, Xiao-Dong  
; APPLICANT: Gallo, Michael  
; APPLICANT: Jia, Xiao-Chi  
; TITLE OF INVENTION: Human Monoclonal Antibodies to Epidermal  
; FILE REFERENCE: Cell 4.20 CIP2  
; CURRENT APPLICATION NUMBER: US/11/021,795  
; CURRENT FILING DATE: 2004-12-22  
; PRIOR APPLICATION NUMBER: US/09/187,693  
; PRIOR FILING DATE: 1998-11-05  
; PRIOR APPLICATION NUMBER: 09/162,280  
; PRIOR FILING DATE: 1998-09-29  
; PRIOR APPLICATION NUMBER: 08/851,362  
; PRIOR FILING DATE: 1997-05-05  
; NUMBER OF SEQ ID NOS: 75  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 66  
; LENGTH: 159  
; TYPE: PRT  
; ORGANISM: human  
; FEATURE:  
; NAME/KEY: VARIANT  
; LOCATION: (1)...(159)  
; OTHER INFORMATION: Xaa = Any Amino Acid  
US-11-021-795-66

Query Match 71.4%; Score 40; DB 6; Length 159;  
Best Local Similarity 66.7%; Pred. No. 56;  
Matches 6; Conservative 0; Mismatches 3; Indels 3; Gaps 0;

QY 1 HQYSKLPWT 9

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Db      88 HQYSTPWT 96
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RESULT 40
US-09-056-160B-6
; Sequence 6, Application US/09056160B
; Patent No. US20020032315A1
; GENERAL INFORMATION:
; APPLICANT: Baca, Manuel
; APPLICANT: Wells, James A.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Lowman, Henry B.
; APPLICANT: Chen, Yvonne M.
; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
; NUMBER OF SEQUENCES: 131
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/056,160B
; FILING DATE: 06-Apr-1998
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/054,856
; FILING DATE: 06-AUG-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hasak, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: P1093R2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1896
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-09-056-160B-6
Query Match      69.6%; Score 39; DB 3; Length 9;
Best Local Similarity 75.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      2 QYSKLPWT 9
|||||
Db      2 QYSTVPWT 9
|||||
RESULT 41
US-09-217-268B-31
; Sequence 31, Application US/09217268B
; Patent No. US20020065398A1
; GENERAL INFORMATION:
; APPLICANT: Mateo de Acosta del Rio, Christina M
; APPLICANT: Rodriguez, Rolando P
; APPLICANT: Prias, Ernesto M
; TITLE OF INVENTION: Humanized and Chimeric Monoclonal Antibodies That Recognize Epide
; FILE REFERENCE: 2720.1US
; CURRENT APPLICATION NUMBER: US/09/217,268B
; CURRENT FILING DATE: 1998-12-21
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
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; SEQ ID NO 31
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Murine
; FEATURE:
; NAME/KEY: MISC FEATURE
; OTHER INFORMATION: CDR of murine R3 antibody
US-09-217-268B-31
Query Match      69.6%; Score 39; DB 3; Length 9;
Best Local Similarity 75.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      2 QYSKLPWT 9
|||||
Db      2 QYSHVPWT 9
|||||
RESULT 42
US-10-234-671-6
; Sequence 6, Application US/10234671
; Publication No. US20030190317A1
; GENERAL INFORMATION:
; APPLICANT: Baca, Manuel
; APPLICANT: Wells, James A.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Lowman, Henry B.
; APPLICANT: Chen, Yvonne M.
; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
; NUMBER OF SEQUENCES: 131
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/234,671
; FILING DATE: 03-Sep-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/056160
; FILING DATE: 06-Apr-1998
; APPLICATION NUMBER: 60/126446
; FILING DATE: 07-Apr-1997
; APPLICATION NUMBER: 60/054856
; FILING DATE: 06-AUG-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Cui, Steven X.
; REGISTRATION NUMBER: 44,637
; REFERENCE/DOCKET NUMBER: P1093R2C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-8674
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-234-671-6
Query Match      69.6%; Score 39; DB 4; Length 9;
Best Local Similarity 75.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      2 QYSKLPWT 9
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; PRIOR APPLICATION NUMBER: US 60/360,843  
; PRIOR FILING DATE: 2002-03-01  
; PRIOR APPLICATION NUMBER: US 60/384,197  
; PRIOR FILING DATE: 2002-05-29  
; NUMBER OF SEQ ID NOS: 184  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 100  
; LENGTH: 103  
; TYPE: PRT  
; ORGANISM: Unknown  
; FEATURE:  
; OTHER INFORMATION: Humanized  
US-10-379-392-100

Query Match 69.6%; Score 39; DB 4; Length 103;  
Best Local Similarity 75.0%; Pred. No. 55;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYSKLPWT 9  
|||:|  
DB 90 QYSTVPEWT 97

RESULT 47  
US-10-379-392-121  
; Sequence 121, Application US/10379392  
; Publication No. US20040110226A1  
; GENERAL INFORMATION:  
; APPLICANT: Lazar, Gregory Alan  
; APPLICANT: Desjarlais, John Rudolf  
; APPLICANT: Marshall, Shannon Alicia  
; APPLICANT: Dahiyat, Bassil I.  
; TITLE OF INVENTION: ANTIBODY OPTIMIZATION  
; FILE REFERENCE: A-71386-3 463077-236  
; CURRENT APPLICATION NUMBER: US/10/379,392  
; CURRENT FILING DATE: 2003-03-03  
; PRIOR APPLICATION NUMBER: US 60/360,843  
; PRIOR FILING DATE: 2002-03-01  
; PRIOR APPLICATION NUMBER: US 60/384,197  
; PRIOR FILING DATE: 2002-05-29  
; NUMBER OF SEQ ID NOS: 184  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 121  
; LENGTH: 103  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-10-379-392-121

Query Match 69.6%; Score 39; DB 4; Length 103;  
Best Local Similarity 75.0%; Pred. No. 55;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYSKLPWT 9  
|||:|  
DB 90 QYSTVPEWT 97

RESULT 48  
US-10-379-392-123  
; Sequence 123, Application US/10379392  
; Publication No. US20040110226A1  
; GENERAL INFORMATION:  
; APPLICANT: Lazar, Gregory Alan  
; APPLICANT: Desjarlais, John Rudolf  
; APPLICANT: Marshall, Shannon Alicia  
; APPLICANT: Dahiyat, Bassil I.  
; TITLE OF INVENTION: ANTIBODY OPTIMIZATION  
; FILE REFERENCE: A-71386-3 463077-236  
; CURRENT APPLICATION NUMBER: US/10/379,392  
; CURRENT FILING DATE: 2003-03-03  
; PRIOR APPLICATION NUMBER: US 60/360,843

; PRIOR FILING DATE: 2002-03-01  
; PRIOR APPLICATION NUMBER: US 60/384,197  
; PRIOR FILING DATE: 2002-05-29  
; NUMBER OF SEQ ID NOS: 184  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 123  
; LENGTH: 103  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-10-379-392-123

Query Match 69.6%; Score 39; DB 4; Length 103;  
Best Local Similarity 75.0%; Pred. No. 55;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYSKLPWT 9  
|||:|  
DB 90 QYSTVPEWT 97

RESULT 49  
US-10-379-392-129  
; Sequence 129, Application US/10379392  
; Publication No. US20040110226A1  
; GENERAL INFORMATION:  
; APPLICANT: Lazar, Gregory Alan  
; APPLICANT: Desjarlais, John Rudolf  
; APPLICANT: Marshall, Shannon Alicia  
; APPLICANT: Dahiyat, Bassil I.  
; TITLE OF INVENTION: ANTIBODY OPTIMIZATION  
; FILE REFERENCE: A-71386-3 463077-236  
; CURRENT APPLICATION NUMBER: US/10/379,392  
; CURRENT FILING DATE: 2003-03-03  
; PRIOR APPLICATION NUMBER: US 60/360,843  
; PRIOR FILING DATE: 2002-03-01  
; PRIOR APPLICATION NUMBER: US 60/384,197  
; PRIOR FILING DATE: 2002-05-29  
; NUMBER OF SEQ ID NOS: 184  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 129  
; LENGTH: 103  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-10-379-392-129

Query Match 69.6%; Score 39; DB 4; Length 103;  
Best Local Similarity 75.0%; Pred. No. 55;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYSKLPWT 9  
|||:|  
DB 90 QYSTVPEWT 97

RESULT 50  
US-10-379-392-129  
; Sequence 129, Application US/10379392  
; Publication No. US20040110226A1  
; GENERAL INFORMATION:  
; APPLICANT: Lazar, Gregory Alan  
; APPLICANT: Desjarlais, John Rudolf  
; APPLICANT: Marshall, Shannon Alicia  
; APPLICANT: Dahiyat, Bassil I.  
; TITLE OF INVENTION: ANTIBODY OPTIMIZATION  
; FILE REFERENCE: A-71386-3 463077-236  
; CURRENT APPLICATION NUMBER: US/10/379,392  
; CURRENT FILING DATE: 2003-03-03  
; PRIOR APPLICATION NUMBER: US 60/360,843

QY 2 QYSKLPWT 9  
 |||: |||  
 Db 90 QYSTVPEWT 97

RESULT 50  
 US-10-379-392-131  
 ; Sequence 131, Application US/10379392  
 ; Publication No. US20040110226A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Lazar, Gregory Alan  
 ; APPLICANT: Desjarlais, John Rudolf  
 ; APPLICANT: Marshall, Shannon Alicia  
 ; APPLICANT: Dahiyat, Bassil I.  
 ; TITLE OF INVENTION: ANTIBODY OPTIMIZATION  
 ; FILE REFERENCE: A-71386-3 463077-236  
 ; CURRENT APPLICATION NUMBER: US/10/379,392  
 ; CURRENT FILING DATE: 2003-03-03  
 ; PRIOR APPLICATION NUMBER: US 60/360,843  
 ; PRIOR FILING DATE: 2002-03-01  
 ; PRIOR APPLICATION NUMBER: US 60/384,197  
 ; PRIOR FILING DATE: 2002-05-29  
 ; NUMBER OF SEQ ID NOS: 184  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 131  
 ; LENGTH: 103  
 ; TYPE: PRT  
 ; ORGANISM: Artificial sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Synthetic  
 US-10-379-392-131

Query Match 69.6%; Score 39; DB 4; Length 103;  
 Best Local Similarity 75.0%; Pred. No. 55;  
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYSKLPWT 9  
 |||: |||  
 Db 90 QYSTVPEWT 97

Search completed: April 6, 2006, 09:22:06  
 Job time : 81.7627 secs

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: April 6, 2006, 08:58:56 ; Search time 12.0508 Seconds  
(without alignments)  
61.745 Million cell updates/sec

Title: US-10-089-500-8

Perfect score: 56

Sequence: 1 HQYSKLPT 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Issued Patents AA:\*

1: /cgn2\_6/prodata/1/iaa/5 COMB pep:\*

2: /cgn2\_6/prodata/1/iaa/6 COMB pep:\*

3: /cgn2\_6/prodata/1/iaa/H COMB pep:\*

4: /cgn2\_6/prodata/1/iaa/PCITUS COMB pep:\*

5: /cgn2\_6/prodata/1/iaa/RE COMB pep:\*

6: /cgn2\_6/prodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	56	100.0	128	2	US-09-225-322B-10
2	56	100.0	128	2	US-09-225-322B-19
3	56	100.0	128	2	US-09-764-304-10
4	56	100.0	128	2	US-09-764-304-19
5	40	71.4	9	2	US-09-440-781-24
6	40	71.4	9	2	US-09-440-781-26
7	40	71.4	107	1	US-07-934-373C-18
8	40	71.4	107	2	US-08-437-642B-18
9	40	71.4	107	2	US-08-146-206C-18
10	40	71.4	107	2	US-09-648-067A-14
11	40	71.4	107	2	US-09-705-686-18
12	40	71.4	107	2	US-09-705-392A-18
13	40	71.4	107	2	US-09-705-398-18
14	40	71.4	107	2	US-09-602-812A-5
15	40	71.4	107	4	PCT-US93-07832-18
16	40	71.4	108	2	US-08-974-899-3
17	40	71.4	108	2	US-09-065-059-3
18	40	71.4	108	2	US-09-795-798-3
19	40	71.4	108	2	US-08-908-469-12
20	40	71.4	108	2	US-08-913-555-3
21	40	71.4	108	2	US-08-913-555-21
22	39	69.6	9	1	US-08-560-558E-31
23	39	69.6	9	2	US-09-217-268B-31
24	39	69.6	9	2	US-09-440-781-25
25	39	69.6	9	2	US-08-908-469-6
26	39	69.6	107	2	US-08-908-469-13
27	39	69.6	107	2	US-08-908-469-15

28	69.6	108	2	US-08-908-469-8	Sequence 8, Appl
29	69.6	108	2	US-08-908-469-10	Sequence 10, Appl
30	69.6	108	2	US-08-908-469-126	Sequence 126, App
31	69.6	110	2	US-09-440-781-94	Sequence 94, Appl
32	69.6	110	2	US-09-440-781-95	Sequence 95, Appl
33	69.6	110	2	US-08-908-469-103	Sequence 103, App
34	69.6	110	2	US-08-908-469-105	Sequence 105, App
35	69.6	110	2	US-08-908-469-107	Sequence 107, App
36	69.6	110	2	US-08-908-469-109	Sequence 109, App
37	69.6	110	2	US-08-908-469-111	Sequence 111, App
38	69.6	110	2	US-08-908-469-113	Sequence 113, App
39	69.6	110	2	US-08-908-469-115	Sequence 115, App
40	69.6	110	2	US-08-908-469-117	Sequence 117, App
41	69.6	113	1	US-08-497-312-18	Sequence 18, Appl
42	69.6	114	1	US-08-560-558E-27	Sequence 27, Appl
43	69.6	114	2	US-09-217-268B-37	Sequence 27, Appl
44	69.6	114	2	US-09-217-268B-35	Sequence 35, Appl
45	69.6	116	1	US-08-497-312-14	Sequence 14, Appl
46	69.6	237	2	US-08-908-469-100	Sequence 100, App
47	69.6	491	2	US-10-011-125A-2	Sequence 2, Appl
48	69.6	491	2	US-09-270-767-37260	Sequence 37260, A
49	69.6	491	2	US-09-270-767-52477	Sequence 52477, A
50	69.6	249	1	US-08-797-689-18	Sequence 18, Appl
51	69.6	249	1	US-09-984-186-18	Sequence 18, Appl
52	69.6	572	6	5200183-5	Patent No. 5200183
53	69.6	572	6	5215909-12	Patent No. 5215909
54	69.6	602	2	US-08-446-100-1	Sequence 1, Appl
55	69.6	602	2	US-08-446-100-2	Sequence 2, Appl
56	69.6	602	2	US-08-446-100-3	Sequence 3, Appl
57	69.6	602	2	US-08-446-100-4	Sequence 4, Appl
58	69.6	602	2	US-08-446-100-5	Sequence 5, Appl
59	69.6	602	2	US-08-446-100-6	Sequence 6, Appl
60	69.6	602	2	US-08-446-100-7	Sequence 7, Appl
61	69.6	602	2	US-08-446-100-8	Sequence 8, Appl
62	69.6	602	2	US-08-446-100-9	Sequence 9, Appl
63	69.6	602	2	US-08-446-100-10	Sequence 10, Appl
64	69.6	602	2	US-08-446-100-11	Sequence 11, Appl
65	69.6	602	2	US-08-446-100-12	Sequence 12, Appl
66	69.6	602	2	US-08-446-100-13	Sequence 13, Appl
67	69.6	602	2	US-08-446-100-14	Sequence 14, Appl
68	69.6	602	2	US-08-446-100-15	Sequence 15, Appl
69	69.6	602	2	US-08-446-100-16	Sequence 16, Appl
70	69.6	602	2	US-08-446-100-17	Sequence 17, Appl
71	69.6	602	2	US-08-446-100-18	Sequence 18, Appl
72	69.6	602	2	US-08-446-100-24	Sequence 24, Appl
73	69.6	602	2	US-09-334-489-3	Sequence 3, Appl
74	69.6	602	2	US-09-334-489-4	Sequence 4, Appl
75	69.6	602	6	5215909-11	Patent No. 5215909
76	69.6	635	6	5215909-10	Patent No. 5215909
77	69.6	643	2	US-09-949-016-11146	Sequence 11146, A
78	66.1	9	2	US-09-440-781-23	Sequence 23, Appl
79	66.1	9	2	US-08-908-469-125	Sequence 125, App
80	66.1	108	2	US-09-726-219A-242	Sequence 242, App
81	66.1	108	2	US-09-196-522-242	Sequence 242, App
82	66.1	112	2	US-08-487-761-13	Sequence 13, Appl
83	66.1	174	2	US-09-240-796A-17845	Sequence 17845, A
84	66.1	1498	1	US-08-404-531B-28	Sequence 28, Appl
85	66.1	1498	1	US-08-404-531B-29	Sequence 29, Appl
86	66.1	1498	2	US-08-476-900A-28	Sequence 28, Appl
87	66.1	1498	2	US-08-476-900A-29	Sequence 29, Appl
88	66.1	1498	2	US-08-488-546A-28	Sequence 28, Appl
89	66.1	1498	2	US-08-488-546A-29	Sequence 29, Appl
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91	66.1	1581	2	US-08-476-900A-6	Sequence 6, Appl
92	66.1	1581	2	US-08-488-546A-6	Sequence 6, Appl
93	66.1	1581	2	US-08-726-320-4	Sequence 4, Appl
94	66.1	1581	2	US-08-208-716-4	Sequence 4, Appl
95	66.1	1582	1	US-08-404-531B-9	Sequence 9, Appl
96	66.1	1582	2	US-08-476-900A-9	Sequence 9, Appl
97	66.1	1582	2	US-08-488-546A-9	Sequence 9, Appl
98	66.1	1582	2	US-08-726-320-5	Sequence 5, Appl
99	66.1	1582	2	US-09-208-716-5	Sequence 5, Appl
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101	36	64.3	239	2	US-10-092-246-33	Sequence 33, Appl	174	34	60.7	240	2	US-08-839-765-148	Sequence 148, App
102	36	64.3	239	2	US-10-096-246A-33	Sequence 33, Appl	175	34	60.7	240	2	US-09-136-389-147	Sequence 147, App
103	36	64.3	240	2	US-10-092-246-36	Sequence 36, Appl	176	34	60.7	240	2	US-09-136-389-148	Sequence 148, App
104	36	64.3	240	2	US-10-092-246-37	Sequence 37, Appl	177	34	60.7	240	2	US-09-610-838-147	Sequence 147, App
105	36	64.3	240	2	US-10-096-246A-34	Sequence 34, Appl	178	34	60.7	240	2	US-09-610-838-148	Sequence 148, App
106	36	64.3	240	2	US-10-096-246A-35	Sequence 35, Appl	179	34	60.7	240	2	US-10-092-246-34	Sequence 34, Appl
107	36	64.3	240	2	US-10-096-246A-36	Sequence 36, Appl	180	34	60.7	240	2	US-10-092-246-35	Sequence 35, Appl
108	36	64.3	240	2	US-10-096-246A-37	Sequence 37, Appl	181	34	60.7	240	2	US-09-711-485-147	Sequence 147, App
109	36	64.3	622	2	US-09-843-598-11	Sequence 11, Appl	182	34	60.7	240	2	US-09-711-485-148	Sequence 148, App
110	35	62.5	9	2	US-08-030-175-15	Sequence 15, Appl	183	34	60.7	257	2	US-10-092-246-2	Sequence 2, Appl1
111	35	62.5	109	2	US-09-386-650A-4	Sequence 4, Appl1	184	34	60.7	257	2	US-10-096-246A-2	Sequence 2, Appl1
112	35	62.5	233	2	US-08-030-175-43	Sequence 43, Appl	185	34	60.7	264	2	US-09-252-991A-16915	Sequence 16915, A
113	35	62.5	338	2	US-09-248-796A-18877	Sequence 18877, A	186	34	60.7	284	2	US-09-328-352-5979	Sequence 5979, Ap
114	35	62.5	343	2	US-09-252-991A-29205	Sequence 29205, A	187	34	60.7	303	2	US-09-248-796A-17696	Sequence 17696, A
115	35	62.5	396	2	US-09-134-001C-4546	Sequence 4546, Ap	188	34	60.7	310	1	US-08-943-600A-3	Sequence 3, Appl1
116	35	62.5	614	2	US-09-949-016-10772	Sequence 10772, A	189	34	60.7	310	2	US-09-354-942-3	Sequence 3, Appl1
117	35	62.5	728	2	US-09-252-991A-22187	Sequence 22187, A	190	34	60.7	426	2	US-09-063-893A-4	Sequence 4, Appl1
118	35	62.5	738	2	US-09-252-991A-27291	Sequence 27291, A	191	34	60.7	426	2	US-08-826-246-4	Sequence 4, Appl1
119	34	60.7	107	1	US-08-425-336-123	Sequence 123, App	192	34	60.7	426	2	US-08-944-495-4	Sequence 4, Appl1
120	34	60.7	107	1	US-08-425-336-125	Sequence 125, App	193	34	60.7	426	2	US-09-126-640-8	Sequence 8, Appl1
121	34	60.7	107	1	US-08-488-113B-123	Sequence 123, App	194	34	60.7	426	2	US-08-925-588-4	Sequence 4, Appl1
122	34	60.7	107	1	US-08-488-113B-125	Sequence 125, App	195	34	60.7	426	2	US-09-082-092-4	Sequence 4, Appl1
123	34	60.7	107	1	US-08-477-484B-123	Sequence 123, App	196	34	60.7	426	2	US-09-082-092-6	Sequence 6, Appl1
124	34	60.7	107	1	US-08-477-484B-125	Sequence 125, App	197	34	60.7	426	2	US-09-288-292A-8	Sequence 8, Appl1
125	34	60.7	107	1	US-08-107-669D-26	Sequence 26, Appl	198	34	60.7	426	2	US-09-372-044-4	Sequence 4, Appl1
126	34	60.7	107	1	US-08-107-669D-27	Sequence 27, Appl	199	34	60.7	426	2	US-08-825-486-4	Sequence 4, Appl1
127	34	60.7	107	1	US-08-107-669D-65	Sequence 65, Appl	200	34	60.7	426	2	US-09-885-722A-4	Sequence 4, Appl1
128	34	60.7	107	1	US-08-472-788A-26	Sequence 26, Appl	201	34	60.7	426	2	US-09-885-722A-6	Sequence 6, Appl1
129	34	60.7	107	1	US-08-472-788A-27	Sequence 27, Appl	202	34	60.7	426	2	US-08-826-248-4	Sequence 4, Appl1
130	34	60.7	107	1	US-08-472-788A-87	Sequence 87, Appl	203	34	60.7	526	2	US-09-949-016-7634	Sequence 7634, Ap
131	34	60.7	107	1	US-08-477-531B-26	Sequence 26, Appl	204	33	58.9	61	2	US-09-513-999C-4480	Sequence 4480, Ap
132	34	60.7	107	1	US-08-477-531B-27	Sequence 27, Appl	205	33	58.9	62	2	US-09-471-276-933	Sequence 933, App
133	34	60.7	107	1	US-08-477-531B-65	Sequence 65, Appl	206	33	58.9	65	2	US-09-248-796A-23293	Sequence 23293, A
134	34	60.7	107	1	US-08-646-360-123	Sequence 123, App	207	33	58.9	93	2	US-09-248-796A-15092	Sequence 15092, A
135	34	60.7	107	1	US-08-646-360-125	Sequence 125, App	208	33	58.9	105	2	US-08-851-362D-30	Sequence 30, Appl
136	34	60.7	107	1	US-08-652-558-2	Sequence 2, Appl1	209	33	58.9	108	2	US-09-240-274-178	Sequence 178, App
137	34	60.7	107	1	US-08-652-558-35	Sequence 35, Appl	210	33	58.9	108	2	US-09-848-798-178	Sequence 178, App
138	34	60.7	107	1	US-08-082-842A-26	Sequence 26, Appl	211	33	58.9	118	1	US-08-481-377-10	Sequence 10, Appl
139	34	60.7	107	1	US-08-082-842A-27	Sequence 27, Appl	212	33	58.9	118	1	US-08-491-835-8	Sequence 8, Appl1
140	34	60.7	107	1	US-08-082-842A-87	Sequence 87, Appl	213	33	58.9	118	2	US-09-153-733A-10	Sequence 10, Appl
141	34	60.7	107	2	US-08-839-765-123	Sequence 123, App	214	33	58.9	118	2	US-08-946-092A-8	Sequence 8, Appl1
142	34	60.7	107	2	US-08-839-765-125	Sequence 125, App	215	33	58.9	118	2	US-09-172-062-8	Sequence 8, Appl1
143	34	60.7	107	2	US-09-136-389-123	Sequence 123, App	216	33	58.9	118	2	US-09-301-520D-8	Sequence 8, Appl1
144	34	60.7	107	2	US-09-136-389-125	Sequence 125, App	217	33	58.9	118	2	US-09-389-705D-10	Sequence 10, Appl
145	34	60.7	107	2	US-09-254-189-1	Sequence 1, Appl1	218	33	58.9	118	4	PCT-US94-00666-10	Sequence 10, Appl
146	34	60.7	107	2	US-09-610-838-123	Sequence 123, App	219	33	58.9	128	1	US-08-455-550-16	Sequence 16, Appl
147	34	60.7	107	2	US-09-610-838-125	Sequence 125, App	220	33	58.9	128	1	US-08-065-844A-6	Sequence 6, Appl1
148	34	60.7	107	2	US-09-711-485-123	Sequence 123, App	221	33	58.9	144	2	US-10-002-278-6	Sequence 6, Appl1
149	34	60.7	107	2	US-09-711-485-125	Sequence 125, App	222	33	58.9	144	2	US-09-330-914A-6	Sequence 6, Appl1
150	34	60.7	108	2	US-09-726-219A-267	Sequence 267, App	223	33	58.9	150	2	US-09-732-210-39	Sequence 39, Appl
151	34	60.7	108	2	US-09-196-522-267	Sequence 267, App	224	33	58.9	159	2	US-09-270-767-44932	Sequence 44932, A
152	34	60.7	109	1	US-08-713-939A-74	Sequence 74, Appl	225	33	58.9	184	2	US-09-252-991A-18317	Sequence 18317, A
153	34	60.7	109	2	US-09-036-579-74	Sequence 74, Appl	226	33	58.9	209	2	US-09-248-796A-21096	Sequence 21096, A
154	34	60.7	109	2	US-09-550-374-74	Sequence 74, Appl	227	33	58.9	239	2	US-09-540-236-2733	Sequence 2733, Ap
155	34	60.7	109	2	US-09-943-906-74	Sequence 74, Appl	228	33	58.9	254	2	US-09-902-540-10473	Sequence 10473, A
156	34	60.7	109	2	US-10-435-602-74	Sequence 74, Appl	229	33	58.9	264	2	US-09-092-540-16352	Sequence 16352, A
157	34	60.7	110	2	US-10-092-246-13	Sequence 13, Appl	230	33	58.9	279	2	US-09-118-270-39	Sequence 39, Appl
158	34	60.7	110	2	US-10-096-246A-13	Sequence 13, Appl	231	33	58.9	326	1	PCT-US93-08528-39	Sequence 39, Appl
159	34	60.7	128	2	US-08-444-644-15	Sequence 15, Appl	232	33	58.9	326	2	US-08-988-876-9	Sequence 9, Appl1
160	34	60.7	128	2	US-08-444-644-25	Sequence 25, Appl	233	33	58.9	342	2	US-09-054-272-2	Sequence 2, Appl1
161	34	60.7	128	2	US-08-232-246A-15	Sequence 15, Appl	234	33	58.9	342	2	US-09-826-509-555	Sequence 555, App
162	34	60.7	128	2	US-08-232-246A-25	Sequence 25, Appl	235	33	58.9	346	1	US-08-702-153-4	Sequence 4, Appl1
163	34	60.7	129	1	US-08-270-767-48787	Sequence 2, Appl1	236	33	58.9	346	1	US-08-702-153-4	Sequence 4, Appl1
164	34	60.7	236	2	US-09-270-767-48787	Sequence 48787, A	237	33	58.9	360	1	US-08-459-346-13	Sequence 13, Appl
165	34	60.7	239	2	US-10-092-246-32	Sequence 32, Appl	238	33	58.9	360	1	US-08-411-607A-4	Sequence 4, Appl1
166	34	60.7	239	2	US-08-488-113B-147	Sequence 147, App	239	33	58.9	360	2	US-08-889-419-13	Sequence 13, Appl
167	34	60.7	240	1	US-08-488-113B-148	Sequence 148, App	240	33	58.9	360	2	US-08-402-542-13	Sequence 13, Appl
168	34	60.7	240	1	US-08-477-484B-148	Sequence 147, App	241	33	58.9	360	2	US-09-361-741-4	Sequence 4, Appl1
169	34	60.7	240	1	US-08-477-484B-148	Sequence 148, App	242	33	58.9	360	2	US-09-461-418-4	Sequence 4, Appl1
170	34	60.7	240	1	US-08-646-360-147	Sequence 147, App	243	33	58.9	360	4	PCT-US93-07189-13	Sequence 13, Appl
171	34	60.7	240	1	US-08-646-360-148	Sequence 148, App	244	33	58.9	388	2	US-09-538-092-804	Sequence 804, App
172	34	60.7	240	1	US-08-839-765-147	Sequence 147, App	245	33	58.9	399	2	US-09-252-991A-23589	Sequence 23589, A
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247	33	58.9	499	2	US-09-252-991A-23848	Sequence 23848, A	320		57.1	614	2	US-09-919-039-378	Sequence 378, App
248	33	58.9	503	2	US-09-248-796A-16650	Sequence 16650, A	321		57.1	614	4	PCT-US94-00119-2	Sequence 2, Appli
249	33	58.9	635	1	US-07-879-617A-9	Sequence 9, Appli	322		57.1	614	4	PCT-US95-10579-8	Sequence 8, Appli
250	33	58.9	635	1	US-08-753-985-9	Sequence 9, Appli	323		57.1	614	4	PCT-US95-10579-8	Sequence 34, Appl
251	33	58.9	877	2	US-09-492-709A-353	Sequence 353, App	324		57.1	632	2	US-09-232-200-34	Sequence 35, Appl
252	33	58.9	1073	1	US-07-695-564-1	Sequence 1, Appli	325		57.1	632	2	US-09-232-200-35	Sequence 39, Appl
253	33	58.9	1073	1	US-08-241-387-1	Sequence 1, Appli	326		57.1	632	2	US-09-232-200-35	Sequence 35, Appl
254	33	58.9	1073	2	US-09-949-002-293	Sequence 293, App	327		57.1	632	2	US-09-232-197-34	Sequence 34, Appl
255	33	58.9	1091	1	US-07-695-564-3	Sequence 3, Appli	328		57.1	632	2	US-09-232-197-35	Sequence 35, Appl
256	33	58.9	1091	1	US-08-241-387-3	Sequence 3, Appli	329		57.1	632	2	US-09-232-197-39	Sequence 39, Appl
257	33	58.9	1580	2	US-08-726-320-1	Sequence 1, Appli	330		57.1	632	2	US-09-232-201-34	Sequence 34, Appl
258	33	58.9	1580	2	US-09-208-716-1	Sequence 1, Appli	331		57.1	632	2	US-09-232-201-35	Sequence 35, Appl
259	33	58.9	1581	2	US-08-726-320-3	Sequence 3, Appli	332		57.1	632	2	US-09-232-201-39	Sequence 39, Appl
260	33	58.9	1581	2	US-09-208-716-3	Sequence 3, Appli	333		57.1	632	2	US-09-232-195-34	Sequence 34, Appl
261	32.5	58.0	473	2	US-09-902-540-16631	Sequence 16631, A	334		57.1	632	2	US-09-232-195-35	Sequence 35, Appl
262	32.5	58.0	910	2	US-08-460-269C-2	Sequence 2, Appli	335		57.1	632	2	US-09-232-195-35	Sequence 35, Appl
263	32.5	58.0	911	2	US-08-460-269C-4	Sequence 4, Appli	336		57.1	634	2	US-09-949-016-7681	Sequence 7681, Ap
264	32.5	58.0	922	2	US-08-460-269C-6	Sequence 6, Appli	337		57.1	643	2	US-09-232-200-41	Sequence 27, Appl
265	32	57.1	9	1	US-08-360-125-21	Sequence 21, Appl	338		57.1	643	2	US-09-232-200-41	Sequence 41, Appl
266	32	57.1	9	1	US-08-450-578-21	Sequence 21, Appl	339		57.1	643	2	US-09-232-200-42	Sequence 42, Appl
267	32	57.1	9	1	US-09-017-828-21	Sequence 21, Appl	340		57.1	643	2	US-09-232-200-45	Sequence 45, Appl
268	32	57.1	9	1	US-09-014-880-21	Sequence 21, Appl	341		57.1	643	2	US-09-232-200-53	Sequence 53, Appl
269	32	57.1	9	2	US-08-649-100-15	Sequence 15, Appl	342		57.1	643	2	US-09-232-200-71	Sequence 71, Appl
270	32	57.1	9	2	US-08-649-100-31	Sequence 31, Appl	343		57.1	643	2	US-09-232-197-27	Sequence 27, Appl
271	32	57.1	9	2	US-08-450-363-21	Sequence 21, Appl	344		57.1	643	2	US-09-232-197-41	Sequence 41, Appl
272	32	57.1	9	2	US-09-467-903-21	Sequence 21, Appl	345		57.1	643	2	US-09-232-197-42	Sequence 42, Appl
273	32	57.1	91	2	US-09-248-796A-27490	Sequence 27490, A	346		57.1	643	2	US-09-232-197-45	Sequence 45, Appl
274	32	57.1	108	1	US-08-276-852-86	Sequence 86, Appl	347		57.1	643	2	US-09-232-197-53	Sequence 53, Appl
275	32	57.1	108	1	US-08-899-575-86	Sequence 86, Appl	348		57.1	643	2	US-09-232-197-71	Sequence 71, Appl
276	32	57.1	108	1	US-08-899-575-86	Sequence 86, Appl	349		57.1	643	2	US-09-232-201-27	Sequence 27, Appl
277	32	57.1	108	2	US-08-483-749A-8	Sequence 8, Appli	350		57.1	643	2	US-09-232-201-41	Sequence 41, Appl
278	32	57.1	108	4	PCT-US95-08743-86	Sequence 86, Appli	351		57.1	643	2	US-09-232-201-42	Sequence 42, Appl
279	32	57.1	110	2	US-09-949-016-8827	Sequence 8827, Ap	352		57.1	643	2	US-09-232-201-45	Sequence 45, Appl
280	32	57.1	114	1	US-08-360-125-6	Sequence 6, Appli	353		57.1	643	2	US-09-232-201-53	Sequence 53, Appl
281	32	57.1	114	1	US-08-450-578-6	Sequence 6, Appli	354		57.1	643	2	US-09-232-201-71	Sequence 71, Appl
282	32	57.1	114	1	US-09-017-628-6	Sequence 6, Appli	355		57.1	643	2	US-09-232-195-27	Sequence 27, Appl
283	32	57.1	114	1	US-09-014-880-6	Sequence 6, Appli	356		57.1	643	2	US-09-232-195-41	Sequence 41, Appl
284	32	57.1	114	2	US-08-450-363-6	Sequence 6, Appli	357		57.1	643	2	US-09-232-195-42	Sequence 42, Appl
285	32	57.1	114	2	US-09-467-903-6	Sequence 6, Appli	358		57.1	643	2	US-09-232-195-45	Sequence 45, Appl
286	32	57.1	127	2	US-08-649-100-17	Sequence 17, Appl	359		57.1	643	2	US-09-232-201-53	Sequence 53, Appl
287	32	57.1	127	2	US-08-649-100-33	Sequence 33, Appl	360		57.1	643	2	US-09-232-195-71	Sequence 71, Appl
288	32	57.1	141	2	US-09-472-087-88	Sequence 88, Appl	361		57.1	670	2	US-09-949-016-11710	Sequence 11710, A
289	32	57.1	200	2	US-09-949-016-8732	Sequence 8732, Ap	362		57.1	688	2	US-10-262-083-22	Sequence 22, Appl
290	32	57.1	215	2	US-09-270-767-45569	Sequence 45569, A	363		57.1	688	2	US-10-262-083-26	Sequence 26, Appl
291	32	57.1	223	2	US-09-066-408-7	Sequence 7, Appli	364		57.1	785	1	US-07-841-997A-4	Sequence 4, Appli
292	32	57.1	223	2	US-09-066-408-8	Sequence 8, Appli	365		57.1	785	1	US-08-290-301-4	Sequence 4, Appli
293	32	57.1	223	2	US-09-066-408-9	Sequence 9, Appli	366		57.1	785	1	US-09-013-598-4	Sequence 4, Appli
294	32	57.1	223	2	US-09-066-408-11	Sequence 11, Appl	367		57.1	1098	1	US-08-290-301-82	Sequence 82, Appl
295	32	57.1	235	2	US-09-472-087-14	Sequence 14, Appl	368		57.1	1098	2	US-09-013-598-82	Sequence 82, Appl
296	32	57.1	235	2	US-09-472-087-65	Sequence 65, Appl	369		57.1	1587	2	US-09-000-094-46	Sequence 46, Appl
297	32	57.1	261	2	US-09-605-703B-190	Sequence 190, App	370		57.1	1587	2	US-10-011-749-46	Sequence 46, Appl
298	32	57.1	314	2	US-09-270-767-42737	Sequence 42737, A	371	31.5	56.2	257	2	US-09-902-540-12797	Sequence 12797, A
299	32	57.1	339	2	US-09-248-796A-19599	Sequence 19599, A	372	31	55.4	71	2	US-09-206-551-32	Sequence 32, Appl
300	32	57.1	346	2	US-09-540-236-3202	Sequence 3202, Ap	373	31	55.4	74	2	US-09-621-976-5631	Sequence 5631, Ap
301	32	57.1	370	2	US-09-134-000C-5356	Sequence 5356, App	374	31	55.4	74	2	US-08-270-767-36536	Sequence 36536, A
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303	32	57.1	404	2	US-09-252-991A-22779	Sequence 22779, A	376	31	55.4	86	2	US-08-658-207A-471	Sequence 471, App
304	32	57.1	430	2	US-09-252-991A-29287	Sequence 29287, A	377	31	55.4	93	1	US-08-633-682-2	Sequence 2, Appli
305	32	57.1	437	2	US-09-252-991A-24355	Sequence 24355, A	378	31	55.4	93	2	US-08-936-772-2	Sequence 2, Appli
306	32	57.1	442	2	US-09-787-083-2	Sequence 2, Appli	379	31	55.4	93	2	US-09-395-918-2	Sequence 2, Appli
307	32	57.1	442	2	US-09-787-083-4	Sequence 4, Appli	380	31	55.4	94	2	US-08-646-899-2	Sequence 2, Appli
308	32	57.1	442	2	US-09-787-083-6	Sequence 6, Appli	381	31	55.4	107	2	US-09-240-274-29	Sequence 29, Appl
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310	32	57.1	463	2	US-09-252-991A-18413	Sequence 18413, A	383	31	55.4	107	2	US-10-007-790-4	Sequence 4, Appli
311	32	57.1	480	2	US-09-540-236-3551	Sequence 3551, Ap	384	31	55.4	107	2	US-09-848-798-29	Sequence 29, Appl
312	32	57.1	483	2	US-09-543-681A-6157	Sequence 6157, Ap	385	31	55.4	109	1	US-07-934-373C-3	Sequence 3, Appli
313	32	57.1	525	2	US-10-101-464A-613	Sequence 613, App	386	31	55.4	109	2	US-08-437-642B-3	Sequence 3, Appli
314	32	57.1	560	2	US-09-252-991A-22343	Sequence 22343, A	387	31	55.4	109	2	US-08-146-206C-3	Sequence 3, Appli
315	32	57.1	614	1	US-08-295-8145-12	Sequence 12, Appl	388	31	55.4	109	2	US-09-705-686-3	Sequence 3, Appli
316	32	57.1	614	1	US-08-543-881-2	Sequence 2, Appli	389	31	55.4	109	2	US-09-705-392A-3	Sequence 3, Appli
317	32	57.1	614	1	US-08-291-299-2	Sequence 2, Appli	390	31	55.4	109	2	US-09-705-398-3	Sequence 3, Appli
318	32	57.1	614	1	US-08-291-299-8	Sequence 8, Appli	391	31	55.4	109	4	PCT-US93-07832-3	Sequence 3, Appli
319	32	57.1	614	2	US-09-343-361-12	Sequence 12, Appli	392	31	55.4	110	2	US-09-270-767-37321	Sequence 37321, A

393	31	55.4	110	2	US-09-270-767-52538	Sequence 52538, A	466	31	55.4	1058	2	US-09-826-312A-2	Sequence 2, Appli
394	31	55.4	111	1	US-08-887-3528-7	Sequence 7, Appli	467	31	55.4	1058	2	US-09-538-092-985	Sequence 985, App
395	31	55.4	111	2	US-09-109-207C-7	Sequence 7, Appli	468	31	55.4	1059	2	US-09-542-437A-2	Sequence 2, Appli
396	31	55.4	111	2	US-09-296-005-7	Sequence 7, Appli	469	31	55.4	1059	2	US-10-108-767-2	Sequence 2, Appli
397	31	55.4	111	2	US-09-920-171-7	Sequence 7, Appli	470	31	55.4	1300	2	US-09-503-540-9932	Sequence 9932, Ap
398	31	55.4	111	2	US-09-716-028-7	Sequence 7, Appli	471	31	55.4	2037	2	US-09-543-681A-5538	Sequence 5538, Ap
399	31	55.4	111	2	US-10-113-996-7	Sequence 7, Appli	472	31	55.4	138	2	US-09-270-767-56946	Sequence 56946, A
400	31	55.4	131	2	US-09-284-768A-14	Sequence 14, Appli	473	30.5	54.5	333	2	US-09-270-767-41703	Sequence 41703, A
401	31	55.4	145	2	US-09-949-016-9003	Sequence 9003, Ap	474	30.5	54.5	333	2	US-08-300-386A-57	Sequence 57, Appli
402	31	55.4	165	2	US-09-252-991A-24486	Sequence 24486, A	475	30.5	54.5	9	1	US-08-931-645-57	Sequence 57, Appli
403	31	55.4	165	2	US-09-893-737-196	Sequence 196, App	476	30	53.6	9	2	PCT-US94-01258-57	Sequence 57, Appli
404	31	55.4	169	2	US-09-614-913-54	Sequence 54, Appli	477	30	53.6	9	4	PCT-US95-11235-57	Sequence 57, Appli
405	31	55.4	177	2	US-09-252-991A-27754	Sequence 27754, A	478	30	53.6	15	2	US-09-613-092B-5	Sequence 5, Appli
406	31	55.4	184	2	US-09-270-767-35271	Sequence 35271, A	479	30	53.6	23	1	US-08-303-569B-9	Sequence 9, Appli
407	31	55.4	184	2	US-09-270-767-50488	Sequence 50488, A	480	30	53.6	23	2	US-08-795-513-9	Sequence 9, Appli
408	31	55.4	199	2	US-09-710-279-2546	Sequence 2546, Ap	481	30	53.6	60	2	US-08-905-223-457	Sequence 457, App
409	31	55.4	203	2	US-09-710-279-3138	Sequence 3138, Ap	482	30	53.6	76	2	US-09-540-236-2637	Sequence 2637, Ap
410	31	55.4	214	2	US-09-489-039A-14324	Sequence 14324, A	483	30	53.6	88	2	US-09-543-681A-7793	Sequence 7793, Ap
411	31	55.4	220	2	US-08-952-235-1	Sequence 1, Appli	484	30	53.6	106	2	US-09-248-796A-19225	Sequence 19225, A
412	31	55.4	220	2	US-09-669-971-1	Sequence 1, Appli	485	30	53.6	106	2	US-09-471-276-1316	Sequence 1316, Ap
413	31	55.4	227	2	US-09-134-001C-4350	Sequence 4350, Ap	486	30	53.6	107	1	US-08-561-521-6	Sequence 6, Appli
414	31	55.4	248	2	US-10-012-231A-194	Sequence 194, App	487	30	53.6	107	1	US-08-561-521-8	Sequence 8, Appli
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416	31	55.4	248	2	US-10-006-768A-194	Sequence 194, App	489	30	53.6	107	1	US-08-652-558-47	Sequence 47, Appli
417	31	55.4	248	2	US-10-015-671A-194	Sequence 194, App	490	30	53.6	107	1	US-08-318-157B-6	Sequence 6, Appli
418	31	55.4	248	2	US-10-015-393A-194	Sequence 194, App	491	30	53.6	107	2	US-09-025-203-15	Sequence 15, Appli
419	31	55.4	248	2	US-10-011-833A-194	Sequence 194, App	492	30	53.6	107	2	US-09-253-794-6	Sequence 6, Appli
420	31	55.4	248	2	US-10-006-041A-194	Sequence 194, App	493	30	53.6	107	2	US-09-999-021-15	Sequence 15, Appli
421	31	55.4	248	2	US-10-012-064A-194	Sequence 194, App	494	30	53.6	107	2	US-09-999-025-15	Sequence 15, Appli
422	31	55.4	249	2	US-09-949-016-8151	Sequence 8151, App	495	30	53.6	107	2	US-10-040-997-15	Sequence 15, Appli
423	31	55.4	254	2	US-09-949-016-6948	Sequence 6948, Ap	496	30	53.6	107	2	US-09-999-040-15	Sequence 15, Appli
424	31	55.4	261	2	US-09-555-510B-13	Sequence 13, Appli	497	30	53.6	107	2	US-09-998-817-15	Sequence 15, Appli
425	31	55.4	261	2	US-10-231-013-13	Sequence 13, Appli	498	30	53.6	107	2	US-10-330-613A-18	Sequence 18, Appli
426	31	55.4	264	2	US-09-583-110-4378	Sequence 4378, Ap	499	30	53.6	107	4	PCT-US95-01219-6	Sequence 6, Appli
427	31	55.4	264	2	US-09-107-433-4635	Sequence 4635, Ap	500	30	53.6	107	4	PCT-US95-01219-8	Sequence 8, Appli
428	31	55.4	269	2	US-09-902-540-11261	Sequence 11261, A	501	30	53.6	108	1	US-08-070-116A-7	Sequence 7, Appli
429	31	55.4	276	2	US-09-949-002-375	Sequence 375, App	502	30	53.6	108	1	US-08-116-247-9	Sequence 9, Appli
430	31	55.4	285	2	US-09-149-476-470	Sequence 470, App	503	30	53.6	108	1	US-08-602-725-29	Sequence 29, Appli
431	31	55.4	296	2	US-09-614-912-40	Sequence 40, Appli	504	30	53.6	108	2	US-08-557-050-7	Sequence 7, Appli
432	31	55.4	311	2	US-10-184-563-2	Sequence 2, Appli	505	30	53.6	108	2	US-08-454-899G-100	Sequence 100, App
433	31	55.4	326	2	US-09-134-001C-4837	Sequence 4837, Ap	506	30	53.6	108	2	US-09-348-224-9	Sequence 9, Appli
434	31	55.4	327	2	US-09-252-991A-32961	Sequence 32961, A	507	30	53.6	112	2	US-10-148-737A-2	Sequence 2, Appli
435	31	55.4	333	2	US-09-949-002-502	Sequence 502, App	508	30	53.6	121	2	US-09-253-991A-21694	Sequence 21694, A
436	31	55.4	359	2	US-09-842-164A-4	Sequence 4, Appli	509	30	53.6	121	2	US-09-471-276-1394	Sequence 1394, Ap
437	31	55.4	371	2	US-09-614-912-50	Sequence 50, Appli	510	30	53.6	123	2	US-09-583-110-3813	Sequence 3813, Ap
438	31	55.4	372	2	US-09-949-016-7140	Sequence 7140, Ap	511	30	53.6	127	2	US-09-107-433-4052	Sequence 4052, Ap
439	31	55.4	393	2	US-09-614-912-36	Sequence 36, Appli	512	30	53.6	133	2	US-09-284-768A-16	Sequence 16, Appli
440	31	55.4	418	2	US-09-270-767-44129	Sequence 44129, A	513	30	53.6	136	2	US-09-710-279-526	Sequence 526, App
441	31	55.4	422	2	US-09-248-796A-16762	Sequence 16762, A	514	30	53.6	140	2	US-09-270-767-35445	Sequence 35445, A
442	31	55.4	424	2	US-09-173-581-7	Sequence 7, Appli	515	30	53.6	140	2	US-09-270-767-50662	Sequence 50662, A
443	31	55.4	424	2	US-09-420-915-7	Sequence 7, Appli	516	30	53.6	141	2	US-09-582-337-16	Sequence 16, Appli
444	31	55.4	448	2	US-09-284-768A-23	Sequence 23, Appli	517	30	53.6	143	2	US-09-328-352-7409	Sequence 7409, Ap
445	31	55.4	479	2	US-09-540-236-3627	Sequence 3627, Ap	518	30	53.6	144	2	US-09-252-991A-17329	Sequence 17329, A
446	31	55.4	511	2	US-09-252-991A-21619	Sequence 21619, A	519	30	53.6	153	2	US-08-829-402-3	Sequence 3, Appli
447	31	55.4	519	2	US-09-538-092-1292	Sequence 1292, Ap	520	30	53.6	162	2	US-08-992-176-9	Sequence 9, Appli
448	31	55.4	523	2	US-09-538-092-571	Sequence 571, App	521	30	53.6	162	2	US-09-602-472A-64	Sequence 64, Appli
449	31	55.4	542	2	US-09-949-016-6778	Sequence 6778, Ap	522	30	53.6	173	2	US-09-284-768A-15	Sequence 15, Appli
450	31	55.4	548	2	US-09-252-991A-25684	Sequence 25684, A	523	30	53.6	180	2	US-09-328-352-5455	Sequence 5455, Ap
451	31	55.4	554	2	US-09-949-016-11687	Sequence 11687, A	524	30	53.6	188	2	US-09-489-039A-13948	Sequence 13948, A
452	31	55.4	575	2	US-09-252-991A-22037	Sequence 22037, A	525	30	53.6	195	2	US-10-358-790-5	Sequence 5, Appli
453	31	55.4	577	2	US-09-902-540-15872	Sequence 15872, A	526	30	53.6	196	2	US-09-538-092-593	Sequence 593, App
454	31	55.4	584	2	US-09-911-909B-14	Sequence 14, Appli	527	30	53.6	198	2	US-09-198-452A-175	Sequence 175, App
455	31	55.4	629	2	US-09-949-016-11700	Sequence 11700, A	528	30	53.6	204	2	US-09-489-039A-13948	Sequence 517, App
456	31	55.4	637	2	US-09-284-768A-20	Sequence 20, Appli	529	30	53.6	207	1	US-08-793-229-30	Sequence 30, Appli
457	31	55.4	674	2	US-09-284-768A-21	Sequence 21, Appli	530	30	53.6	207	2	US-09-285-957-30	Sequence 30, Appli
458	31	55.4	784	2	US-09-949-016-8793	Sequence 8793, Ap	531	30	53.6	215	2	US-10-358-790-1	Sequence 1, Appli
459	31	55.4	861	2	US-09-949-016-8794	Sequence 8794, Ap	532	30	53.6	223	2	US-09-328-352-4358	Sequence 4358, Ap
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461	31	55.4	861	2	US-09-252-991A-29422	Sequence 29422, A	534	30	53.6	241	2	US-09-605-703B-1950	Sequence 1950, Ap
462	31	55.4	1046	2	US-09-199-637A-13	Sequence 13, Appli	535	30	53.6	242	2	US-09-949-016-10911	Sequence 10911, A
463	31	55.4	1049	2	US-09-252-991A-26475	Sequence 26475, A	536	30	53.6	260	2	US-09-248-796A-16370	Sequence 16370, A
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465	31	55.4	1058	2	US-08-767-942A-15	Sequence 15, Appli	538	30	53.6	273	2	US-09-134-591-5	Sequence 5, Appli

539	30	53.6	278	2	US-09-252-991A-25529	Sequence 25529, A	612	30	53.6	909	2	US-09-301-085-142	Sequence 142, App
540	30	53.6	302	2	US-09-949-016-9576	Sequence 9576, Ap	613	30	53.6	909	4	PCT-US95-04589-142	Sequence 142, App
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542	30	53.6	322	2	US-09-489-039A-9408	Sequence 9408, Ap	615	30	53.6	911	2	US-09-388-774-4	Sequence 4, Appli
543	30	53.6	327	2	US-09-252-991A-17609	Sequence 17609, A	616	30	53.6	947	2	US-09-377-850-3	Sequence 3, Appli
544	30	53.6	340	2	US-09-134-001C-3448	Sequence 3448, Ap	617	30	53.6	956	2	US-09-438-185A-541	Sequence 541, App
545	30	53.6	342	2	US-09-252-991A-32983	Sequence 32983, A	618	30	53.6	1627	2	US-09-252-991A-20395	Sequence 20395, A
546	30	53.6	348	2	US-09-252-991A-27446	Sequence 27446, A	619	30	53.6	1722	2	US-09-194-612A-1	Sequence 1, Appli
547	30	53.6	349	2	US-09-270-767-43051	Sequence 43051, A	620	30	53.6	1722	2	US-09-949-002-311	Sequence 311, App
548	30	53.6	360	2	US-09-134-001C-4684	Sequence 4684, Ap	621	30	53.6	1740	2	US-09-949-002-535	Sequence 535, App
549	30	53.6	360	2	US-09-248-796A-14454	Sequence 14454, A	622	30	53.6	2176	2	US-09-949-016-9923	Sequence 9923, Ap
550	30	53.6	365	1	US-08-089-755A-5	Sequence 5, Appli	623	29.5	52.7	10	2	US-09-563-222C-7	Sequence 7, Appli
551	30	53.6	365	1	US-08-421-791-5	Sequence 5, Appli	624	29.5	52.7	21	1	US-08-712-212-2	Sequence 2, Appli
552	30	53.6	365	1	US-08-421-791-5	Sequence 5, Appli	625	29.5	52.7	21	1	PCT-US95-05160-2	Sequence 2, Appli
553	30	53.6	365	1	US-08-851-088-4	Sequence 4, Appli	626	29.5	52.7	21	1	US-08-726-368A-137	Sequence 137, App
554	30	53.6	365	2	US-08-851-089-10	Sequence 10, Appl	627	29.5	52.7	67	2	US-09-513-999C-7228	Sequence 7228, Ap
555	30	53.6	371	2	US-09-198-452A-712	Sequence 712, App	628	29.5	52.7	114	1	US-08-561-521-43	Sequence 43, Appl
556	30	53.6	371	2	US-09-438-185A-676	Sequence 676, App	629	29.5	52.7	114	4	PCT-US95-01219-43	Sequence 43, Appl
557	30	53.6	375	2	US-09-311-021-8	Sequence 8, Appli	630	29.5	52.7	212	2	US-09-506-286B-66	Sequence 66, Appl
558	30	53.6	377	2	US-09-543-681A-7473	Sequence 7473, Ap	631	29.5	52.7	212	2	US-10-065-133A-66	Sequence 66, Appl
559	30	53.6	383	2	US-09-328-352-7965	Sequence 7965, Ap	632	29.5	52.7	263	2	US-09-069-821-3	Sequence 3, Appli
560	30	53.6	408	2	US-09-248-796A-19407	Sequence 19407, A	633	29.5	52.7	263	2	US-09-956-086-3	Sequence 3, Appli
561	30	53.6	417	2	US-09-252-991A-29521	Sequence 29521, A	634	29.5	52.7	263	2	US-09-956-086-3	Sequence 3, Appli
562	30	53.6	446	2	US-09-248-796A-15947	Sequence 15947, A	635	29.5	52.7	283	2	US-09-420-592A-6	Sequence 6, Appli
563	30	53.6	452	2	US-09-284-768A-22	Sequence 22, Appl	636	29.5	52.7	283	2	US-09-985-442-6	Sequence 6, Appli
564	30	53.6	473	2	US-09-248-796A-15735	Sequence 15735, A	637	29.5	52.7	283	2	US-09-983-580-6	Sequence 6, Appli
565	30	53.6	474	2	US-09-543-681A-6873	Sequence 6873, Ap	638	29.5	52.7	291	2	US-09-252-991A-22804	Sequence 22804, A
566	30	53.6	478	2	US-09-902-540-15753	Sequence 15753, A	639	29.5	52.7	395	2	US-09-506-286B-69	Sequence 69, Appl
567	30	53.6	500	2	US-09-949-016-7131	Sequence 7131, Ap	640	29.5	52.7	395	2	US-10-065-133A-104	Sequence 104, App
568	30	53.6	503	2	US-10-104-047-3516	Sequence 3516, Ap	641	29.5	52.7	398	2	US-09-506-286B-63	Sequence 63, Appl
569	30	53.6	510	2	US-09-291-922-22	Sequence 22, Appl	642	29.5	52.7	398	2	US-10-065-133A-63	Sequence 63, Appl
570	30	53.6	536	2	US-09-902-540-14532	Sequence 14532, A	643	29.5	52.7	757	2	US-09-506-286B-104	Sequence 104, App
571	30	53.6	543	2	US-10-104-047-3493	Sequence 3493, Ap	644	29.5	52.7	757	2	US-09-506-286B-107	Sequence 107, App
572	30	53.6	548	2	US-09-380-061B-18	Sequence 18, Appl	645	29.5	52.7	757	2	US-10-065-133A-104	Sequence 104, App
573	30	53.6	548	2	US-08-487-183A-16	Sequence 16, Appl	646	29.5	52.7	757	2	US-10-065-133A-107	Sequence 107, App
574	30	53.6	548	2	US-09-396-154-29	Sequence 29, Appl	647	29.5	52.7	759	2	US-10-258-860-6	Sequence 6, Appli
575	30	53.6	548	2	US-09-248-796A-15537	Sequence 15537, A	648	29.5	52.7	762	2	US-10-258-860-2	Sequence 2, Appli
576	30	53.6	556	2	US-09-489-039A-9666	Sequence 9666, Ap	649	29.5	52.7	785	2	US-10-258-860-4	Sequence 4, Appli
577	30	53.6	580	2	US-09-514-245-7	Sequence 7, Appli	650	29	51.8	9	2	US-09-802-083-12	Sequence 12, Appl
578	30	53.6	605	2	US-09-538-092-375	Sequence 375, App	651	29	51.8	26	2	US-09-270-767-62003	Sequence 62003, A
579	30	53.6	608	2	US-09-284-768A-4	Sequence 4, Appli	652	29	51.8	38	2	US-09-280-428A-4	Sequence 4, Appli
580	30	53.6	612	2	US-10-101-464A-813	Sequence 813, App	653	29	51.8	47	2	US-08-341-018-46	Sequence 46, Appl
581	30	53.6	614	2	US-09-270-767-36832	Sequence 36832, A	654	29	51.8	47	2	US-08-470-335-218	Sequence 218, App
582	30	53.6	614	2	US-09-270-767-52049	Sequence 52049, A	655	29	51.8	47	2	US-08-470-339-218	Sequence 218, App
583	30	53.6	619	2	US-10-197-220-77	Sequence 77, Appl	656	29	51.8	47	2	US-08-467-602-412	Sequence 412, App
584	30	53.6	624	2	US-09-198-452A-1089	Sequence 1089, Ap	657	29	51.8	47	2	US-08-411-295F-40	Sequence 40, Appl
585	30	53.6	624	2	US-09-438-185A-1017	Sequence 1017, Ap	658	29	51.8	47	2	US-08-411-295F-91	Sequence 91, Appl
586	30	53.6	657	2	US-09-284-768A-7	Sequence 7, Appli	659	29	51.8	64	2	US-09-270-767-40321	Sequence 40321, A
587	30	53.6	660	2	US-09-198-452A-578	Sequence 578, App	660	29	51.8	64	2	US-09-270-767-55537	Sequence 55537, A
588	30	53.6	673	2	US-09-989-981A-8	Sequence 8, Appli	661	29	51.8	73	1	US-08-687-916-21	Sequence 21, Appl
589	30	53.6	680	2	US-09-538-092-1165	Sequence 1165, Ap	662	29	51.8	73	2	US-09-138-614-21	Sequence 21, Appl
590	30	53.6	680	2	US-09-949-016-6637	Sequence 6637, Ap	663	29	51.8	78	2	US-09-270-767-56782	Sequence 56782, A
591	30	53.6	708	2	US-09-949-016-6638	Sequence 6638, Ap	664	29	51.8	80	2	US-09-330-914A-4	Sequence 4, Appli
592	30	53.6	712	2	US-09-949-016-7340	Sequence 7340, Ap	665	29	51.8	80	2	US-09-252-991A-23455	Sequence 23455, A
593	30	53.6	712	2	US-09-949-016-7341	Sequence 7341, Ap	666	29	51.8	82	2	US-09-198-452A-590	Sequence 590, App
594	30	53.6	714	2	US-09-828-303-21	Sequence 21, Appl	667	29	51.8	86	2	US-09-621-976-3953	Sequence 3953, Ap
595	30	53.6	781	2	US-09-766-387-2	Sequence 2, Appli	668	29	51.8	97	2	US-09-248-796A-16604	Sequence 16604, A
596	30	53.6	781	2	US-09-766-387-4	Sequence 4, Appli	669	29	51.8	102	2	US-09-199-149-10	Sequence 10, Appl
597	30	53.6	781	2	US-09-417-039-10	Sequence 10, Appl	670	29	51.8	102	2	US-09-199-149-29	Sequence 29, Appl
598	30	53.6	781	2	US-09-538-092-1067	Sequence 1067, Ap	671	29	51.8	102	2	US-10-114-716A-44	Sequence 44, Appl
599	30	53.6	868	1	US-08-162-081B-33	Sequence 33, Appl	672	29	51.8	103	2	US-09-199-637A-291	Sequence 291, App
600	30	53.6	868	1	US-08-780-872-33	Sequence 33, Appl	673	29	51.8	103	2	US-09-270-767-34353	Sequence 34353, A
601	30	53.6	868	2	US-09-085-957-33	Sequence 33, Appl	674	29	51.8	103	2	US-09-270-767-49570	Sequence 49570, A
602	30	53.6	868	2	US-09-830-433A-73	Sequence 73, Appl	675	29	51.8	105	2	US-09-199-149-31	Sequence 31, Appl
603	30	53.6	869	2	US-09-830-433A-42	Sequence 42, Appl	676	29	51.8	105	2	US-10-330-613A-80	Sequence 80, Appl
604	30	53.6	875	1	US-09-328-352-4884	Sequence 4884, Ap	677	29	51.8	106	1	US-08-276-852-101	Sequence 101, App
605	30	53.6	885	1	US-08-310-912A-2	Sequence 2, Appli	678	29	51.8	106	1	US-08-899-575-101	Sequence 101, App
606	30	53.6	885	2	US-08-841-089-2	Sequence 2, Appli	679	29	51.8	106	1	US-08-899-575-101	Sequence 101, App
607	30	53.6	885	2	PCT-US95-04570-2	Sequence 2, Appli	680	29	51.8	106	1	PCT-US95-08743-101	Sequence 101, App
608	30	53.6	885	4	PCT-US95-04589-2	Sequence 2, Appli	681	29	51.8	107	1	US-08-458-516-9	Sequence 9, Appli
609	30	53.6	885	4	PCT-US95-04589-2	Sequence 2, Appli	682	29	51.8	107	1	US-08-458-516-9	Sequence 9, Appli
610	30	53.6	907	2	US-08-930-996A-7	Sequence 7, Appli	683	29	51.8	107	1	US-07-934-373C-16	Sequence 16, Appl
611	30	53.6	909	1	US-08-310-912A-142	Sequence 142, App	684	29	51.8	107	1	US-07-934-373C-17	Sequence 17, Appl

685	29	51.8	107	2	US-08-437-642B-16	Sequence 16, Appl	758	29	51.8	247	2	US-10-620-049-21	Sequence 21, Appl
686	29	51.8	107	2	US-08-437-642B-17	Sequence 17, Appl	759	29	51.8	250	2	US-09-252-931A-24075	Sequence 24075, A
687	29	51.8	107	2	US-09-240-274-35	Sequence 35, Appl	760	29	51.8	259	2	US-09-252-931A-27735	Sequence 27735, A
688	29	51.8	107	2	US-09-240-274-157	Sequence 157, Appl	761	29	51.8	263	1	US-08-752-844-66	Sequence 66, Appl
689	29	51.8	107	2	US-09-240-274-164	Sequence 164, Appl	762	29	51.8	263	2	US-09-293-533-66	Sequence 66, Appl
690	29	51.8	107	2	US-09-240-274-170	Sequence 170, Appl	763	29	51.8	266	2	US-09-248-796A-15421	Sequence 15421, A
691	29	51.8	107	2	US-08-146-206C-16	Sequence 16, Appl	764	29	51.8	270	2	US-09-270-767-37404	Sequence 37404, A
692	29	51.8	107	2	US-08-146-206C-16	Sequence 16, Appl	765	29	51.8	270	2	US-09-270-767-52621	Sequence 52621, A
693	29	51.8	107	2	US-09-705-686-16	Sequence 17, Appl	766	29	51.8	274	2	US-09-813-659-30	Sequence 30, Appl
694	29	51.8	107	2	US-09-705-686-17	Sequence 17, Appl	767	29	51.8	274	2	US-09-549-067A-30	Sequence 30, Appl
695	29	51.8	107	2	US-09-705-392A-16	Sequence 16, Appl	768	29	51.8	275	2	US-09-482-273-265	Sequence 265, Appl
696	29	51.8	107	2	US-09-705-392A-17	Sequence 17, Appl	769	29	51.8	281	2	US-09-248-796A-27217	Sequence 27217, A
697	29	51.8	107	2	US-09-705-398-16	Sequence 16, Appl	770	29	51.8	281	2	US-09-543-681A-4801	Sequence 4801, Ap
698	29	51.8	107	2	US-09-705-398-17	Sequence 17, Appl	771	29	51.8	282	2	US-09-107-532A-4057	Sequence 4057, Ap
699	29	51.8	107	2	US-09-848-798-35	Sequence 35, Appl	772	29	51.8	284	1	US-09-014-969-21	Sequence 21, Appl
700	29	51.8	107	2	US-09-848-798-157	Sequence 157, Appl	773	29	51.8	286	2	US-09-205-258-404	Sequence 404, App
701	29	51.8	107	2	US-09-848-798-164	Sequence 164, Appl	774	29	51.8	286	2	US-09-205-258-1063	Sequence 1063, Ap
702	29	51.8	107	2	US-09-848-798-170	Sequence 170, Appl	775	29	51.8	286	2	US-10-004-860-404	Sequence 404, App
703	29	51.8	107	4	PCT-US93-07832-16	Sequence 16, Appl	776	29	51.8	286	2	US-10-004-860-1063	Sequence 1063, Ap
704	29	51.8	107	4	PCT-US93-07832-17	Sequence 17, Appl	777	29	51.8	292	2	US-09-543-681A-5819	Sequence 5819, Ap
705	29	51.8	108	2	US-09-199-149-7	Sequence 7, Appl	778	29	51.8	293	2	US-09-540-236-2400	Sequence 2400, Ap
706	29	51.8	108	2	US-09-199-149-14	Sequence 14, Appl	779	29	51.8	295	2	US-09-270-767-45538	Sequence 45538, A
707	29	51.8	108	2	US-09-905-243-73	Sequence 73, Appl	780	29	51.8	301	2	US-09-252-991A-24016	Sequence 24016, A
708	29	51.8	109	2	US-09-802-083-4	Sequence 4, Appl	781	29	51.8	302	1	US-08-121-054C-18	Sequence 18, Appl
709	29	51.8	112	1	US-08-752-844-15	Sequence 15, Appl	782	29	51.8	302	1	US-08-121-054C-30	Sequence 30, Appl
710	29	51.8	112	1	US-08-591-196-15	Sequence 15, Appl	783	29	51.8	302	2	US-08-539-436-18	Sequence 18, Appl
711	29	51.8	112	1	US-08-293-533-15	Sequence 15, Appl	784	29	51.8	302	2	US-08-539-436-30	Sequence 30, Appl
712	29	51.8	114	1	US-08-202-047-25	Sequence 25, Appl	785	29	51.8	302	2	US-09-813-659-18	Sequence 18, Appl
713	29	51.8	114	2	US-08-964-690-25	Sequence 25, Appl	786	29	51.8	302	2	US-09-813-659-32	Sequence 32, Appl
714	29	51.8	127	1	US-08-458-516-5	Sequence 5, Appl	787	29	51.8	302	2	US-09-549-067A-18	Sequence 18, Appl
715	29	51.8	130	2	US-09-710-278-164	Sequence 164, Appl	788	29	51.8	302	2	US-09-549-067A-32	Sequence 32, Appl
716	29	51.8	131	1	US-08-236-520-2	Sequence 2, Appl	789	29	51.8	308	2	US-09-198-452A-606	Sequence 606, App
717	29	51.8	131	4	PCT-US95-05262-2	Sequence 2, Appl	790	29	51.8	308	2	US-09-438-185A-569	Sequence 569, App
718	29	51.8	140	2	US-09-252-991A-28660	Sequence 28660, A	791	29	51.8	313	2	US-09-489-039A-12108	Sequence 12108, A
719	29	51.8	146	2	US-09-435-054A-8	Sequence 8, Appl	792	29	51.8	313	2	US-09-540-236-2394	Sequence 2394, Ap
720	29	51.8	147	2	US-09-248-796A-15504	Sequence 15504, A	793	29	51.8	314	2	US-09-489-039A-13037	Sequence 13037, A
721	29	51.8	147	2	US-09-302-540-11556	Sequence 11556, A	794	29	51.8	314	2	US-09-482-273-267	Sequence 267, App
722	29	51.8	149	1	US-08-752-844-2	Sequence 2, Appl	795	29	51.8	319	2	US-09-328-352-6404	Sequence 6404, Ap
723	29	51.8	149	1	US-08-591-196-2	Sequence 2, Appl	796	29	51.8	320	2	US-09-482-273-194	Sequence 194, App
724	29	51.8	149	2	US-09-192-838B-2	Sequence 2, Appl	797	29	51.8	320	2	US-09-902-540-12563	Sequence 12563, A
725	29	51.8	149	2	US-09-293-533-2	Sequence 2, Appl	798	29	51.8	321	2	US-09-252-991A-29844	Sequence 29844, A
726	29	51.8	149	2	US-09-324-191-2	Sequence 2, Appl	799	29	51.8	322	2	US-09-667-135-2	Sequence 2, Appl
727	29	51.8	155	2	US-09-472-087-20	Sequence 20, Appl	800	29	51.8	322	2	US-09-910-174B-29	Sequence 29, Appl
728	29	51.8	155	2	US-09-472-087-112	Sequence 112, Appl	801	29	51.8	322	2	US-09-620-461-29	Sequence 29, Appl
729	29	51.8	156	2	US-10-104-047-2055	Sequence 2055, Ap	802	29	51.8	324	2	US-09-489-039A-7896	Sequence 7896, Ap
730	29	51.8	160	1	US-08-162-402B-11	Sequence 11, Appl	803	29	51.8	336	2	US-09-328-352-8202	Sequence 8202, Ap
731	29	51.8	161	2	US-09-621-976-5114	Sequence 5114, Ap	804	29	51.8	337	2	US-09-543-681A-7707	Sequence 7707, Ap
732	29	51.8	166	2	US-10-104-047-2085	Sequence 2085, Ap	805	29	51.8	341	2	US-09-248-796A-26575	Sequence 26575, A
733	29	51.8	176	2	US-09-621-976-5111	Sequence 5111, Ap	806	29	51.8	347	2	US-09-667-135-4	Sequence 4, Appl
734	29	51.8	188	2	US-09-489-039A-8998	Sequence 8998, Ap	807	29	51.8	347	2	US-09-543-681A-5315	Sequence 5315, Ap
735	29	51.8	190	2	US-09-248-796A-14762	Sequence 14762, A	808	29	51.8	352	2	US-09-252-991A-29664	Sequence 29664, A
736	29	51.8	194	2	US-09-202-329-10	Sequence 10, Appl	809	29	51.8	355	2	US-09-248-796A-18246	Sequence 18246, A
737	29	51.8	197	2	US-09-502-540-11820	Sequence 11820, A	810	29	51.8	355	2	US-09-435-054A-18	Sequence 18, Appl
738	29	51.8	198	2	US-09-538-092-367	Sequence 367, Appl	811	29	51.8	357	2	US-09-134-000C-4229	Sequence 4229, Ap
739	29	51.8	202	2	US-09-328-352-5586	Sequence 5586, Ap	812	29	51.8	364	2	US-09-293-322C-7	Sequence 7, Appl
740	29	51.8	203	2	US-09-492-709A-338	Sequence 338, Appl	813	29	51.8	364	2	US-09-839-497A-7	Sequence 7, Appl
741	29	51.8	209	2	US-09-248-796A-19324	Sequence 19324, A	814	29	51.8	365	2	US-09-198-452A-984	Sequence 984, App
742	29	51.8	214	1	US-08-458-516-12	Sequence 12, Appl	815	29	51.8	365	2	US-09-438-185A-913	Sequence 913, App
743	29	51.8	215	2	US-09-270-767-32005	Sequence 32005, A	816	29	51.8	370	2	US-09-902-540-15887	Sequence 15887, A
744	29	51.8	215	2	US-09-270-767-47222	Sequence 47222, A	817	29	51.8	373	2	US-09-489-039A-7685	Sequence 7685, Ap
745	29	51.8	216	2	US-09-516-052-22	Sequence 22, Appl	818	29	51.8	380	1	US-08-244-205-11	Sequence 11, Appl
746	29	51.8	222	2	US-09-252-991A-32998	Sequence 32998, A	819	29	51.8	380	2	US-09-161-994A-13	Sequence 13, Appl
747	29	51.8	227	2	US-09-270-767-47520	Sequence 47520, A	820	29	51.8	380	4	PCT-US92-10284-11	Sequence 2, Appl
748	29	51.8	230	1	US-08-471-371-2	Sequence 2, Appl	821	29	51.8	382	1	US-08-872-302-2	Sequence 2, Appl
749	29	51.8	231	1	US-09-902-540-13238	Sequence 13238, A	822	29	51.8	382	2	US-08-811-177A-2	Sequence 2, Appl
750	29	51.8	236	2	US-08-681-432-1	Sequence 1, Appl	823	29	51.8	401	2	US-10-104-047-3800	Sequence 3800, Ap
751	29	51.8	236	2	US-09-902-540-13131	Sequence 13131, A	824	29	51.8	412	2	US-09-902-540-15974	Sequence 15974, A
752	29	51.8	240	2	US-09-107-433-3542	Sequence 3542, Ap	825	29	51.8	416	2	US-09-228-246-4	Sequence 4, Appl
753	29	51.8	249	2	US-09-435-054A-10	Sequence 10, Appl	826	29	51.8	423	2	US-09-328-352-5667	Sequence 5667, Ap
754	29	51.8	244	1	US-08-230-843-2	Sequence 2, Appl	827	29	51.8	424	2	US-08-311-731A-220	Sequence 220, App
755	29	51.8	244	1	US-08-636-936-2	Sequence 2, Appl	828	29	51.8	427	2	US-09-252-991A-31904	Sequence 31904, A
756	29	51.8	244	2	US-09-489-039A-12635	Sequence 12635, A	829	29	51.8	432	1	US-08-904-278-6	Sequence 6, Appl
757	29	51.8	247	2	US-09-248-796A-19065	Sequence 19065, A	830	29	51.8	432	2	US-09-222-594-6	Sequence 6, Appl

831	29	51.8	432	2	US-09-977-653-6	Sequence 6, Appl1	904	29	51.8	563	2	US-09-600-991-4	Sequence 4, Appl1
832	29	51.8	433	2	US-09-489-039A-9762	Sequence 9762, Ap	905	29	51.8	565	2	US-09-270-767-41555	Sequence 41555, A
833	29	51.8	444	2	US-09-252-991A-18424	Sequence 18424, A	906	29	51.8	566	2	US-09-482-273-173	Sequence 173, App
834	29	51.8	446	2	US-09-826-509-359	Sequence 359, App	907	29	51.8	567	2	US-08-813-150-4	Sequence 4, Appl1
835	29	51.8	453	2	US-09-248-796A-17497	Sequence 17497, A	908	29	51.8	567	2	US-09-546-553-4	Sequence 4, Appl1
836	29	51.8	455	2	US-09-248-796A-17497	Sequence 6, Appl1	909	29	51.8	567	2	US-10-013-231A-84	Sequence 84, Appl
837	29	51.8	456	2	US-09-328-352-7590	Sequence 7590, Ap	910	29	51.8	567	2	US-10-349-805-4	Sequence 4, Appl1
838	29	51.8	457	2	US-09-999-833A-19	Sequence 19, Appl	911	29	51.8	567	2	US-10-015-389A-84	Sequence 84, Appl
839	29	51.8	457	2	US-10-020-445A-19	Sequence 19, Appl	912	29	51.8	567	2	US-10-006-768A-84	Sequence 84, Appl
840	29	51.8	462	2	US-09-489-039A-12427	Sequence 12427, A	913	29	51.8	567	2	US-10-015-671A-84	Sequence 84, Appl
841	29	51.8	463	1	US-08-162-402B-9	Sequence 9, Appl1	914	29	51.8	567	2	US-10-015-393A-84	Sequence 84, Appl
842	29	51.8	468	2	US-09-270-767-60234	Sequence 60234, A	915	29	51.8	567	2	US-10-011-833A-84	Sequence 84, Appl
843	29	51.8	469	2	US-09-583-110-4733	Sequence 4733, Ap	916	29	51.8	567	2	US-10-006-041A-84	Sequence 84, Appl
844	29	51.8	471	2	US-09-543-681A-7497	Sequence 7497, Ap	917	29	51.8	567	2	US-10-012-064A-84	Sequence 84, Appl
845	29	51.8	474	2	US-08-467-602-190	Sequence 190, App	918	29	51.8	580	2	US-09-252-991A-20407	Sequence 20407, A
846	29	51.8	474	2	US-08-411-295F-314	Sequence 314, App	919	29	51.8	582	2	US-09-252-991A-21510	Sequence 21510, A
847	29	51.8	475	1	US-07-715-184-4	Sequence 4, Appl1	920	29	51.8	587	2	US-09-815-923-4	Sequence 4, Appl1
848	29	51.8	475	1	US-07-876-280-7	Sequence 7, Appl1	921	29	51.8	589	2	US-09-543-681A-6155	Sequence 6155, Ap
849	29	51.8	475	1	US-07-876-280-28	Sequence 28, Appl	922	29	51.8	607	1	US-07-959-943-7	Sequence 7, Appl1
850	29	51.8	475	1	US-07-935-310A-2	Sequence 2, Appl1	923	29	51.8	607	1	US-07-878-617A-12	Sequence 12, Appl
851	29	51.8	475	1	US-07-828-788A-2	Sequence 2, Appl1	924	29	51.8	607	1	US-08-753-985-12	Sequence 12, Appl
852	29	51.8	475	1	US-08-049-783-4	Sequence 4, Appl1	925	29	51.8	616	2	US-08-467-602-238	Sequence 238, App
853	29	51.8	475	1	US-08-147-189-2	Sequence 2, Appl1	926	29	51.8	616	2	US-08-411-295F-164	Sequence 164, App
854	29	51.8	475	1	US-08-316-301A-8	Sequence 8, Appl1	927	29	51.8	619	2	US-08-467-602-233	Sequence 233, App
855	29	51.8	475	1	US-08-904-278-2	Sequence 2, Appl1	928	29	51.8	619	2	US-08-411-295F-159	Sequence 159, App
856	29	51.8	475	1	US-08-904-278-4	Sequence 4, Appl1	929	29	51.8	625	2	US-08-467-602-250	Sequence 250, App
857	29	51.8	475	1	US-09-076-137-8	Sequence 8, Appl1	930	29	51.8	625	2	US-08-411-295F-176	Sequence 176, App
858	29	51.8	475	2	US-07-941-650A-6	Sequence 6, Appl1	931	29	51.8	628	2	US-08-467-602-247	Sequence 247, App
859	29	51.8	475	2	US-09-222-594-2	Sequence 2, Appl1	932	29	51.8	628	2	US-08-411-295F-173	Sequence 173, App
860	29	51.8	475	2	US-09-222-594-4	Sequence 4, Appl1	933	29	51.8	630	1	US-07-959-943-9	Sequence 9, Appl1
861	29	51.8	475	2	US-09-738-363-8	Sequence 8, Appl1	934	29	51.8	639	2	US-08-467-602-241	Sequence 241, App
862	29	51.8	475	2	US-09-538-092-796	Sequence 796, App	935	29	51.8	639	2	US-08-411-295F-167	Sequence 167, App
863	29	51.8	475	2	US-09-977-653-2	Sequence 2, Appl1	936	29	51.8	648	2	US-08-467-602-253	Sequence 253, App
864	29	51.8	475	2	US-09-977-653-4	Sequence 4, Appl1	937	29	51.8	648	2	US-08-411-295F-179	Sequence 179, App
865	29	51.8	475	4	PCT-US92-03624-8	Sequence 8, Appl1	938	29	51.8	650	2	US-08-467-602-217	Sequence 217, App
866	29	51.8	475	4	PCT-US92-11337-2	Sequence 2, Appl1	939	29	51.8	650	2	US-08-467-602-280	Sequence 280, App
867	29	51.8	475	4	PCT-US93-07409-2	Sequence 2, Appl1	940	29	51.8	650	2	US-08-411-295F-143	Sequence 143, App
868	29	51.8	476	2	US-09-248-796A-16812	Sequence 16812, A	941	29	51.8	650	2	US-08-411-295F-206	Sequence 206, App
869	29	51.8	477	2	US-08-467-602-185	Sequence 185, App	942	29	51.8	653	1	US-07-782-298-2	Sequence 2, Appl1
870	29	51.8	477	2	US-08-411-295F-309	Sequence 309, App	943	29	51.8	653	2	US-08-467-602-212	Sequence 212, App
871	29	51.8	483	2	US-08-467-602-202	Sequence 202, App	944	29	51.8	653	2	US-08-467-602-275	Sequence 275, App
872	29	51.8	484	2	US-08-411-295F-326	Sequence 326, App	945	29	51.8	653	2	US-08-411-295F-138	Sequence 138, App
873	29	51.8	484	2	US-09-252-991A-31677	Sequence 31677, A	946	29	51.8	653	2	US-08-411-295F-201	Sequence 201, App
874	29	51.8	486	2	US-08-467-602-199	Sequence 199, App	947	29	51.8	659	2	US-08-467-602-229	Sequence 229, App
875	29	51.8	486	2	US-08-411-295F-323	Sequence 323, App	948	29	51.8	659	2	US-08-467-602-232	Sequence 232, App
876	29	51.8	487	2	US-10-418-036-16	Sequence 16, Appl	949	29	51.8	659	2	US-08-411-295F-155	Sequence 155, App
877	29	51.8	488	2	US-09-540-236-2307	Sequence 2307, Ap	950	29	51.8	659	2	US-08-411-295F-218	Sequence 218, App
878	29	51.8	489	2	US-09-667-135-30	Sequence 30, Appl	951	29	51.8	662	2	US-08-467-602-226	Sequence 226, App
879	29	51.8	491	1	US-08-687-916-23	Sequence 23, Appl	952	29	51.8	662	2	US-08-467-602-289	Sequence 289, App
880	29	51.8	491	2	US-09-138-614-23	Sequence 23, Appl	953	29	51.8	662	2	US-08-411-295F-152	Sequence 152, App
881	29	51.8	494	2	US-09-328-352-7025	Sequence 7025, Ap	954	29	51.8	662	2	US-08-411-295F-215	Sequence 215, App
882	29	51.8	495	1	US-08-687-916-22	Sequence 22, Appl	955	29	51.8	673	2	US-08-467-602-202	Sequence 202, App
883	29	51.8	495	1	US-09-138-614-22	Sequence 22, Appl	956	29	51.8	673	2	US-08-467-602-283	Sequence 283, App
884	29	51.8	497	1	US-08-570-311-2	Sequence 2, Appl1	957	29	51.8	673	2	US-08-411-295F-146	Sequence 146, App
885	29	51.8	497	1	US-08-353-485-2	Sequence 2, Appl1	958	29	51.8	673	2	US-08-411-295F-209	Sequence 209, App
886	29	51.8	497	2	US-08-467-602-193	Sequence 193, App	959	29	51.8	682	2	US-08-467-602-232	Sequence 232, App
887	29	51.8	497	2	US-08-411-295F-317	Sequence 317, App	960	29	51.8	682	2	US-08-467-602-295	Sequence 295, App
888	29	51.8	506	2	US-08-467-602-205	Sequence 205, App	961	29	51.8	682	2	US-08-411-295F-158	Sequence 158, App
889	29	51.8	506	2	US-08-411-295F-329	Sequence 329, App	962	29	51.8	682	2	US-08-411-295F-221	Sequence 221, App
890	29	51.8	516	2	US-09-197-063-2	Sequence 2, Appl1	963	29	51.8	684	2	US-08-467-602-259	Sequence 259, App
891	29	51.8	520	2	US-09-583-110-3457	Sequence 3457, Ap	964	29	51.8	684	2	US-08-411-295F-185	Sequence 185, App
892	29	51.8	526	2	US-09-248-796A-16081	Sequence 16081, A	965	29	51.8	687	2	US-08-467-602-234	Sequence 234, App
893	29	51.8	527	2	US-09-302-540-13101	Sequence 13101, A	966	29	51.8	687	2	US-08-411-295F-180	Sequence 180, App
894	29	51.8	527	2	US-09-758-759-123	Sequence 123, App	967	29	51.8	693	2	US-08-467-602-271	Sequence 271, App
895	29	51.8	529	2	US-09-291-922-28	Sequence 28, Appl	968	29	51.8	693	2	US-08-411-295F-197	Sequence 197, App
896	29	51.8	534	2	US-09-087-134-11	Sequence 11, Appl	969	29	51.8	696	2	US-08-467-602-268	Sequence 268, App
897	29	51.8	556	2	US-09-303-518D-466	Sequence 466, App	970	29	51.8	696	2	US-08-411-295F-194	Sequence 194, App
898	29	51.8	560	2	US-08-341-018-58	Sequence 58, Appl	971	29	51.8	707	2	US-08-467-602-262	Sequence 262, App
899	29	51.8	560	2	US-08-470-335-194	Sequence 194, App	972	29	51.8	707	2	US-08-411-295F-188	Sequence 188, App
900	29	51.8	560	2	US-08-470-339-194	Sequence 194, App	973	29	51.8	709	2	US-09-543-681A-6114	Sequence 6114, Ap
901	29	51.8	560	2	US-08-467-602-388	Sequence 388, App	974	29	51.8	711	1	US-08-184-012C-8	Sequence 8, Appl1
902	29	51.8	560	2	US-08-411-295F-51	Sequence 51, Appl	975	29	51.8	711	1	US-08-334-177-2	Sequence 2, Appl1
903	29	51.8	560	2	US-08-411-295F-96	Sequence 96, Appl	976	29	51.8	711	1	US-08-666-082B-1	Sequence 1, Appl1

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979      29 51.8 711 2 US-09-600-991-20 Sequence 20, Appl
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981      29 51.8 711 4 PCT-US95-016-6981 Sequence 6981, Ap
982      29 51.8 711 4 PCT-US95-13830-2 Sequence 2, Appli
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984      29 51.8 716 2 US-09-296-219-1 Sequence 1, Appli
985      29 51.8 716 2 US-08-467-602-274 Sequence 274, App
986      29 51.8 716 2 US-08-411-295F-200 Sequence 200, App
987      29 51.8 737 2 US-09-602-787A-182 Sequence 182, App
988      29 51.8 797 2 US-09-248-796A-16517 Sequence 16517, A
989      29 51.8 816 2 US-10-104-047-3657 Sequence 3657, Ap
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991      29 51.8 865 2 US-08-470-335-235 Sequence 235, App
992      29 51.8 865 2 US-08-467-602-322 Sequence 322, App
993      29 51.8 865 2 US-08-411-295F-248 Sequence 248, App
994      29 51.8 868 2 US-08-470-335-229 Sequence 229, App
995      29 51.8 868 2 US-08-467-602-317 Sequence 317, App
996      29 51.8 868 2 US-08-411-295F-243 Sequence 243, App
997      29 51.8 874 2 US-08-470-335-238 Sequence 238, App
998      29 51.8 874 2 US-08-467-602-334 Sequence 334, App
999      29 51.8 874 2 US-08-411-295F-260 Sequence 260, App
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## ALIGNMENTS

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RESULT 1
US-09-225-322B-10
; Sequence 10, Application US/09225322B
; Patent No. 6437098
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KIWANA, YOSHIHISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/09/225,322B
; PRIOR FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: US 08/454,680
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
; PRIOR APPLICATION NUMBER: US07/947,674
; PRIOR FILING DATE: 1992-09-17
; PRIOR APPLICATION NUMBER: JP 3-238375
; PRIOR FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: cDNA KM-641
; OTHER INFORMATION:
US-09-225-322B-10

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Query Match 100.0%; Score 56; DB 2; Length 128;
Best Local Similarity 100.0%; Pred. No. 0.0049;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 109 HOYSKLPWT 117

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RESULT 2

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US-09-225-322B-19
; Sequence 19, Application US/09225322B
; Patent No. 6437098
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KIWANA, YOSHIHISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/09/225,322B
; PRIOR FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: US 08/454,680
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
; PRIOR APPLICATION NUMBER: US07/947,674
; PRIOR FILING DATE: 1992-09-17
; PRIOR APPLICATION NUMBER: JP 3-238375
; PRIOR FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: light chain
; OTHER INFORMATION: variable region
US-09-225-322B-19

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Query Match 100.0%; Score 56; DB 2; Length 128;
Best Local Similarity 100.0%; Pred. No. 0.0049;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 HOYSKLPWT 9
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DB 109 HOYSKLPWT 117

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RESULT 3
US-09-764-304-10
; Sequence 10, Application US/09764304
; Patent No. 6495666
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KIWANA, YOSHIHISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/09/764,304
; CURRENT FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: 09/225,322
; EARLIER FILING DATE: 1999-01-05
; EARLIER APPLICATION NUMBER: US 08/454,680
; EARLIER FILING DATE: 1995-05-31
; EARLIER APPLICATION NUMBER: US 08/408,133
; EARLIER FILING DATE: 1995-03-21
; EARLIER APPLICATION NUMBER: US 08/292,178
; EARLIER FILING DATE: 1994-08-17
; EARLIER APPLICATION NUMBER: US07/947,674
; EARLIER FILING DATE: 1992-09-17
; EARLIER APPLICATION NUMBER: JP 3-238375
; EARLIER FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 128

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; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: cDNA KM-641
US-09-764-304-10

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Best Local Similarity 100.0%; Pred. No. 0.0049;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 HOYSKLPWT 9
      |||||
Db      109 HOYSKLPWT 117

RESULT 4
US-09-764-304-19
; Sequence 19, Application US/09764304
; Patent No. 6495666
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUWANA, YOSHIOHISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/09/764,304
; CURRENT FILING DATE: 2001-01-19
; EARLIER APPLICATION NUMBER: 09/225,322
; EARLIER FILING DATE: 1999-01-05
; EARLIER APPLICATION NUMBER: US 08/454,680
; EARLIER FILING DATE: 1995-05-31
; EARLIER APPLICATION NUMBER: US 08/408,133
; EARLIER FILING DATE: 1995-03-21
; EARLIER APPLICATION NUMBER: US 08/292,178
; EARLIER FILING DATE: 1994-08-17
; EARLIER APPLICATION NUMBER: US07/947,674
; EARLIER FILING DATE: 1992-09-17
; EARLIER APPLICATION NUMBER: JP 3-238375
; EARLIER FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: light chain
; OTHER INFORMATION: variable region
US-09-764-304-19

Query Match          100.0%; Score 56; DB 2; Length 128;
Best Local Similarity 100.0%; Pred. No. 0.0049;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 HOYSKLPWT 9
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Db      109 HOYSKLPWT 117

RESULT 5
US-09-440-781-24
; Sequence 24, Application US/09440781
; Patent No. 6632926
; GENERAL INFORMATION:
; APPLICANT: Yvonne Man-yea Chen et al.
; TITLE OF INVENTION: ANTIBODY VARIANTS
; FILE REFERENCE: P1469R1
; CURRENT APPLICATION NUMBER: US/09/440,781
; CURRENT FILING DATE: 1999-11-16
; NUMBER OF SEQ ID NOS: 99
; SEQ ID NO 24
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; LENGTH: 9
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: artificial
; LOCATION: 1-9
; OTHER INFORMATION: variant CDR sequence
US-09-440-781-24

Query Match          71.4%; Score 40; DB 2; Length 9;
Best Local Similarity 75.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Db      2 QYSNVPWT 9

RESULT 6
US-09-440-781-26
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; Patent No. 6632926
; GENERAL INFORMATION:
; APPLICANT: Yvonne Man-yea Chen et al.
; TITLE OF INVENTION: ANTIBODY VARIANTS
; FILE REFERENCE: P1469R1
; CURRENT APPLICATION NUMBER: US/09/440,781
; CURRENT FILING DATE: 1999-11-16
; NUMBER OF SEQ ID NOS: 99
; SEQ ID NO 26
; LENGTH: 9
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: artificial
; LOCATION: 1-9
; OTHER INFORMATION: variant CDR sequence
US-09-440-781-26

Query Match          71.4%; Score 40; DB 2; Length 9;
Best Local Similarity 75.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      2 QYSKLPWT 9
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Db      2 QYSSVPWT 9

RESULT 7
US-07-934-373C-18
; Sequence 18, Application US/07934373C
; Patent No. 5821337
; GENERAL INFORMATION:
; APPLICANT: Paul J. Carter
; APPLICANT: Leonard G. Presta
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/934,373C
; FILING DATE: 21-Aug-1992
; CLASSIFICATION: 530
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; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US92/05126  
; FILING DATE: 15-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/715272  
; FILING DATE: 14-JUN-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lee, Wendy M.  
; REGISTRATION NUMBER: 40,378  
; REFERENCE/DOCKET NUMBER: P0709P2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-1994  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 18:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 107 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
US-07-934-373C-18

Query Match 71.4%; Score 40; DB 1; Length 107;  
Best Local Similarity 75.0%; Pred. No. 4;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYSKLPWT 9  
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Db 90 QYNSLPWT 97

RESULT 8  
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; Sequence 18, Application US/08437642B  
; Patent No. 6054297  
; GENERAL INFORMATION:  
; APPLICANT: Paul J. Carter  
; APPLICANT: Leonard G. Presta  
; TITLE OF INVENTION: Immunoglobulin Variants  
; NUMBER OF SEQUENCES: 47  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/437,642B  
; FILING DATE: 09-May-1995  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/934373  
; FILING DATE: 21-AUG-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/146206  
; FILING DATE: 17-NOV-1993  
; PRIOR APPLICATION DATA: PCT/US92/05126  
; FILING DATE: 15-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/715272  
; FILING DATE: 14-JUN-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lee, Wendy M.  
; REGISTRATION NUMBER: 40,378  
; REFERENCE/DOCKET NUMBER: P0709P2C1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-1994  
; TELEFAX: 650/952-9881

; INFORMATION FOR SEQ ID NO: 18:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 107 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
US-08-437-642B-18

Query Match 71.4%; Score 40; DB 2; Length 107;  
Best Local Similarity 75.0%; Pred. No. 4;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYSKLPWT 9  
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Db 90 QYNSLPWT 97

RESULT 9  
US-08-146-206C-18  
; Sequence 18, Application US/08146206C  
; Patent No. 6407213  
; GENERAL INFORMATION:  
; APPLICANT: Carter, Paul J.  
; APPLICANT: Presta, Leonard G.  
; TITLE OF INVENTION: Method for Making Humanized Antibodies  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/146,206C  
; FILING DATE: 17-No. 6407213-1993  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/715272  
; FILING DATE: 14-JUN-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lee, Wendy M.  
; REGISTRATION NUMBER: 40,378  
; REFERENCE/DOCKET NUMBER: P0709P1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-1994  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 18:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 107 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
US-08-146-206C-18

Query Match 71.4%; Score 40; DB 2; Length 107;  
Best Local Similarity 75.0%; Pred. No. 4;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYSKLPWT 9  
||: ||||  
Db 90 QYNSLPWT 97

RESULT 10  
US-09-648-067A-14  
; Sequence 14, Application US/09648067A  
; Patent No. 6627196  
; GENERAL INFORMATION:  
; APPLICANT: Baughman, Sharon A.



APPLICANT: Shak Steven  
TITLE OF INVENTION: Dosages for Treatment with Anti-ErbB2 Antibodies  
FILE REFERENCE: P1775R1  
CURRENT APPLICATION NUMBER: US/09/648,067A  
PRIOR FILING DATE: 2000-08-25  
PRIOR APPLICATION NUMBER: US 60/151,018  
PRIOR FILING DATE: 1999-08-27  
PRIOR APPLICATION NUMBER: US 60/213,822  
PRIOR FILING DATE: 2000-06-23  
NUMBER OF SEQ ID NOS: 15  
SEQ ID NO 14  
LENGTH: 107  
TYPE: PRT  
ORGANISM: Artificial sequence  
FEATURE:  
OTHER INFORMATION: VL consensus sequence  
US-09-648-067A-14

Query Match 71.4%; Score 40; DB 2; Length 107;  
Best Local Similarity 75.0%; Pred. No. 4;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYSKLPWT 9  
||:||||  
Db 90 QYNSLPWT 97

RESULT 11  
US-09-705-686-18  
; Sequence 18, Application US/09705686  
; Patent No. 6639055  
; GENERAL INFORMATION:  
; APPLICANT: Carter, Paul J.  
; Presta, Leonard G.  
; TITLE OF INVENTION: Method for Making Humanized Antibodies  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/705,686  
; FILING DATE: 02-No. 6639055-2000  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/146206  
; FILING DATE: 17-NOV-1993  
; APPLICATION NUMBER: 07/715272  
; FILING DATE: 14-JUN-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lee, Wendy M.  
; REGISTRATION NUMBER: 40,378  
; REFERENCE/DOCKET NUMBER: P0709PID3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-1994  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 18:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 107 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
; SEQUENCE DESCRIPTION: SEQ ID NO: 18:  
US-09-705-686-18

Query Match 71.4%; Score 40; DB 2; Length 107;  
Best Local Similarity 75.0%; Pred. No. 4;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYSKLPWT 9  
||:||||  
Db 90 QYNSLPWT 97

RESULT 13  
US-09-705-398-18  
; Sequence 18, Application US/09705398  
; Patent No. 6800738  
; GENERAL INFORMATION:  
; APPLICANT: Carter, Paul J.  
; Presta, Leonard G.  
; TITLE OF INVENTION: Method for Making Humanized Antibodies  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.

Best Local Similarity 75.0%; Pred. No. 4;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYSKLPWT 9  
||:||||  
Db 90 QYNSLPWT 97

RESULT 12  
US-09-705-392A-18  
; Sequence 18, Application US/09705392A  
; Patent No. 6719971  
; GENERAL INFORMATION:  
; APPLICANT: Carter, Paul J.  
; Presta, Leonard G.  
; TITLE OF INVENTION: Method for Making Humanized Antibodies  
; NUMBER OF SEQUENCES: 36  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/705,392A  
; FILING DATE: 02-No. 6719971-2002  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/146206  
; FILING DATE: 17-NOV-1993  
; APPLICATION NUMBER: 07/715272  
; FILING DATE: 14-JUN-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lee, Wendy M.  
; REGISTRATION NUMBER: 40,378  
; REFERENCE/DOCKET NUMBER: P0709PID1 REVISED  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-1994  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 18:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 107 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
; SEQUENCE DESCRIPTION: SEQ ID NO: 18:  
US-09-705-392A-18

Query Match 71.4%; Score 40; DB 2; Length 107;  
Best Local Similarity 75.0%; Pred. No. 4;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYSKLPWT 9  
||:||||  
Db 90 QYNSLPWT 97

RESULT 13  
US-09-705-398-18  
; Sequence 18, Application US/09705398  
; Patent No. 6800738  
; GENERAL INFORMATION:  
; APPLICANT: Carter, Paul J.  
; Presta, Leonard G.  
; TITLE OF INVENTION: Method for Making Humanized Antibodies  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/705,398  
FILING DATE: 02-Nov-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/146206  
FILING DATE: 17-NOV-1993  
APPLICATION NUMBER: 07/715272  
FILING DATE: 14-JUN-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Lee, Wendy M.  
REGISTRATION NUMBER: 40,378  
REFERENCE/DOCKET NUMBER: P0709PID2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-1994  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 107 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 18:  
US-09-705-398-18

Query Match 71.4%; Score 40; DB 2; Length 107;  
Best Local Similarity 75.0%; Pred. No. 4;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYSLPWT 9  
||:||||  
Db 90 QYNSLPWT 97

RESULT 14  
US-09-602-812A-5  
Sequence 5, Application US/09602812A  
Patent No. 6949245  
GENERAL INFORMATION:  
APPLICANT: Adams, Camellia W.  
APPLICANT: Presta, Leonard G.  
TITLE OF INVENTION: Humanized Anti-ErbB2 Antibodies and Treatment with  
TITLE OF INVENTION: Humanized Anti-ErbB2 Antibodies  
FILE REFERENCE: P1467R2  
CURRENT APPLICATION NUMBER: US/09/602,812A  
CURRENT FILING DATE: 2000-06-23  
PRIOR APPLICATION NUMBER: US 60/141,316  
PRIOR FILING DATE: 1999-06-25  
NUMBER OF SEQ ID NOS: 13  
SEQ ID NO 5  
LENGTH: 107  
TYPE: PRT  
ORGANISM: Artificial sequence  
FEATURE:  
OTHER INFORMATION: light chain consensus sequence  
US-09-602-812A-5

Query Match 71.4%; Score 40; DB 2; Length 107;  
Best Local Similarity 75.0%; Pred. No. 4;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYSLPWT 9  
||:||||

Db 90 QYNSLPWT 97  
RESULT 15  
PCT-US93-07832-18  
Sequence 18, Application PC/TUS9307832  
GENERAL INFORMATION:  
APPLICANT: Genentech, Inc.  
TITLE OF INVENTION: Immunoglobulin Variants  
NUMBER OF SEQUENCES: 40  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: patin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/07832  
FILING DATE: 19930820  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/715272  
FILING DATE: 14-JUN-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/05126  
FILING DATE: 15-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/934373  
FILING DATE: 21-AUG-1992  
ATTORNEY/AGENT INFORMATION:  
NAME:  
REGISTRATION NUMBER:  
REFERENCE/DOCKET NUMBER: 709P2PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE:  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 107 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
PCT-US93-07832-18

Query Match 71.4%; Score 40; DB 4; Length 107;  
Best Local Similarity 75.0%; Pred. No. 4;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYSLPWT 9  
||:||||  
Db 90 QYNSLPWT 97

RESULT 16  
US-08-974-899-3  
Sequence 3, Application US/08974899  
Patent No. 6037454  
GENERAL INFORMATION:  
APPLICANT: Presta, Leonard G.  
APPLICANT: Jardieu, Paula M.  
TITLE OF INVENTION: Humanized Anti-CD11a Antibodies  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California

```
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,899
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/031971
; FILING DATE: 11/27/96
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P1014R1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-974-899-3

Query Match 71.4%; Score 40; DB 2; Length 108;
Best Local Similarity 75.0%; Pred. No. 4.1;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYSLPWT 9
Db 90 QYNSLPWT 97

RESULT 17
US-09-065-059-3
; Sequence 3, Application US/09065059
; Patent No. 6068841
; GENERAL INFORMATION:
; APPLICANT: SEINO, Ken-ichiro
; APPLICANT: KAYAGAKI, No. 6068841uhiko
; APPLICANT: YAGITA, Hideo
; APPLICANT: OKUMURA, Ko
; APPLICANT: NAKATA, Motomi
; TITLE OF INVENTION: THERAPEUTIC AGENT FOR HEPATITIS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDermott, Will & Emery
; STREET: 99 Canal Center Plaza
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/065,059
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Bucca Ph.D., Daniel
; REGISTRATION NUMBER: P-42,368
; REFERENCE/DOCKET NUMBER: 50356-151
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-518-5100
; TELEFAX: 703-694-1124
; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-065-059-3

Query Match 71.4%; Score 40; DB 2; Length 108;
Best Local Similarity 75.0%; Pred. No. 4.1;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYSLPWT 9
Db 90 QYNSLPWT 97

RESULT 18
US-09-795-798-3
; Sequence 3, Application US/09795798
; Patent No. 6703018
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.
; Jardieu, Paula M.
; TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/795,798
; FILING DATE: 28-Feb-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/974,899
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P1014R1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-795-798-3

Query Match 71.4%; Score 40; DB 2; Length 108;
Best Local Similarity 75.0%; Pred. No. 4.1;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYSLPWT 9
Db 90 QYNSLPWT 97

RESULT 19
US-08-908-469-12
; Sequence 12, Application US/08908469
; Patent No. 6884879
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;
; GENERAL INFORMATION:
; APPLICANT: Baca, Manuel
;           Wells, James A.
;           Presta, Leonard G.
;           Lowman, Henry B.
;           Chen, Yvonne M.
;
; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
;
; NUMBER OF SEQUENCES: 131
; CORRESPONDENCE ADDRESS:
;   ADDRESS: Genentech, Inc.
;   STREET: 1 DNA Way
;   CITY: South San Francisco
;   STATE: California
;   COUNTRY: USA
;   ZIP: 94080
;
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: WinPatIn (Genentech)
;
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/908,469
;   FILING DATE: 21-May-2001
;   CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/833,504
;   FILING DATE: 07-APR-1997
;
; ATTORNEY/AGENT INFORMATION:
;   NAME: Cui, Steven X.
;   REGISTRATION NUMBER: 44,637
;   REFERENCE/DOCKET NUMBER: P1093P1
;
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 650/225-8674
;   TELEFAX: 650/952-9881
;
; INFORMATION FOR SEQ ID NO: 12:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 108 amino acids
;     TYPE: Amino Acid
;     TOPOLOGY: Linear
;   SEQUENCE DESCRIPTION: SEQ ID NO: 12:
;
; US-08-908-469-12
;
; Query Match 71.4%; Score 40; DB 2; Length 108;
; Best Local Similarity 75.0%; Pred. No. 4.1;
; Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
;
; QY 2 QYSKLPWT 9
; Db 90 QYNSLPWT 97
;
; RESULT 20
; US-08-913-555-3
; Sequence 3, Application US/08913555
; Patent No. 6946255
;
; GENERAL INFORMATION:
; APPLICANT: KAYAGAKI, No. 6946255uhiko
; APPLICANT: YAGITA, Kideo
; APPLICANT: OKUMURA, Ko
; APPLICANT: NAKATA, Motomi
; TITLE OF INVENTION: MONOCLONAL ANTIBODY SPECIFICALLY
;   REACTING WITH Fas LIGAND AND PRODUCTION PROCESS THEREOF
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: McDermott, Will & Emery
;   STREET: 99 Canal Center Plaza, Suite 300
;   CITY: Alexandria
;   STATE: Virginia
;   COUNTRY: USA
;   ZIP: 22314
;
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/913,555
;   FILING DATE: 19-SEP-1997
;   CLASSIFICATION: 530
;
; ATTORNEY/AGENT INFORMATION:
;   NAME: Bucca Ph.D., Daniel
;   REGISTRATION NUMBER: 42,368
;   REFERENCE/DOCKET NUMBER: 50356-150
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 202-756-8600
;     TELEFAX: 202-756-8699
;
; INFORMATION FOR SEQ ID NO: 21:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 108 amino acids
;     TYPE: amino acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
;   MOLECULE TYPE: peptide
;
; US-08-913-555-3
;
; Query Match 71.4%; Score 40; DB 2; Length 108;
; Best Local Similarity 75.0%; Pred. No. 4.1;
; Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
;
; QY 2 QYSKLPWT 9
; Db 90 QYSEFPWT 97
;
; RESULT 21
; US-08-913-555-21
; Sequence 21, Application US/08913555
; Patent No. 6946255
;
; GENERAL INFORMATION:
; APPLICANT: KAYAGAKI, No. 6946255uhiko
; APPLICANT: YAGITA, Kideo
; APPLICANT: OKUMURA, Ko
; APPLICANT: NAKATA, Motomi
; TITLE OF INVENTION: MONOCLONAL ANTIBODY SPECIFICALLY
;   REACTING WITH Fas LIGAND AND PRODUCTION PROCESS THEREOF
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: McDermott, Will & Emery
;   STREET: 99 Canal Center Plaza, Suite 300
;   CITY: Alexandria
;   STATE: Virginia
;   COUNTRY: USA
;   ZIP: 22314
;
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/913,555
;   FILING DATE: 19-SEP-1997
;   CLASSIFICATION: 530
;
; ATTORNEY/AGENT INFORMATION:
;   NAME: Bucca Ph.D., Daniel
;   REGISTRATION NUMBER: 42,368
;   REFERENCE/DOCKET NUMBER: 50356-150
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 202-756-8600
;     TELEFAX: 202-756-8699
;
; INFORMATION FOR SEQ ID NO: 21:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 108 amino acids
;     TYPE: amino acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
;   MOLECULE TYPE: peptide
;
; US-08-913-555-3
;
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/913,555
;   FILING DATE: 19-SEP-1997
;   CLASSIFICATION: 530
;
; ATTORNEY/AGENT INFORMATION:
;   NAME: Bucca Ph.D., Daniel
;   REGISTRATION NUMBER: 42,368
;   REFERENCE/DOCKET NUMBER: 50356-150
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 202-756-8600
;     TELEFAX: 202-756-8699
;
; INFORMATION FOR SEQ ID NO: 3:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 108 amino acids
;     TYPE: amino acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
;   MOLECULE TYPE: peptide
;
; US-08-913-555-3
```

US-08-913-555-21

Query Match 71.4%; Score 40; DB 2; Length 108;  
Best Local Similarity 75.0%; Pred. No. 4.1;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYSKLPWT 9  
|||: |||  
Db 90 QYSEFPWT 97

RESULT 22

US-08-560-558E-31  
; Sequence 31, Application US/08560558E  
; Patent No. 5891996  
; GENERAL INFORMATION:  
; APPLICANT:  
; TITLE OF INVENTION: Humanized and chimeric monoclonal  
; TITLE OF INVENTION: antibodies that recognize epidermal growth factor receptor  
; TITLE OF INVENTION: (EGF-R); diagnostic and therapeutic use.  
; NUMBER OF SEQUENCES: 34  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Allen C. Turner, TRASK, BRITT & ROSSA  
; STREET: P.O. Box 2250  
; CITY: Salt Lake City  
; STATE: Utah  
; COUNTRY: United States of America  
; ZIP: 84110

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: WINDOWS95  
; SOFTWARE: WordPerfect 5.1/5.2  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/560,558E  
; FILING DATE: No. 5891996ember 17, 1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Turner, Allen C.  
; REGISTRATION NUMBER: 33,041  
; REFERENCE/DOCKET NUMBER: 2720US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (801) 532-1922  
; TELEFAX: (801) 531-9168

INFORMATION FOR SEQ ID NO: 31:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: NO  
US-08-560-558E-31

Query Match 69.6%; Score 39; DB 1; Length 9;  
Best Local Similarity 75.0%; Pred. No. 4.6e+05;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYSKLPWT 9  
|||: |||  
Db 2 QYSHVPWT 9

RESULT 23

US-09-217-268B-31  
; Sequence 31, Application US/09217268B  
; Patent No. 6506883  
; GENERAL INFORMATION:  
; APPLICANT: Mateo de Acosta del Rio, Christina M  
; APPLICANT: Rodriguez, Rolando P  
; APPLICANT: Frias, Ernesto M  
; TITLE OF INVENTION: Humanized and Chimeric Monoclonal Antibodies That Recognize Epide  
; TITLE OF INVENTION: Growth Factor Receptor (EGF-R); Diagnostic and Therapeutic Use  
; FILE REFERENCE: 2720.105

; CURRENT APPLICATION NUMBER: US/09/217,268B

; CURRENT FILING DATE: 1998-12-21

; NUMBER OF SEQ ID NOS: 36

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 31

; LENGTH: 9

; TYPE: PRT

; ORGANISM: Murine

; FEATURE:

; NAME/KEY: MISC FEATURE

; OTHER INFORMATION: CDR of murine R3 antibody

US-09-217-268B-31

Query Match

69.6%; Score 39; DB 2; Length 9;

Best Local Similarity 75.0%; Pred. No. 4.6e+05;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYSKLPWT 9

|||: |||

Db 2 QYSHVPWT 9

RESULT 24

US-09-440-781-25  
; Sequence 25, Application US/09440781  
; Patent No. 6632926  
; GENERAL INFORMATION:  
; APPLICANT: Yvonne Man-yeet Chen et al.  
; TITLE OF INVENTION: ANTIBODY VARIANTS  
; FILE REFERENCE: P1469R1  
; CURRENT APPLICATION NUMBER: US/09/440,781  
; CURRENT FILING DATE: 1999-11-16  
; NUMBER OF SEQ ID NOS: 99  
; SEQ ID NO 25

; LENGTH: 9

; TYPE: PRT

; ORGANISM: artificial sequence

; FEATURE:

; NAME/KEY: artificial

; LOCATION: 1-9

; OTHER INFORMATION: variant CDR sequence

US-09-440-781-25

Query Match

69.6%; Score 39; DB 2; Length 9;

Best Local Similarity 75.0%; Pred. No. 4.6e+05;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYSKLPWT 9

|||: |||

Db 2 QYSHVPWT 9

RESULT 25

US-08-908-469-6

; Sequence 6, Application US/08908469

; Patent No. 6884879

; GENERAL INFORMATION:

; APPLICANT: Baca, Manuel

; Wells, James A.

; Presta, Leonard G.

; Lowman, Henry B.

; Chen, Yvonne M.

; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES

; NUMBER OF SEQUENCES: 131

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.

; STREET: 1 DNA Way

; CITY: South San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94080

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

```
;
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/908,469
; FILING DATE: 21-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/833,504
; FILING DATE: 07-APR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Cui, Steven X.
; REGISTRATION NUMBER: 44,637
; REFERENCE/DOCKET NUMBER: P1093P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-8674
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-08-908-469-6

Query Match          69.6%; Score 39; DB 2; Length 9;
Best Local Similarity 75.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      2 QYSKLPWT 9
Db      2 QYSTVPWT 9

RESULT 26
US-08-908-469-13
; Sequence 13, Application US/08908469
; Patent No. 6884879
; GENERAL INFORMATION:
; APPLICANT: Baca, Manuel
; Wells, James A.
; Presta, Leonard G.
; Lowman, Henry B.
; Chen, Yvonne M.
; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
; NUMBER OF SEQUENCES: 131
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/908,469
; FILING DATE: 21-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/833,504
; FILING DATE: 07-APR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Cui, Steven X.
; REGISTRATION NUMBER: 44,637
; REFERENCE/DOCKET NUMBER: P1093P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-8674
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-08-908-469-15

Query Match          69.6%; Score 39; DB 2; Length 107;
Best Local Similarity 75.0%; Pred. No. 6.2;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      2 QYSKLPWT 9
Db      90 QYSTVPWT 97

RESULT 27
US-08-908-469-15
; Sequence 15, Application US/08908469
; Patent No. 6884879
; GENERAL INFORMATION:
; APPLICANT: Baca, Manuel
; Wells, James A.
; Presta, Leonard G.
; Lowman, Henry B.
; Chen, Yvonne M.
; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
; NUMBER OF SEQUENCES: 131
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/908,469
; FILING DATE: 21-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/833,504
; FILING DATE: 07-APR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Cui, Steven X.
; REGISTRATION NUMBER: 44,637
; REFERENCE/DOCKET NUMBER: P1093P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-8674
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-08-908-469-15

Query Match          69.6%; Score 39; DB 2; Length 107;
Best Local Similarity 75.0%; Pred. No. 6.2;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      2 QYSKLPWT 9
Db      90 QYSTVPWT 97

RESULT 28
US-08-908-469-8
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; Sequence 8, Application US/08908469  
; Patent No. 6884879  
; GENERAL INFORMATION:  
; APPLICANT: Baca, Manuel  
; Wells, James A.  
; Presta, Leonard G.  
; Lowman, Henry B.  
; Chen, Yvonne M.  
; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES  
; NUMBER OF SEQUENCES: 131  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/908,469  
; FILING DATE: 21-May-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/833,504  
; FILING DATE: 07-APR-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Cui, Steven X.  
; REGISTRATION NUMBER: 44,637  
; REFERENCE/DOCKET NUMBER: P1093P1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-8674  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 108 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:  
US-08-908-469-8

Query Match 69.6%; Score 39; DB 2; Length 108;  
Best Local Similarity 75.0%; Pred. No. 6.3;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYSKLPWT 9  
DB 90 QYSTVPWT 97

RESULT 29  
US-08-908-469-10  
; Sequence 10, Application US/08908469  
; Patent No. 6884879  
; GENERAL INFORMATION:  
; APPLICANT: Baca, Manuel  
; Wells, James A.  
; Presta, Leonard G.  
; Lowman, Henry B.  
; Chen, Yvonne M.  
; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES  
; NUMBER OF SEQUENCES: 131  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/908,469  
; FILING DATE: 21-May-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/833,504  
; FILING DATE: 07-APR-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Cui, Steven X.  
; REGISTRATION NUMBER: 44,637  
; REFERENCE/DOCKET NUMBER: P1093P1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-8674  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 108 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
; SEQUENCE DESCRIPTION: SEQ ID NO: 10:  
US-08-908-469-10

Query Match 69.6%; Score 39; DB 2; Length 108;  
Best Local Similarity 75.0%; Pred. No. 6.3;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYSKLPWT 9  
DB 90 QYSTVPWT 97

RESULT 30  
US-08-908-469-126  
; Sequence 126, Application US/08908469  
; Patent No. 6884879  
; GENERAL INFORMATION:  
; APPLICANT: Baca, Manuel  
; Wells, James A.  
; Presta, Leonard G.  
; Lowman, Henry B.  
; Chen, Yvonne M.  
; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES  
; NUMBER OF SEQUENCES: 131  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/908,469  
; FILING DATE: 21-May-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/833,504  
; FILING DATE: 07-APR-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Cui, Steven X.  
; REGISTRATION NUMBER: 44,637  
; REFERENCE/DOCKET NUMBER: P1093P1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-8674  
; TELEFAX: 650/952-9881

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; INFORMATION FOR SEQ ID NO: 126:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 108 amino acids
;   TYPE: Amino Acid
;   TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 126:
US-08-908-469-126

Query Match          69.6%; Score 39; DB 2; Length 108;
Best Local Similarity 75.0%; Pred. No. 6.3;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      2 QYSKLPWT 9
Db      90 QYSTVPWT 97

RESULT 31
US-09-440-781-94
; Sequence 94, Application US/09440781
; Patent No. 6632926
; GENERAL INFORMATION:
; APPLICANT: Yvonne Man-yea Chen et al.
; TITLE OF INVENTION: ANTIBODY VARIANTS
; FILE REFERENCE: P1469R1
; CURRENT APPLICATION NUMBER: US/09/440,781
; CURRENT FILING DATE: 1999-11-16
; NUMBER OF SEQ ID NOS: 99
; SEQ ID NO 94
; LENGTH: 110
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: artificial
; LOCATION: 1-110
; OTHER INFORMATION: humanized antibody light chain variable domain
US-09-440-781-94

Query Match          69.6%; Score 39; DB 2; Length 110;
Best Local Similarity 75.0%; Pred. No. 6.4;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      2 QYSKLPWT 9
Db      90 QYSTVPWT 97

RESULT 32
US-09-440-781-95
; Sequence 95, Application US/09440781
; Patent No. 6632926
; GENERAL INFORMATION:
; APPLICANT: Yvonne Man-yea Chen et al.
; TITLE OF INVENTION: ANTIBODY VARIANTS
; FILE REFERENCE: P1469R1
; CURRENT APPLICATION NUMBER: US/09/440,781
; CURRENT FILING DATE: 1999-11-16
; NUMBER OF SEQ ID NOS: 99
; SEQ ID NO 95
; LENGTH: 110
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: artificial
; LOCATION: 1-110
; OTHER INFORMATION: humanized antibody light chain variable domain
US-09-440-781-95

Query Match          69.6%; Score 39; DB 2; Length 110;
Best Local Similarity 75.0%; Pred. No. 6.4;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      2 QYSKLPWT 9
Db      90 QYSTVPWT 97

RESULT 33
US-08-908-469-103
; Sequence 103, Application US/08908469
; Patent No. 6884879
; GENERAL INFORMATION:
; APPLICANT: Baca, Manuel
;               Wells, James A.
;               Presta, Leonard G.
;               Lowman, Henry B.
;               Chen, Yvonne M.
; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
; NUMBER OF SEQUENCES: 131
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/908,469
; FILING DATE: 21-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/833,504
; FILING DATE: 07-APR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Cui, Steven X.
; REGISTRATION NUMBER: 44,637
; REFERENCE/DOCKET NUMBER: P1093P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-8674
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 103:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 110 amino acids
;   TYPE: Amino Acid
;   TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 103:
US-08-908-469-103

Query Match          69.6%; Score 39; DB 2; Length 110;
Best Local Similarity 75.0%; Pred. No. 6.4;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      2 QYSKLPWT 9
Db      90 QYSTVPWT 97

RESULT 34
US-08-908-469-105
; Sequence 105, Application US/08908469
; Patent No. 6884879
; GENERAL INFORMATION:
; APPLICANT: Baca, Manuel
;               Wells, James A.
;               Presta, Leonard G.
;               Lowman, Henry B.
;               Chen, Yvonne M.
; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
; NUMBER OF SEQUENCES: 131
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/908,469
; FILING DATE: 21-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/833,504
; FILING DATE: 07-APR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Cui, Steven X.
; REGISTRATION NUMBER: 44,637
; REFERENCE/DOCKET NUMBER: P1093P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-8674
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 103:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 110 amino acids
;   TYPE: Amino Acid
;   TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 103:
US-08-908-469-105

Query Match          69.6%; Score 39; DB 2; Length 110;
Best Local Similarity 75.0%; Pred. No. 6.4;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      2 QYSKLPWT 9
Db      90 QYSTVPWT 97
```



```

; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/908,469
; FILING DATE: 21-May-2001
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/833,504
; FILING DATE: 07-APR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Cui, Steven X.
; REGISTRATION NUMBER: 44,637
; REFERENCE/DOCKET NUMBER: P1093P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-8674
; TELEFAX: 650/952-9881
;
; INFORMATION FOR SEQ ID NO: 105:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 110 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 105:
;
; US-08-908-469-105
;
; Query Match 69.6%; Score 39; DB 2; Length 110;
; Best Local Similarity 75.0%; Pred. No. 6.4;
; Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
;
; QY 2 QYSKLPWT 9
; DB 90 QYSTVPWT 97
;
; RESULT 35
; US-08-908-469-107
; Sequence 107, Application US/08908469
; Patent No. 6884879
; GENERAL INFORMATION:
; APPLICANT: Baca, Manuel
; Wells, James A.
; Presta, Leonard G.
; Lowman, Henry B.
; Chen, Yvonne M.
;
; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
; NUMBER OF SEQUENCES: 131
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/908,469
; FILING DATE: 21-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/833,504
; FILING DATE: 07-APR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Cui, Steven X.
; REGISTRATION NUMBER: 44,637
; REFERENCE/DOCKET NUMBER: P1093P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-8674
; TELEFAX: 650/952-9881
;
; INFORMATION FOR SEQ ID NO: 109:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 110 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 109:
;
; US-08-908-469-109
;
; Query Match 69.6%; Score 39; DB 2; Length 110;
; Best Local Similarity 75.0%; Pred. No. 6.4;
; Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
;
; QY 2 QYSKLPWT 9
; DB 90 QYSTVPWT 97
;
; RESULT 36
; US-08-908-469-109
; Sequence 109, Application US/08908469
; Patent No. 6884879
; GENERAL INFORMATION:
; APPLICANT: Baca, Manuel
; Wells, James A.
; Presta, Leonard G.
; Lowman, Henry B.
; Chen, Yvonne M.
;
; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
; NUMBER OF SEQUENCES: 131
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/908,469
; FILING DATE: 21-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/833,504
; FILING DATE: 07-APR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Cui, Steven X.
; REGISTRATION NUMBER: 44,637
; REFERENCE/DOCKET NUMBER: P1093P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-8674
; TELEFAX: 650/952-9881
;
; INFORMATION FOR SEQ ID NO: 109:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 110 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 109:
;
; US-08-908-469-109
;
; Query Match 69.6%; Score 39; DB 2; Length 110;
; Best Local Similarity 75.0%; Pred. No. 6.4;
; Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
;
; QY 2 QYSKLPWT 9
; DB 90 QYSTVPWT 97
;
; RESULT 35
; US-08-908-469-107
; Sequence 107, Application US/08908469
; Patent No. 6884879
; GENERAL INFORMATION:
; APPLICANT: Baca, Manuel
; Wells, James A.
; Presta, Leonard G.
; Lowman, Henry B.
; Chen, Yvonne M.
;
; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
; NUMBER OF SEQUENCES: 131
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/908,469
; FILING DATE: 21-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/833,504
; FILING DATE: 07-APR-1997
; ATTORNEY/AGENT INFORMATION:

```

```

; NAME: Cui, Steven X.
; REGISTRATION NUMBER: 44,637
; REFERENCE/DOCKET NUMBER: P1093P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-8674
; TELEFAX: 650/952-9881
;
; INFORMATION FOR SEQ ID NO: 107:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 110 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 107:
;
; US-08-908-469-107
;
; Query Match 69.6%; Score 39; DB 2; Length 110;
; Best Local Similarity 75.0%; Pred. No. 6.4;
; Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
;
; QY 2 QYSKLPWT 9
; DB 90 QYSTVPWT 97
;
; RESULT 36
; US-08-908-469-109
; Sequence 109, Application US/08908469
; Patent No. 6884879
; GENERAL INFORMATION:
; APPLICANT: Baca, Manuel
; Wells, James A.
; Presta, Leonard G.
; Lowman, Henry B.
; Chen, Yvonne M.
;
; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
; NUMBER OF SEQUENCES: 131
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/908,469
; FILING DATE: 21-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/833,504
; FILING DATE: 07-APR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Cui, Steven X.
; REGISTRATION NUMBER: 44,637
; REFERENCE/DOCKET NUMBER: P1093P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-8674
; TELEFAX: 650/952-9881
;
; INFORMATION FOR SEQ ID NO: 109:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 110 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 109:
;
; US-08-908-469-109
;
; Query Match 69.6%; Score 39; DB 2; Length 110;
; Best Local Similarity 75.0%; Pred. No. 6.4;
; Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
;
; QY 2 QYSKLPWT 9
; DB 90 QYSTVPWT 97
;
; RESULT 35
; US-08-908-469-107
; Sequence 107, Application US/08908469
; Patent No. 6884879
; GENERAL INFORMATION:
; APPLICANT: Baca, Manuel
; Wells, James A.
; Presta, Leonard G.
; Lowman, Henry B.
; Chen, Yvonne M.
;
; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
; NUMBER OF SEQUENCES: 131
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/908,469
; FILING DATE: 21-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/833,504
; FILING DATE: 07-APR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Cui, Steven X.
; REGISTRATION NUMBER: 44,637
; REFERENCE/DOCKET NUMBER: P1093P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-8674
; TELEFAX: 650/952-9881
;
; INFORMATION FOR SEQ ID NO: 109:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 110 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 109:
;
; US-08-908-469-109
;
; Query Match 69.6%; Score 39; DB 2; Length 110;
; Best Local Similarity 75.0%; Pred. No. 6.4;
; Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
;
; QY 2 QYSKLPWT 9
; DB 90 QYSTVPWT 97
;
; RESULT 35
; US-08-908-469-107
; Sequence 107, Application US/08908469
; Patent No. 6884879
; GENERAL INFORMATION:
; APPLICANT: Baca, Manuel
; Wells, James A.
; Presta, Leonard G.
; Lowman, Henry B.
; Chen, Yvonne M.
;
; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
; NUMBER OF SEQUENCES: 131
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/908,469
; FILING DATE: 21-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/833,504
; FILING DATE: 07-APR-1997
; ATTORNEY/AGENT INFORMATION:

```

Qy 2 QYSLPWT 9  
Db 90 QYSTVPWT 97

## RESULT 37

US-08-908-469-111  
; Sequence 111, Application US/08908469  
; Patent No. 6884879  
; GENERAL INFORMATION:  
; APPLICANT: Baca, Manuel  
; Wells, James A.  
; Presta, Leonard G.  
; Lowman, Henry B.  
; Chen, Yvonne M.  
; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES  
; NUMBER OF SEQUENCES: 131  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/908,469  
; FILING DATE: 21-May-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/833,504  
; FILING DATE: 07-APR-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Cui, Steven X.  
; REGISTRATION NUMBER: 44,637  
; REFERENCE/DOCKET NUMBER: P1093P1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-8674  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 111:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 110 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
; SEQUENCE DESCRIPTION: SEQ ID NO: 111:  
US-08-908-469-111

Query Match 69.6%; Score 39; DB 2; Length 110;  
Best Local Similarity 75.0%; Pred. No. 6.4;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QYSLPWT 9  
Db 90 QYSTVPWT 97

## RESULT 38

US-08-908-469-113  
; Sequence 113, Application US/08908469  
; Patent No. 6884879  
; GENERAL INFORMATION:  
; APPLICANT: Baca, Manuel  
; Wells, James A.  
; Presta, Leonard G.  
; Lowman, Henry B.  
; Chen, Yvonne M.  
; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES  
; NUMBER OF SEQUENCES: 131  
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/908,469  
; FILING DATE: 21-May-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/833,504  
; FILING DATE: 07-APR-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Cui, Steven X.  
; REGISTRATION NUMBER: 44,637  
; REFERENCE/DOCKET NUMBER: P1093P1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-8674  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 113:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 110 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
; SEQUENCE DESCRIPTION: SEQ ID NO: 113:  
US-08-908-469-113

Query Match 69.6%; Score 39; DB 2; Length 110;  
Best Local Similarity 75.0%; Pred. No. 6.4;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QYSLPWT 9  
Db 90 QYSTVPWT 97

## RESULT 39

US-08-908-469-115  
; Sequence 115, Application US/08908469  
; Patent No. 6884879  
; GENERAL INFORMATION:  
; APPLICANT: Baca, Manuel  
; Wells, James A.  
; Presta, Leonard G.  
; Lowman, Henry B.  
; Chen, Yvonne M.  
; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES  
; NUMBER OF SEQUENCES: 131  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/908,469  
; FILING DATE: 21-May-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/833,504  
; FILING DATE: 07-APR-1997

ATTORNEY/AGENT INFORMATION:  
NAME: Cui, Steven X.  
REGISTRATION NUMBER: 44,637  
REFERENCE/DOCKET NUMBER: P1093P1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-8674  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 115:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 110 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 115:  
US-08-908-469-115

Query Match 69.6%; Score 39; DB 2; Length 110;  
Best Local Similarity 75.0%; Pred. No. 6.4;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYSKLPWT 9  
DB 90 QYSTVPWT 97

RESULT 40  
US-08-908-469-117  
Sequence 117, Application US/08908469  
Patent No. 6884879  
GENERAL INFORMATION:  
APPLICANT: Baca, Manuel  
Wells, James A.  
Presta, Leonard G.  
Lowman, Henry B.  
Chen, Yvonne M.  
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES  
NUMBER OF SEQUENCES: 131  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/908,469  
FILING DATE: 21-May-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/833,504  
FILING DATE: 07-APR-1997

ATTORNEY/AGENT INFORMATION:  
NAME: Cui, Steven X.  
REGISTRATION NUMBER: 44,637  
REFERENCE/DOCKET NUMBER: P1093P1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-8674  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 117:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 110 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 117:  
US-08-908-469-117

Query Match 69.6%; Score 39; DB 2; Length 110;  
Best Local Similarity 75.0%; Pred. No. 6.4;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYSKLPWT 9  
DB 90 QYSTVPWT 97

RESULT 41  
US-08-497-312-18  
Sequence 18, Application US/08497312  
Patent No. 5712120  
GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: Method for obtaining modified  
TITLE OF INVENTION: immunoglobulins with reduced immunogenicity of murine  
TITLE OF INVENTION: antibody variable domains, compositions containing them.  
NUMBER OF SEQUENCES: 31  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CENTRO DE INMUNOLOGIA MOLECULAR  
STREET: 215 Y 15, ATABEY PLAYA  
CITY: HAVANA  
STATE:  
COUNTRY: CUBA  
ZIP: 11600

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/497,312  
FILING DATE: 30-JUN-1995

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: CU 80/94  
FILING DATE: 30-JUN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: BOND, LAURENCE B.  
REGISTRATION NUMBER: 30,549  
REFERENCE/DOCKET NUMBER: 2629US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 801/532-1922  
TELEFAX: 801/531-9168  
TELEX: 388961 1PM04UT  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 113 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
US-08-497-312-18

Query Match 69.6%; Score 39; DB 1; Length 113;  
Best Local Similarity 75.0%; Pred. No. 6.6;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYSKLPWT 9  
DB 95 QYSHVPWT 102

RESULT 42  
US-08-560-558E-27  
Sequence 27, Application US/08560558E  
Patent No. 5891996  
GENERAL INFORMATION:  
APPLICANT:

TITLE OF INVENTION: Humanized and chimeric monoclonal  
TITLE OF INVENTION: antibodies that recognize epidermal growth factor receptor  
TITLE OF INVENTION: EGF-R; diagnostic and therapeutic use.  
NUMBER OF SEQUENCES: 34  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Allen C. Turner, TRASK, BRITT & ROSSA

; STREET: P.O. Box 2250  
; CITY: Salt Lake City  
; STATE: Utah  
; COUNTRY: United States of America  
; ZIP: 84110  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: WINDOWS95  
; SOFTWARE: WordPerfect 5.1/5.2  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/560,558E  
; FILING DATE: No. 5891996ember 17, 1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Turner, Allen C.  
; REGISTRATION NUMBER: 33,041  
; REFERENCE/DOCKET NUMBER: 2720US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (801) 532-1922  
; TELEFAX: (801) 531-9168  
; INFORMATION FOR SEQ ID NO: 27:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 114 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: NO  
US-08-560-558E-27

Query Match 69.6%; Score 39; DB 1; Length 114;

Best Local Similarity 75.0%; Pred. No. 6.7; Mismatches 1; Indels 0; Gaps 0;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYSKLPWT 9  
|||:||||  
DB 95 QYSHVPWT 102

## RESULT 43

US-09-217-268B-27

; Sequence 27, Application US/09217268B

; Patent No. 6506883

; GENERAL INFORMATION:

; APPLICANT: Mateo de Acosta del Rio, Christina M

; APPLICANT: Rodriguez, Rolando P

; APPLICANT: Frias, Ernesto M

; TITLE OF INVENTION: Humanized and Chimeric Monoclonal Antibodies That Recognize Epide

; TITLE OF INVENTION: Growth Factor Receptor (EGF-R); Diagnostic and Therapeutic Use

; FILE REFERENCE: 2720.1US

; CURRENT APPLICATION NUMBER: US/09/217,268B

; CURRENT FILING DATE: 1998-12-21

; NUMBER OF SEQ ID NOS: 36

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 27

; LENGTH: 114

; TYPE: PRT

; ORGANISM: Murine R3 antibody

; FEATURE:

; NAME/KEY: MISC FEATURE

; OTHER INFORMATION: Deduced amino acid sequence of VK of murine R3 antibody

US-09-217-268B-27

Query Match 69.6%; Score 39; DB 2; Length 114;

Best Local Similarity 75.0%; Pred. No. 6.7;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYSKLPWT 9  
|||:||||  
DB 95 QYSHVPWT 102

## RESULT 44

US-09-217-268B-35  
; Sequence 35, Application US/09217268B  
; Patent No. 6506883  
; GENERAL INFORMATION:  
; APPLICANT: Mateo de Acosta del Rio, Christina M  
; APPLICANT: Rodriguez, Rolando P  
; APPLICANT: Frias, Ernesto M  
; TITLE OF INVENTION: Humanized and Chimeric Monoclonal Antibodies That Recognize Epide  
; TITLE OF INVENTION: Growth Factor Receptor (EGF-R); Diagnostic and Therapeutic Use  
; FILE REFERENCE: 2720.1US  
; CURRENT APPLICATION NUMBER: US/09/217,268B  
; CURRENT FILING DATE: 1998-12-21  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 35  
; LENGTH: 114  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Amino acid sequence of humanized VK of murine R3 antibody contain  
; OTHER INFORMATION: ing mAb CDRs  
US-09-217-268B-35

Query Match 69.6%; Score 39; DB 2; Length 114;

Best Local Similarity 75.0%; Pred. No. 6.7; Mismatches 1; Indels 0; Gaps 0;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYSKLPWT 9  
|||:||||  
DB 95 QYSHVPWT 102

## RESULT 45

US-08-497-312-14

; Sequence 14, Application US/08497312

; Patent No. 5712120

; GENERAL INFORMATION:

; APPLICANT:

; TITLE OF INVENTION: Method for obtaining modified

; TITLE OF INVENTION: immunoglobulins with reduced immunogenicity of murine

; NUMBER OF SEQUENCES: 31

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: CENTRO DE INMUNOLOGIA MOLECULAR

; STREET: 215 Y 15, ATABEY PLAYA

; CITY: HAVANA

; STATE:

; COUNTRY: CUBA

; ZIP: 11600

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/497,312

; FILING DATE: 30-JUN-1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: CU 80/94

; FILING DATE: 30-JUN-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: BOND, LAURENCE B.

; REGISTRATION NUMBER: 30,549

; REFERENCE/DOCKET NUMBER: 2629US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 801/532-1922

; TELEFAX: 801/531-9168

; TELEX: 388961 LPW04UT

; INFORMATION FOR SEQ ID NO: 14:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 116 amino acids

; TYPE: amino acid

; STRANDEDNESS: unknown

```
;
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-497-312-14

Query Match 69.6%; Score 39; DB 1; Length 116;
Best Local Similarity 75.0%; Pred. No. 6.8;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYSKLPWT 9
DB 97 QYSHVPWT 104

RESULT 46
US-08-908-469-100
; Sequence 100, Application US/08908469
; Patent No. 6884879
; GENERAL INFORMATION:
; APPLICANT: Baca, Manuel
; Wells, James A.
; Presta, Leonard G.
; Lowman, Henry B.
; Chen, Yvonne M.
; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
; NUMBER OF SEQUENCES: 131
; CORRESPONDENCE ADDRESS:
; ADDRESS: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/908,469
; FILING DATE: 21-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/833,504
; FILING DATE: 07-APR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Cui, Steven X.
; REGISTRATION NUMBER: 44,637
; REFERENCE/DOCKET NUMBER: P1093P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-8674
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 100:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 237 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 100:
US-08-908-469-100

Query Match 69.6%; Score 39; DB 2; Length 237;
Best Local Similarity 75.0%; Pred. No. 14;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYSKLPWT 9
DB 113 QYSTVPWT 120

RESULT 47
US-10-011-125A-2
; Sequence 2, Application US/10011125A
; Patent No. 6828121
; GENERAL INFORMATION:
; APPLICANT: Chen, Christina Yu-Ching
; TITLE OF INVENTION: BACTERIAL HOST STRAINS
; FILE REFERENCE: P1804R1
; CURRENT APPLICATION NUMBER: US/10/011,125A
; CURRENT FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: US 60/256,162
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 12
; SEQ ID NO 2
; LENGTH: 491
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized.
; Patent No. 6828121
US-10-011-125A-2

Query Match 69.6%; Score 39; DB 2; Length 491;
Best Local Similarity 75.0%; Pred. No. 31;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYSKLPWT 9
DB 113 QYSTVPWT 120

RESULT 48
US-09-270-767-37260
; Sequence 37260, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 37260
; LENGTH: 191
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-37260

Query Match 67.9%; Score 38; DB 2; Length 191;
Best Local Similarity 55.6%; Pred. No. 18;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 HQYSKLPWT 9
DB 147 HRYSORPWS 155

RESULT 49
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; Sequence 52477, Application US/09270767
; Patent No. 6703491
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; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
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; ORGANISM: Drosophila melanogaster
; FEATURE:
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; OTHER INFORMATION: Xaa means any amino acid  
US-09-270-767-52477

Query Match 67.9%; Score 38; DB 2; Length 191;  
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; Sequence 18, Application US/08797689  
; Patent No. 5876969  
; GENERAL INFORMATION:  
; APPLICANT: Fleer, Reinhard  
; APPLICANT: Fournier, Alain  
; APPLICANT: Guitten, Jean-Dominique  
; APPLICANT: Jung, Gerard  
; APPLICANT: Yeh, Patrice  
; TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,  
; TITLE OF INVENTION: PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION  
; TITLE OF INVENTION: CONTAINING SAID POLYPEPTIDES  
; NUMBER OF SEQUENCES: 36  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Rhone-Poulenc Rorer Inc.  
; STREET: 500 Arcola Road, 3C43  
; CITY: Collegeville  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19426

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Macintosh  
; OPERATING SYSTEM: System 7.1  
; SOFTWARE: Word 5.1 (Patentin)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/797,689  
; FILING DATE: 31-JAN-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/256,927  
; FILING DATE: 28-JUL-1994  
; APPLICATION NUMBER: FR 92/01064  
; FILING DATE: 31-JAN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/FR93/00085  
; FILING DATE: 28-JAN-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith Ph.D., Julie K.  
; REGISTRATION NUMBER: P-38,619  
; REFERENCE/DOCKET NUMBER: ST92006-US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (610) 454-3839  
; TELEFAX: (610) 454-3808  
; INFORMATION FOR SEQ ID NO: 18:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 249 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-797-689-18

Query Match 67.9%; Score 38; DB 1; Length 249;  
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OM protein - protein search, using sw model

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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157	31	55.4	174	7	US-11-096-568A-15697	Sequence 15697, A	230	30	53.6	236	7	US-11-182-343-52	Sequence 52, Appl
158	31	55.4	181	6	US-10-485-517-338	Sequence 338, App	231	30	53.6	237	7	US-11-096-568A-15482	Sequence 15482, A
159	31	55.4	182	6	US-10-485-517-328	Sequence 328, App	232	30	53.6	250	7	US-11-054-515-1174	Sequence 1174, Ap
160	31	55.4	182	6	US-11-087-099-2660	Sequence 2660, Ap	233	30	53.6	250	7	US-11-266-444-1174	Sequence 1174, Ap
161	31	55.4	189	6	US-11-096-568A-10728	Sequence 10728, A	234	30	53.6	269	7	US-11-087-099-602	Sequence 602, App
162	31	55.4	199	6	US-10-793-626-2546	Sequence 2546, Ap	235	30	53.6	293	7	US-11-096-568A-16325	Sequence 16325, A
163	31	55.4	203	6	US-10-793-626-3138	Sequence 3138, Ap	236	30	53.6	294	7	US-11-096-568A-15481	Sequence 15481, A
164	31	55.4	203	7	US-11-096-568A-15695	Sequence 15695, A	237	30	53.6	294	7	US-11-096-568A-24728	Sequence 24728, A
165	31	55.4	224	6	US-10-942-698-11	Sequence 11, Appl	238	30	53.6	342	6	US-10-729-895-2	Sequence 2, Appli
166	31	55.4	261	6	US-10-883-512-2	Sequence 2, Appli	239	30	53.6	363	6	US-10-729-895-4	Sequence 4, Appli
167	31	55.4	267	7	US-11-134-795-12	Sequence 12, Appl	240	30	53.6	381	7	US-11-087-099-1083	Sequence 1083, Ap
168	31	55.4	265	7	US-11-096-568A-31762	Sequence 31762, A	241	30	53.6	381	7	US-11-087-099-12001	Sequence 12001, A
169	31	55.4	269	7	US-11-096-568A-31761	Sequence 31761, A	242	30	53.6	385	7	US-11-087-099-3154	Sequence 3154, Ap
170	31	55.4	270	7	US-11-096-568A-10727	Sequence 10727, A	243	30	53.6	404	7	US-11-124-368A-258	Sequence 258, App
171	31	55.4	270	7	US-11-096-568A-16837	Sequence 16837, A	244	30	53.6	431	7	US-11-087-099-1524	Sequence 1524, Ap



245	30	53.6	435	7	US-11-087-099-9359	Sequence 9359, Ap	318	29	51.8	155	7	US-11-128-900-112	Sequence 112, App
246	30	53.6	447	7	US-11-087-099-6982	Sequence 6952, Ap	319	29	51.8	156	7	US-11-072-512-2055	Sequence 2055, Ap
247	30	53.6	463	7	US-11-087-099-7203	Sequence 7203, Ap	320	29	51.8	157	7	US-11-096-568A-14031	Sequence 14031, A
248	30	53.6	463	7	US-11-087-099-7203	Sequence 10390, A	321	29	51.8	166	7	US-11-176-830-1010	Sequence 1010, Ap
249	30	53.6	500	7	US-11-120-308-1338	Sequence 138, App	322	29	51.8	166	7	US-11-072-512-2085	Sequence 2085, Ap
250	30	53.6	503	7	US-11-072-512-3516	Sequence 3516, Ap	323	29	51.8	199	7	US-11-096-568A-29189	Sequence 29189, A
251	30	53.6	504	7	US-11-096-568A-24727	Sequence 24727, A	324	29	51.8	214	7	US-11-183-205-55	Sequence 55, Appl
252	30	53.6	510	7	US-11-210-316-22	Sequence 22, Appl	325	29	51.8	223	6	US-10-506-454-1361	Sequence 1261, Ap
253	30	53.6	516	7	US-11-096-568A-16324	Sequence 16324, A	326	29	51.8	240	7	US-11-087-099-1831	Sequence 1831, Ap
254	30	53.6	543	7	US-11-072-512-3493	Sequence 3493, Ap	327	29	51.8	246	7	US-11-172-740-222	Sequence 222, App
255	30	53.6	580	6	US-10-718-264-7	Sequence 7, Appl	328	29	51.8	246	7	US-11-172-740-1695	Sequence 1695, Ap
256	30	53.6	580	6	US-10-718-264-7	Sequence 7, Appl	329	29	51.8	247	7	US-11-084-717-21	Sequence 21, Appl
257	30	53.6	673	6	US-11-124-368A-257	Sequence 257, App	330	29	51.8	247	7	US-11-179-244-21	Sequence 21, Appl
258	30	53.6	694	6	US-10-491-468-24	Sequence 24, Appl	331	29	51.8	247	7	US-11-084-0558-21	Sequence 21, Appl
259	29.5	52.7	101	6	US-10-771-257-2	Sequence 2, Appl	332	29	51.8	260	7	US-11-053-822-906	Sequence 906, App
260	29.5	52.7	101	7	US-11-127-677-2	Sequence 2, Appl	333	29	51.8	262	7	US-11-089-266-66	Sequence 66, Appl
261	29.5	52.7	111	7	US-11-217-402-2	Sequence 2, Appl	334	29	51.8	283	7	US-11-087-099-11561	Sequence 11561, A
262	29.5	52.7	112	7	US-11-127-933-15	Sequence 15, Appl	335	29	51.8	284	7	US-11-124-367A-431	Sequence 431, App
263	29.5	52.7	112	7	US-11-127-903-15	Sequence 15, Appl	336	29	51.8	286	7	US-11-124-368A-221	Sequence 221, App
264	29.5	52.7	113	7	US-11-096-074-53	Sequence 53, Appl	337	29	51.8	290	7	US-11-032-773-957	Sequence 957, App
265	29.5	52.7	113	7	US-11-095-822-53	Sequence 53, Appl	338	29	51.8	290	7	US-11-096-568A-29188	Sequence 29188, A
266	29.5	52.7	380	7	US-11-087-099-5720	Sequence 5720, Ap	339	29	51.8	301	7	US-11-098-686-11244	Sequence 11244, A
267	29.5	52.7	380	7	US-11-087-099-6472	Sequence 6472, Ap	340	29	51.8	312	6	US-10-858-730-122	Sequence 122, App
268	29.5	52.7	386	7	US-11-087-099-4397	Sequence 4397, Ap	341	29	51.8	319	7	US-11-032-773-955	Sequence 955, App
269	29	51.8	9	6	US-10-982-357-20	Sequence 20, Appl	342	29	51.8	326	7	US-11-096-568A-23304	Sequence 23304, A
270	29	51.8	9	6	US-10-982-357-37	Sequence 37, Appl	343	29	51.8	331	7	US-11-087-099-11371	Sequence 11371, A
271	29	51.8	9	7	US-11-012-353-6	Sequence 6, Appl	344	29	51.8	339	7	US-11-096-568A-29187	Sequence 29187, A
272	29	51.8	9	7	US-11-125-837-15	Sequence 15, Appl	345	29	51.8	342	7	US-11-024-959-456	Sequence 456, App
273	29	51.8	9	7	US-11-105-708-19	Sequence 19, Appl	346	29	51.8	376	7	US-11-087-099-6961	Sequence 6961, Ap
274	29	51.8	48	6	US-10-856-751-34	Sequence 34, Appl	347	29	51.8	376	7	US-11-087-099-12395	Sequence 12395, A
275	29	51.8	98	7	US-11-000-463-920	Sequence 920, App	348	29	51.8	377	7	US-11-096-568A-24504	Sequence 24504, A
276	29	51.8	98	7	US-11-000-463-921	Sequence 921, App	349	29	51.8	380	7	US-11-087-099-1772	Sequence 1772, Ap
277	29	51.8	102	7	US-11-096-568A-14033	Sequence 14033, A	350	29	51.8	380	7	US-11-087-099-9164	Sequence 9164, Ap
278	29	51.8	105	7	US-11-097-812-53	Sequence 53, Appl	351	29	51.8	380	7	US-11-087-099-9819	Sequence 9819, Ap
279	29	51.8	107	6	US-10-982-357-6	Sequence 6, Appl	352	29	51.8	380	7	US-11-146-428-73	Sequence 73, Appl
280	29	51.8	107	6	US-10-982-357-42	Sequence 42, Appl	353	29	51.8	383	7	US-11-087-099-2347	Sequence 2347, Ap
281	29	51.8	107	6	US-10-982-357-44	Sequence 44, Appl	354	29	51.8	383	7	US-11-087-099-7341	Sequence 7341, Ap
282	29	51.8	107	6	US-10-982-357-48	Sequence 48, Appl	355	29	51.8	384	7	US-11-087-099-8427	Sequence 8427, Ap
283	29	51.8	107	6	US-10-982-357-50	Sequence 50, Appl	356	29	51.8	384	7	US-11-096-568A-10142	Sequence 10142, A
284	29	51.8	107	6	US-11-064-174-35	Sequence 35, Appl	357	29	51.8	400	7	US-11-087-099-4318	Sequence 4318, Ap
285	29	51.8	107	7	US-11-064-174-157	Sequence 157, App	358	29	51.8	401	7	US-11-072-512-3800	Sequence 3800, Ap
286	29	51.8	107	7	US-11-064-174-164	Sequence 164, App	359	29	51.8	401	7	US-11-096-568A-10141	Sequence 10141, A
287	29	51.8	107	7	US-11-064-174-170	Sequence 170, App	360	29	51.8	416	7	US-11-096-568A-10140	Sequence 10140, A
288	29	51.8	107	7	US-11-183-205-51	Sequence 51, Appl	361	29	51.8	421	7	US-11-055-822-902	Sequence 902, App
289	29	51.8	107	7	US-11-183-205-52	Sequence 52, Appl	362	29	51.8	432	7	US-11-096-568A-23303	Sequence 23303, A
290	29	51.8	109	7	US-11-221-281-47	Sequence 47, Appl	363	29	51.8	436	7	US-11-087-099-5918	Sequence 5918, Ap
291	29	51.8	110	7	US-11-097-812-96	Sequence 96, Appl	364	29	51.8	447	7	US-11-087-099-5814	Sequence 5814, Ap
292	29	51.8	110	7	US-11-097-812-114	Sequence 114, App	365	29	51.8	447	7	US-11-096-568A-24503	Sequence 24503, A
293	29	51.8	111	7	US-11-097-812-106	Sequence 106, App	366	29	51.8	448	7	US-11-087-099-3085	Sequence 3085, Ap
294	29	51.8	111	7	US-11-097-812-115	Sequence 115, App	367	29	51.8	456	7	US-11-087-099-6259	Sequence 6259, Ap
295	29	51.8	112	7	US-11-012-353-54	Sequence 54, Appl	368	29	51.8	457	6	US-10-063-703-12	Sequence 12, Appl
296	29	51.8	112	7	US-11-012-353-56	Sequence 56, Appl	369	29	51.8	457	7	US-11-102-240-12	Sequence 12, Appl
297	29	51.8	112	7	US-11-012-353-61	Sequence 61, Appl	370	29	51.8	457	7	US-11-087-099-5761	Sequence 5761, Ap
298	29	51.8	112	7	US-11-012-353-65	Sequence 65, Appl	371	29	51.8	457	7	US-11-103-195-12	Sequence 12, Appl
299	29	51.8	112	7	US-11-089-266-15	Sequence 15, Appl	372	29	51.8	474	7	US-11-096-568A-26621	Sequence 26621, A
300	29	51.8	114	7	US-11-037-199-26	Sequence 26, Appl	373	29	51.8	510	7	US-11-096-568A-24502	Sequence 24502, A
301	29	51.8	114	7	US-11-037-199-34	Sequence 34, Appl	374	29	51.8	520	7	US-11-024-959-272	Sequence 272, App
302	29	51.8	118	7	US-11-172-740-2417	Sequence 2417, Ap	375	29	51.8	529	7	US-11-210-316-28	Sequence 28, Appl
303	29	51.8	122	7	US-11-012-353-49	Sequence 49, Appl	376	29	51.8	567	6	US-10-131-826A-476	Sequence 476, App
304	29	51.8	123	7	US-11-172-740-2416	Sequence 2416, Ap	377	29	51.8	567	6	US-10-973-115B-476	Sequence 476, App
305	29	51.8	124	7	US-11-172-740-2415	Sequence 2415, Ap	378	29	51.8	567	6	US-10-501-035-257	Sequence 257, App
306	29	51.8	126	7	US-11-098-686-10771	Sequence 10771, A	379	29	51.8	569	7	US-11-096-568A-26620	Sequence 26620, A
307	29	51.8	126	7	US-11-172-740-2418	Sequence 2418, Ap	380	29	51.8	576	7	US-11-096-568A-8957	Sequence 8957, Ap
308	29	51.8	127	6	US-10-982-357-28	Sequence 28, Appl	381	29	51.8	576	7	US-11-096-568A-8959	Sequence 8959, Ap
309	29	51.8	130	6	US-10-793-626-164	Sequence 164, App	382	29	51.8	608	7	US-11-096-568A-26619	Sequence 26619, A
310	29	51.8	131	7	US-11-012-353-63	Sequence 63, Appl	383	29	51.8	617	7	US-11-096-568A-8956	Sequence 8956, Ap
311	29	51.8	131	7	US-11-012-353-67	Sequence 67, Appl	384	29	51.8	636	6	US-10-506-454-910	Sequence 910, App
312	29	51.8	131	7	US-11-125-837-23	Sequence 23, Appl	385	29	51.8	639	7	US-11-098-686-10424	Sequence 10424, A
313	29	51.8	136	7	US-11-096-568A-25027	Sequence 25027, A	386	29	51.8	643	7	US-11-127-877-72	Sequence 72, Appl
314	29	51.8	141	7	US-11-096-568A-14032	Sequence 14032, A	387	29	51.8	798	7	US-11-087-099-2368	Sequence 2368, Ap
315	29	51.8	141	7	US-11-096-568A-14034	Sequence 14034, A	388	29	51.8	816	7	US-11-073-512-3657	Sequence 3657, Ap
316	29	51.8	149	7	US-11-089-266-2	Sequence 2, Appl	389	29	51.8	817	7	US-11-012-762-2	Sequence 2, Appl
317	29	51.8	155	7	US-11-128-900-20	Sequence 20, Appl	390	29	51.8	879	7	US-11-098-686-10290	Sequence 10290, A

391	29	51.8	1328	6	US-10-649-591-2	Sequence 2, Appli	464	28	50.0	245	7	US-11-054-515-1521	Sequence 1521, Ap
392	29	51.8	1331	6	US-10-649-591-1	Sequence 1, Appli	465	28	50.0	245	7	US-11-054-515-1839	Sequence 1839, Ap
393	29	51.8	1361	7	US-10-649-591-13	Sequence 13, Appli	466	28	50.0	245	7	US-11-054-515-1864	Sequence 1864, Ap
394	29	51.8	1385	7	US-11-129-741-3655	Sequence 3655, Ap	467	28	50.0	245	7	US-11-054-515-1950	Sequence 1950, Ap
395	29	51.8	1694	7	US-11-135-855-36	Sequence 36, Appl	468	28	50.0	245	7	US-11-266-444-1516	Sequence 1516, Ap
396	29	51.8	1700	6	US-10-453-372-398	Sequence 398, App	469	28	50.0	245	7	US-11-266-444-1521	Sequence 1521, Ap
397	29	51.8	1700	6	US-10-453-372-412	Sequence 412, App	470	28	50.0	245	7	US-11-266-444-1839	Sequence 1839, Ap
398	29	51.8	1700	6	US-10-453-372-414	Sequence 414, App	471	28	50.0	245	7	US-11-266-444-1864	Sequence 1864, Ap
399	29	51.8	1700	6	US-10-453-372-416	Sequence 416, App	472	28	50.0	245	7	US-11-266-444-1950	Sequence 1950, Ap
400	29	51.8	1700	6	US-10-453-372-418	Sequence 418, App	473	28	50.0	246	7	US-11-054-515-1847	Sequence 1847, Ap
401	29	51.8	1709	6	US-10-995-561-973	Sequence 973, App	474	28	50.0	246	7	US-11-266-444-1847	Sequence 1847, Ap
402	29	51.8	1709	6	US-10-453-372-410	Sequence 410, App	475	28	50.0	247	6	US-10-533-811-9	Sequence 9, Appli
403	29	51.8	1709	6	US-11-135-855-35	Sequence 35, Appl	476	28	50.0	247	7	US-11-054-515-1885	Sequence 1885, Ap
404	28.5	50.9	404	6	US-10-507-662-60	Sequence 60, Appl	477	28	50.0	247	7	US-11-054-515-1892	Sequence 1892, Ap
405	28.5	50.9	406	6	US-10-507-662-64	Sequence 64, Appl	478	28	50.0	247	7	US-11-054-515-2092	Sequence 2092, Ap
406	28.5	50.9	262	7	US-11-098-686-11125	Sequence 11125, A	479	28	50.0	247	7	US-11-054-515-2124	Sequence 2124, Ap
407	28	50.0	9	6	US-10-507-662-59	Sequence 59, Appl	480	28	50.0	247	7	US-11-054-515-2126	Sequence 2126, Ap
408	28	50.0	9	7	US-11-097-812-122	Sequence 122, App	481	28	50.0	247	7	US-11-054-515-2127	Sequence 2127, Ap
409	28	50.0	9	7	US-11-097-812-196	Sequence 196, App	482	28	50.0	247	7	US-11-266-444-1885	Sequence 1885, Ap
410	28	50.0	30	7	US-11-108-185-28	Sequence 28, Appl	483	28	50.0	247	7	US-11-266-444-1892	Sequence 2092, Ap
411	28	50.0	56	6	US-10-997-201A-16	Sequence 16, Appl	484	28	50.0	247	7	US-11-266-444-2092	Sequence 2124, Ap
412	28	50.0	89	7	US-11-096-568A-24975	Sequence 568, Ap	485	28	50.0	247	7	US-11-266-444-2124	Sequence 2126, Ap
413	28	50.0	99	7	US-11-084-554-199	Sequence 199, App	486	28	50.0	247	7	US-11-266-444-2126	Sequence 2127, Ap
414	28	50.0	99	7	US-11-136-250-199	Sequence 199, App	487	28	50.0	247	7	US-11-266-444-2127	Sequence 2071, Ap
415	28	50.0	100	7	US-11-084-554-196	Sequence 196, App	488	28	50.0	248	7	US-11-054-515-2071	Sequence 2071, Ap
416	28	50.0	100	7	US-11-136-250-196	Sequence 196, App	489	28	50.0	248	7	US-11-266-444-2071	Sequence 1962, Ap
417	28	50.0	100	7	US-11-096-568A-24975	Sequence 24975, A	490	28	50.0	249	7	US-11-054-515-1968	Sequence 1968, Ap
418	28	50.0	101	5	US-09-995-493-107	Sequence 107, App	491	28	50.0	249	7	US-11-054-515-1970	Sequence 1970, Ap
419	28	50.0	107	6	US-10-507-662-63	Sequence 63, Appl	492	28	50.0	249	7	US-11-054-515-1984	Sequence 1984, Ap
420	28	50.0	107	6	US-11-064-174-45	Sequence 45, Appl	493	28	50.0	249	7	US-11-054-515-1997	Sequence 1997, Ap
421	28	50.0	109	7	US-11-097-812-113	Sequence 113, App	494	28	50.0	249	7	US-11-054-515-1999	Sequence 1999, Ap
422	28	50.0	110	7	US-11-064-174-65	Sequence 65, Appl	495	28	50.0	249	7	US-11-266-444-1962	Sequence 1962, Ap
423	28	50.0	111	7	US-11-112-240-4	Sequence 4, Appli	496	28	50.0	249	7	US-11-266-444-1968	Sequence 1968, Ap
424	28	50.0	111	7	US-11-112-304A-4	Sequence 20, Appli	497	28	50.0	249	7	US-11-266-444-1970	Sequence 1970, Ap
425	28	50.0	111	7	US-11-201-825-20	Sequence 20, Appl	498	28	50.0	249	7	US-11-266-444-1984	Sequence 1984, Ap
426	28	50.0	111	7	US-11-201-825-33	Sequence 33, Appl	499	28	50.0	249	7	US-11-266-444-1997	Sequence 1997, Ap
427	28	50.0	111	7	US-11-221-281-43	Sequence 43, Appl	500	28	50.0	249	7	US-11-266-444-1999	Sequence 1999, Ap
428	28	50.0	112	7	US-11-165-023-8	Sequence 8, Appli	501	28	50.0	250	7	US-11-054-515-1280	Sequence 1280, Ap
429	28	50.0	112	7	US-11-072-512-2912	Sequence 2912, Ap	502	28	50.0	250	7	US-11-054-515-1280	Sequence 2074, Ap
430	28	50.0	113	7	US-11-097-812-188	Sequence 188, App	503	28	50.0	250	7	US-11-054-515-2074	Sequence 2093, Ap
431	28	50.0	113	7	US-11-096-568A-5657	Sequence 5657, Ap	504	28	50.0	250	7	US-11-054-515-2097	Sequence 2097, Ap
432	28	50.0	117	7	US-11-000-463-271	Sequence 271, App	505	28	50.0	250	7	US-11-054-515-1280	Sequence 1280, Ap
433	28	50.0	122	6	US-10-993-543-38	Sequence 38, Appl	506	28	50.0	250	7	US-11-266-444-2074	Sequence 2074, Ap
434	28	50.0	125	6	US-11-156-084-152	Sequence 152, App	507	28	50.0	250	7	US-11-266-444-2093	Sequence 2093, Ap
435	28	50.0	127	6	US-10-721-763-35	Sequence 35, Appl	508	28	50.0	250	7	US-11-266-444-2097	Sequence 2097, Ap
436	28	50.0	127	7	US-11-089-872-5	Sequence 5, Appli	509	28	50.0	251	6	US-10-527-500-3	Sequence 3, Appli
437	28	50.0	139	7	US-11-096-568A-110	Sequence 110, App	510	28	50.0	251	7	US-11-054-515-904	Sequence 904, App
438	28	50.0	142	7	US-11-096-568A-5656	Sequence 5656, Ap	511	28	50.0	251	7	US-11-054-515-1133	Sequence 1133, Ap
439	28	50.0	144	7	US-11-072-512-3457	Sequence 3457, Ap	512	28	50.0	251	7	US-11-054-515-1154	Sequence 1154, Ap
440	28	50.0	164	7	US-11-098-686-11392	Sequence 11392, A	513	28	50.0	251	7	US-11-054-515-1213	Sequence 1213, Ap
441	28	50.0	164	7	US-11-124-367A-453	Sequence 453, App	514	28	50.0	251	7	US-11-054-515-1225	Sequence 1225, Ap
442	28	50.0	164	7	US-11-124-367A-454	Sequence 454, App	515	28	50.0	251	7	US-11-266-444-1225	Sequence 1225, Ap
443	28	50.0	168	7	US-11-096-568A-23106	Sequence 23106, A	516	28	50.0	251	7	US-11-266-444-1585	Sequence 1585, Ap
444	28	50.0	177	7	US-11-087-099-6716	Sequence 6716, Ap	517	28	50.0	251	7	US-11-054-515-1712	Sequence 1712, Ap
445	28	50.0	177	7	US-11-096-568A-8297	Sequence 8297, Ap	518	28	50.0	251	7	US-11-054-515-2001	Sequence 2001, Ap
446	28	50.0	192	6	US-10-980-388-85	Sequence 85, Appl	519	28	50.0	251	7	US-11-266-444-904	Sequence 904, App
447	28	50.0	207	7	US-11-129-076-10	Sequence 10, Appl	520	28	50.0	251	7	US-11-266-444-1133	Sequence 1133, Ap
448	28	50.0	210	7	US-11-096-568A-20894	Sequence 20894, A	521	28	50.0	251	7	US-11-266-444-1154	Sequence 1213, Ap
449	28	50.0	213	7	US-11-096-568A-5618	Sequence 5618, App	522	28	50.0	251	7	US-11-266-444-1213	Sequence 1225, Ap
450	28	50.0	226	7	US-11-096-568A-10736	Sequence 10736, A	523	28	50.0	251	7	US-11-266-444-1585	Sequence 1585, Ap
451	28	50.0	232	7	US-11-096-568A-26802	Sequence 26802, A	524	28	50.0	251	7	US-11-266-444-1712	Sequence 1712, Ap
452	28	50.0	232	7	US-11-172-740-2256	Sequence 2226, Ap	525	28	50.0	251	7	US-11-266-444-2001	Sequence 2001, Ap
453	28	50.0	233	7	US-11-096-568A-2884	Sequence 2884, Ap	526	28	50.0	252	6	US-10-527-500-19	Sequence 19, Appl
454	28	50.0	233	7	US-11-096-568A-2886	Sequence 2886, Ap	527	28	50.0	252	7	US-11-054-515-1144	Sequence 1144, Ap
455	28	50.0	235	6	US-10-537-897-15	Sequence 15, Appl	528	28	50.0	252	7	US-11-054-515-1221	Sequence 1221, Ap
456	28	50.0	235	7	US-11-172-740-556	Sequence 556, App	529	28	50.0	252	7	US-11-054-515-1378	Sequence 1378, Ap
457	28	50.0	236	7	US-11-139-499-10	Sequence 10, Appl	530	28	50.0	252	7	US-11-054-515-1505	Sequence 1505, Ap
458	28	50.0	236	7	US-11-096-568A-21748	Sequence 21748, A	531	28	50.0	252	7	US-11-054-515-1506	Sequence 1506, Ap
459	28	50.0	241	7	US-11-096-568A-5617	Sequence 5617, Ap	532	28	50.0	252	7	US-11-054-515-1575	Sequence 1575, Ap
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463	28	50.0	245	7	US-11-054-515-1516	Sequence 1516, Ap	536	28	50.0	252	7	US-11-266-444-1378	

537	28	50.0	252	7	US-11-266-444-1505	Sequence 1505, Ap	610	28	50.0	352	6	US-10-498-026-116	Sequence 116, App
538	28	50.0	252	7	US-11-266-444-1506	Sequence 1506, Ap	611	28	50.0	356	6	US-10-055-877-184	Sequence 184, App
539	28	50.0	252	7	US-11-266-444-1507	Sequence 1507, Ap	612	28	50.0	356	6	US-10-055-877-185	Sequence 185, App
540	28	50.0	253	7	US-11-054-515-1235	Sequence 1235, Ap	613	28	50.0	361	7	US-11-129-143-108	Sequence 108, App
541	28	50.0	253	7	US-11-054-515-1358	Sequence 1358, Ap	614	28	50.0	363	7	US-11-087-099-12394	Sequence 12394, A
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543	28	50.0	253	7	US-11-054-515-1895	Sequence 1895, Ap	616	28	50.0	369	7	US-11-087-099-9549	Sequence 9549, Ap
544	28	50.0	253	7	US-11-054-515-1981	Sequence 1951, Ap	617	28	50.0	369	7	US-11-096-568A-28415	Sequence 28415, A
545	28	50.0	253	7	US-11-054-515-2098	Sequence 2098, Ap	618	28	50.0	371	7	US-11-096-568A-8074	Sequence 8074, Ap
546	28	50.0	253	7	US-11-054-515-2101	Sequence 2101, Ap	619	28	50.0	377	7	US-11-152-892-8	Sequence 8, Appl
547	28	50.0	253	7	US-11-266-444-1235	Sequence 1235, Ap	620	28	50.0	378	7	US-11-152-892-7	Sequence 7, Appl
548	28	50.0	253	7	US-11-266-444-1358	Sequence 1358, Ap	621	28	50.0	383	6	US-10-506-454-82	Sequence 82, Appl
549	28	50.0	253	7	US-11-266-444-1359	Sequence 1359, Ap	622	28	50.0	384	7	US-11-087-099-5448	Sequence 5448, Ap
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552	28	50.0	253	7	US-11-266-444-2098	Sequence 2098, Ap	625	28	50.0	392	7	US-11-087-099-12003	Sequence 12003, A
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555	28	50.0	254	7	US-11-054-515-1594	Sequence 1584, Ap	628	28	50.0	417	7	US-11-096-568A-20641	Sequence 20641, A
556	28	50.0	254	7	US-11-054-515-1981	Sequence 1961, Ap	629	28	50.0	423	7	US-11-031-206-204	Sequence 204, App
557	28	50.0	254	7	US-11-054-515-1973	Sequence 1973, Ap	630	28	50.0	426	7	US-11-031-206-160	Sequence 160, App
558	28	50.0	254	7	US-11-054-515-1983	Sequence 1983, Ap	631	28	50.0	437	7	US-11-096-568A-20640	Sequence 20640, A
559	28	50.0	254	7	US-11-067-323-925	Sequence 925, App	632	28	50.0	446	7	US-11-108-172-1121	Sequence 1121, Ap
560	28	50.0	254	7	US-11-266-444-1508	Sequence 1508, Ap	633	28	50.0	447	7	US-11-096-568A-32518	Sequence 32518, A
561	28	50.0	254	7	US-11-266-444-1584	Sequence 1584, Ap	634	28	50.0	457	6	US-10-131-826A-236	Sequence 236, App
562	28	50.0	254	7	US-11-266-444-1981	Sequence 1961, Ap	635	28	50.0	457	6	US-10-973-115B-236	Sequence 236, App
563	28	50.0	254	7	US-11-266-444-1973	Sequence 1973, Ap	636	28	50.0	464	7	US-11-096-568A-3439	Sequence 3439, Ap
564	28	50.0	254	7	US-11-266-444-1983	Sequence 1983, Ap	637	28	50.0	465	7	US-11-087-099-11818	Sequence 11818, A
565	28	50.0	255	7	US-11-054-515-1012	Sequence 1012, Ap	638	28	50.0	482	7	US-11-096-568A-8958	Sequence 8958, Ap
566	28	50.0	255	7	US-11-054-515-1828	Sequence 1828, Ap	639	28	50.0	489	7	US-11-096-568A-3438	Sequence 3438, Ap
567	28	50.0	255	7	US-11-266-444-1012	Sequence 1012, Ap	640	28	50.0	494	6	US-10-934-944-234	Sequence 234, App
568	28	50.0	255	7	US-11-266-444-1828	Sequence 1828, Ap	641	28	50.0	494	7	US-11-116-881A-443	Sequence 443, App
569	28	50.0	256	7	US-11-054-515-1967	Sequence 1967, Ap	642	28	50.0	495	7	US-11-072-512-3469	Sequence 3469, Ap
570	28	50.0	256	7	US-11-096-568A-26801	Sequence 26801, A	643	28	50.0	498	7	US-11-096-568A-30759	Sequence 30759, A
571	28	50.0	256	7	US-11-266-444-1967	Sequence 1967, Ap	644	28	50.0	502	7	US-11-087-099-8024	Sequence 8024, Ap
572	28	50.0	257	7	US-11-087-099-6897	Sequence 6897, Ap	645	28	50.0	521	6	US-10-793-626-532	Sequence 532, App
573	28	50.0	257	7	US-11-054-515-1841	Sequence 1841, Ap	646	28	50.0	525	7	US-11-096-568A-12402	Sequence 12402, A
574	28	50.0	258	7	US-11-201-825-8	Sequence 8, Appl	647	28	50.0	531	7	US-11-193-544-31	Sequence 31, Appl
575	28	50.0	258	7	US-11-201-825-25	Sequence 25, Appl	648	28	50.0	532	7	US-11-183-914-12	Sequence 12, Appl
576	28	50.0	258	7	US-11-266-444-1841	Sequence 1841, Ap	649	28	50.0	560	7	US-11-096-568A-12401	Sequence 12401, A
577	28	50.0	259	7	US-11-054-515-1043	Sequence 1043, Ap	650	28	50.0	574	6	US-10-527-771-14	Sequence 14, Appl
578	28	50.0	259	7	US-11-054-515-1497	Sequence 1497, Ap	651	28	50.0	586	7	US-11-096-568A-32517	Sequence 32517, A
579	28	50.0	259	7	US-11-266-444-1043	Sequence 1043, Ap	652	28	50.0	589	7	US-11-096-568A-32516	Sequence 32516, A
580	28	50.0	259	7	US-11-266-444-1497	Sequence 1497, Ap	653	28	50.0	617	6	US-10-993-561-890	Sequence 890, App
581	28	50.0	260	7	US-11-054-515-1282	Sequence 1282, Ap	654	28	50.0	645	6	US-10-793-626-2984	Sequence 2984, Ap
582	28	50.0	260	7	US-11-266-444-1282	Sequence 1282, Ap	655	28	50.0	656	6	US-10-993-561-871	Sequence 871, App
583	28	50.0	262	7	US-11-054-515-1836	Sequence 1836, Ap	656	28	50.0	663	6	US-10-501-035-369	Sequence 369, App
584	28	50.0	262	7	US-11-266-444-1836	Sequence 1836, Ap	657	28	50.0	679	6	US-10-993-561-872	Sequence 872, App
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586	28	50.0	266	7	US-11-096-568A-20343	Sequence 20343, A	659	28	50.0	693	7	US-11-098-686-11343	Sequence 11343, A
587	28	50.0	272	7	US-11-119-212-31	Sequence 31, Appl	660	28	50.0	707	7	US-11-052-554A-214	Sequence 214, App
588	28	50.0	276	7	US-11-096-568A-20342	Sequence 20342, A	661	28	50.0	730	6	US-10-821-234-1019	Sequence 1019, Ap
589	28	50.0	277	7	US-11-096-568A-20893	Sequence 20893, A	662	28	50.0	761	7	US-11-057-047-6	Sequence 6, Appl
590	28	50.0	280	7	US-11-096-568A-10735	Sequence 10735, A	663	28	50.0	774	7	US-11-070-627-7	Sequence 7, Appl
591	28	50.0	281	7	US-11-087-099-6234	Sequence 6234, Ap	664	28	50.0	797	6	US-10-514-531-5	Sequence 5, Appl
592	28	50.0	288	7	US-11-096-568A-23817	Sequence 23817, A	665	28	50.0	798	6	US-10-514-531-2	Sequence 2, Appl
593	28	50.0	298	7	US-11-074-176-6	Sequence 6, Appl	666	28	50.0	835	6	US-10-501-039-4	Sequence 4, Appl
594	28	50.0	299	7	US-11-044-347B-9	Sequence 9, Appl	667	28	50.0	902	7	US-11-182-016-36	Sequence 36, Appl
595	28	50.0	303	7	US-11-072-512-3997	Sequence 3997, Ap	668	28	50.0	952	7	US-11-087-099-3514	Sequence 3514, Ap
596	28	50.0	305	7	US-11-096-568A-3440	Sequence 3440, Ap	669	28	50.0	952	7	US-11-087-099-7009	Sequence 7009, Ap
597	28	50.0	307	6	US-10-467-657-7006	Sequence 7006, Ap	670	28	50.0	1039	7	US-11-096-568A-30324	Sequence 30324, A
598	28	50.0	310	7	US-11-245-053-11	Sequence 11, Appl	671	28	50.0	1055	7	US-11-096-568A-30323	Sequence 30323, A
599	28	50.0	315	7	US-11-044-347B-2	Sequence 2, Appl	672	28	50.0	1059	7	US-11-062	Sequence 5, Appl
600	28	50.0	318	6	US-10-548-748-40	Sequence 40, Appl	673	28	50.0	1063	7	US-11-096-568A-30322	Sequence 148, App
601	28	50.0	324	7	US-11-096-568A-28417	Sequence 28417, A	674	28	50.0	1066	7	US-11-169-041-148	Sequence 8, Appl
602	28	50.0	327	7	US-11-096-568A-8076	Sequence 8076, Ap	675	28	50.0	1084	7	US-11-062	Sequence 69, Appl
603	28	50.0	327	7	US-11-096-568A-23291	Sequence 23291, A	676	28	50.0	1236	7	US-11-193-544-69	Sequence 69, Appl
604	28	50.0	328	7	US-11-096-568A-28416	Sequence 28416, A	677	28	50.0	1366	7	US-11-169-041-174	Sequence 174, App
605	28	50.0	330	7	US-11-072-512-2839	Sequence 2839, Ap	678	28	50.0	1501	6	US-10-793-626-2850	Sequence 2850, Ap
606	28	50.0	337	7	US-11-096-568A-8075	Sequence 8075, Ap	679	28	50.0	1728	7	US-11-019-711-72	Sequence 72, Appl
607	28	50.0	342	7	US-11-087-099-4284	Sequence 4284, Ap	680	28	50.0	1992	7	US-11-069-834-58	Sequence 58, Appl
608	28	50.0	344	7	US-11-186-284-138	Sequence 138, App	681	28	50.0	1995	7	US-11-069-834-60	Sequence 60, Appl
609	28	50.0	348	7	US-11-096-568A-10734	Sequence 10734, A	682	28	50.0	2000	7	US-11-069-834-56	Sequence 56, Appl

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684	27.5	49.1	242	6	US-10-506-454-364	Sequence 364, App	757	27	48.2	164	7	US-11-087-099-5431	Sequence 5431, Ap
685	27.5	49.1	349	7	US-11-108-528-44	Sequence 44, App	758	27	48.2	170	7	US-11-096-568A-22202	Sequence 22202, A
686	27.5	49.1	349	7	US-11-108-528-46	Sequence 46, App	759	27	48.2	172	7	US-11-087-099-9391	Sequence 9391, Ap
687	27.5	49.1	368	7	US-11-060-008-13	Sequence 13, App	760	27	48.2	175	7	US-11-096-568A-842	Sequence 842, App
688	27.5	49.1	546	7	US-11-072-512-2051	Sequence 2051, Ap	761	27	48.2	177	6	US-10-821-234-1350	Sequence 1350, Ap
689	27.5	49.1	571	7	US-11-121-438-12	Sequence 12, App	762	27	48.2	178	7	US-11-087-099-2412	Sequence 2412, Ap
690	27.5	49.1	915	6	US-10-647-956A-6	Sequence 6, App	763	27	48.2	181	7	US-11-087-099-10726	Sequence 10726, A
691	27.5	49.1	1126	7	US-11-110-480-7	Sequence 7, App	764	27	48.2	185	7	US-11-096-568A-22587	Sequence 22587, A
692	27.5	49.1	1126	7	US-11-110-480-9	Sequence 9, App	765	27	48.2	189	6	US-10-131-826A-232	Sequence 232, App
693	27.5	49.1	1126	7	US-11-110-480-16	Sequence 16, App	766	27	48.2	189	6	US-10-973-115B-232	Sequence 232, App
694	27.5	49.1	1126	7	US-11-110-480-27	Sequence 27, App	767	27	48.2	196	7	US-11-087-099-7577	Sequence 7577, Ap
695	27.5	49.1	1126	7	US-11-110-480-37	Sequence 37, App	768	27	48.2	196	7	US-11-135-603-10	Sequence 10, Appl
696	27.5	49.1	1126	7	US-11-110-480-47	Sequence 47, App	769	27	48.2	207	7	US-11-096-568A-19059	Sequence 19059, A
697	27.5	49.1	1126	7	US-11-110-480-59	Sequence 59, App	770	27	48.2	208	6	US-10-467-657-2658	Sequence 2658, Ap
698	27.5	49.1	1126	7	US-11-110-480-82	Sequence 82, App	771	27	48.2	213	7	US-11-096-568A-3517	Sequence 3517, Ap
699	27.5	49.1	1126	7	US-11-110-480-88	Sequence 88, App	772	27	48.2	219	7	US-11-224-623-11	Sequence 11, Appl
700	27	48.2	9	6	US-10-880-238-184	Sequence 184, App	773	27	48.2	222	6	US-10-512-512-1	Sequence 1, Appl
701	27	48.2	9	7	US-11-102-743-5	Sequence 5, App	774	27	48.2	222	7	US-11-096-568A-14563	Sequence 14563, A
702	27	48.2	9	7	US-11-051-453-18	Sequence 18, App	775	27	48.2	228	7	US-11-096-568A-17939	Sequence 17939, A
703	27	48.2	9	7	US-11-224-623-3	Sequence 3, App	776	27	48.2	232	7	US-11-096-568A-28090	Sequence 28090, A
704	27	48.2	9	7	US-11-221-470-22	Sequence 22, App	777	27	48.2	232	7	US-11-087-099-9351	Sequence 9351, Ap
705	27	48.2	17	7	US-11-062-186-41	Sequence 41, App	778	27	48.2	236	7	US-11-096-568A-10192	Sequence 10192, A
706	27	48.2	19	7	US-11-228-293-16	Sequence 16, App	779	27	48.2	236	6	US-10-927-641-68	Sequence 68, Appl
707	27	48.2	19	7	US-11-228-319-16	Sequence 16, App	780	27	48.2	238	7	US-10-219-510-21	Sequence 21, Appl
708	27	48.2	22	6	US-10-512-512-22	Sequence 22, App	781	27	48.2	239	7	US-11-072-512-2603	Sequence 2603, Ap
709	27	48.2	26	6	US-10-512-512-8	Sequence 8, App	782	27	48.2	240	7	US-11-239-510-11	Sequence 11, Appl
710	27	48.2	27	6	US-10-512-512-23	Sequence 23, App	783	27	48.2	247	7	US-11-054-515-1978	Sequence 1978, Ap
711	27	48.2	31	6	US-10-512-512-9	Sequence 9, App	784	27	48.2	247	7	US-11-096-568A-21177	Sequence 21177, A
712	27	48.2	34	6	US-10-467-657-498	Sequence 498, Ap	785	27	48.2	247	7	US-11-266-444-1978	Sequence 1978, Ap
713	27	48.2	36	6	US-10-532-480-23	Sequence 23, App	786	27	48.2	249	7	US-11-054-515-1986	Sequence 1986, Ap
714	27	48.2	53	7	US-11-004-399-2901	Sequence 2901, Ap	787	27	48.2	249	7	US-11-266-444-1986	Sequence 1986, Ap
715	27	48.2	54	5	US-09-978-360A-514	Sequence 514, App	788	27	48.2	250	7	US-11-239-510-15	Sequence 15, Appl
716	27	48.2	78	6	US-10-467-657-8126	Sequence 8126, Ap	789	27	48.2	251	7	US-11-096-568A-10191	Sequence 10191, A
717	27	48.2	79	7	US-11-096-568A-4038	Sequence 4038, Ap	790	27	48.2	252	7	US-11-054-515-1557	Sequence 1557, Ap
718	27	48.2	82	6	US-10-821-234-1594	Sequence 1594, Ap	791	27	48.2	252	7	US-11-054-515-2100	Sequence 2100, Ap
719	27	48.2	82	6	US-11-096-568A-4037	Sequence 4037, Ap	792	27	48.2	252	7	US-11-096-568A-33167	Sequence 33167, A
720	27	48.2	87	6	US-10-506-454-125	Sequence 125, App	793	27	48.2	252	7	US-11-266-444-1557	Sequence 1557, Ap
721	27	48.2	102	7	US-11-049-536-42	Sequence 42, App	794	27	48.2	252	6	US-10-524-647-84	Sequence 84, Appl
722	27	48.2	102	7	US-11-199-739-42	Sequence 42, App	795	27	48.2	253	6	US-10-524-972-92	Sequence 92, Appl
723	27	48.2	103	6	US-10-771-257-99	Sequence 99, App	796	27	48.2	253	6	US-10-541-513-4	Sequence 4, Appl
724	27	48.2	103	6	US-10-771-257-100	Sequence 100, App	797	27	48.2	253	6	US-11-239-510-17	Sequence 17, Appl
725	27	48.2	103	6	US-10-771-257-110	Sequence 110, App	798	27	48.2	253	7	US-11-054-515-1862	Sequence 1862, Ap
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## ALIGNMENTS

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; Publication No. US20050260206A1
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; APPLICANT: KYOWA HAKKO KOGYO CO., LTD.
; TITLE OF INVENTION: Agents for treatment of cancer using recombinant anti-GD3 antibody
; FILE REFERENCE: 11374WO1
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: JP2001-097483
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 9
; TYPE: PRT
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US-10-473-037-8
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Best Local Similarity 100.0%; Pred. No. 1.4e+05;
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; APPLICANT: KYOWA HAKKO KOGYO CO., LTD.
; TITLE OF INVENTION: Agents for treatment of cancer using recombinant anti-GD3 antibody
; FILE REFERENCE: 11374WO1
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: JP2001-097483
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; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.0
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US-10-473-037-10
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; TITLE OF INVENTION: Agents for treatment of cancer using recombinant anti-GD3 antibody
; FILE REFERENCE: 11374WO1
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: JP2001-097483
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 50
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; TITLE OF INVENTION: Agents for treatment of cancer using recombinant anti-GD3 antibody
; FILE REFERENCE: 11374WO1
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: JP2001-097483
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 50
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; GENERAL INFORMATION:  
; APPLICANT: SHITARA, KENYA  
; APPLICANT: HANAI, NOBUO  
; APPLICANT: HASEGAWA, MAMORU  
; APPLICANT: MIYAJI, HIROMASA  
; APPLICANT: KUMANA, YOSHIHISA  
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY  
; FILE REFERENCE: 249-101  
; CURRENT APPLICATION NUMBER: US/11/228,293  
; CURRENT FILING DATE: 2005-09-19  
; PRIOR APPLICATION NUMBER: US/09/225,322  
; PRIOR FILING DATE: 1999-01-05  
; PRIOR APPLICATION NUMBER: US 08/454,680  
; PRIOR FILING DATE: 1995-05-31  
; PRIOR APPLICATION NUMBER: US 08/408,133  
; PRIOR FILING DATE: 1995-03-21  
; PRIOR APPLICATION NUMBER: US 08/292,178  
; PRIOR FILING DATE: 1994-08-17  
; PRIOR APPLICATION NUMBER: US/07/947,674  
; PRIOR FILING DATE: 1992-09-17  
; PRIOR APPLICATION NUMBER: JP 3-238375  
; PRIOR FILING DATE: 1991-09-18  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 10  
; LENGTH: 128  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: cDNA KM-641  
US-11-228-293-10

Query Match 100.0%; Score 56; DB 7; Length 128;  
Best Local Similarity 100.0%; Pred. No. 0.0011;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HOYSKLPWT 9  
|||||  
Db 109 HOYSKLPWT 117

## RESULT 6

US-11-228-293-19  
; Sequence 19, Application US/11228293  
; Publication No. US20060057139A1  
; GENERAL INFORMATION:  
; APPLICANT: SHITARA, KENYA  
; APPLICANT: HANAI, NOBUO  
; APPLICANT: HASEGAWA, MAMORU  
; APPLICANT: MIYAJI, HIROMASA  
; APPLICANT: KUMANA, YOSHIHISA  
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY  
; FILE REFERENCE: 249-101  
; CURRENT APPLICATION NUMBER: US/11/228,293  
; CURRENT FILING DATE: 2005-09-19  
; PRIOR APPLICATION NUMBER: US/09/225,322  
; PRIOR FILING DATE: 1999-01-05  
; PRIOR APPLICATION NUMBER: US 08/454,680  
; PRIOR FILING DATE: 1995-05-31  
; PRIOR APPLICATION NUMBER: US 08/408,133  
; PRIOR FILING DATE: 1995-03-21  
; PRIOR APPLICATION NUMBER: US 08/292,178

; PRIOR FILING DATE: 1994-08-17  
; PRIOR APPLICATION NUMBER: US/07/947,674  
; PRIOR FILING DATE: 1992-09-17  
; PRIOR APPLICATION NUMBER: JP 3-238375  
; PRIOR FILING DATE: 1991-09-18  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 19  
; LENGTH: 128  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: light chain  
; OTHER INFORMATION: variable region  
US-11-228-293-19

Query Match 100.0%; Score 56; DB 7; Length 128;  
Best Local Similarity 100.0%; Pred. No. 0.0011;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HOYSKLPWT 9  
|||||  
Db 109 HOYSKLPWT 117

## RESULT 7

US-11-228-319-10  
; Sequence 10, Application US/11228319  
; Publication No. US20060058512A1  
; GENERAL INFORMATION:  
; APPLICANT: SHITARA, KENYA  
; APPLICANT: HANAI, NOBUO  
; APPLICANT: HASEGAWA, MAMORU  
; APPLICANT: MIYAJI, HIROMASA  
; APPLICANT: KUMANA, YOSHIHISA  
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY  
; FILE REFERENCE: 249-101  
; CURRENT APPLICATION NUMBER: US/11/228,319  
; CURRENT FILING DATE: 2005-09-19  
; PRIOR APPLICATION NUMBER: US/09/225,322  
; PRIOR FILING DATE: 1999-01-05  
; PRIOR APPLICATION NUMBER: US 08/454,680  
; PRIOR FILING DATE: 1995-05-31  
; PRIOR APPLICATION NUMBER: US 08/408,133  
; PRIOR FILING DATE: 1995-03-21  
; PRIOR APPLICATION NUMBER: US 08/292,178  
; PRIOR FILING DATE: 1994-08-17  
; PRIOR APPLICATION NUMBER: US/07/947,674  
; PRIOR FILING DATE: 1992-09-17  
; PRIOR APPLICATION NUMBER: JP 3-238375  
; PRIOR FILING DATE: 1991-09-18  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 10  
; LENGTH: 128  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: cDNA KM-641  
US-11-228-319-10

Query Match 100.0%; Score 56; DB 7; Length 128;  
Best Local Similarity 100.0%; Pred. No. 0.0011;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HOYSKLPWT 9  
|||||  
Db 109 HOYSKLPWT 117

## RESULT 8

US-11-228-319-19  
; Sequence 19, Application US/11228319



```
; Publication No. US20060058512A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUMANA, YOSHIHISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/11/228,319
; CURRENT FILING DATE: 2005-09-19
; PRIOR APPLICATION NUMBER: US/09/225,322
; PRIOR FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: US 08/454,680
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
; PRIOR APPLICATION NUMBER: US07/947,674
; PRIOR FILING DATE: 1992-09-17
; PRIOR APPLICATION NUMBER: JP 3-238375
; PRIOR FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:light chain
; OTHER INFORMATION: variable region
US-11-228-319-19

Query Match 100.0%; Score 56; DB 7; Length 128;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HOYSKLPWT 9
Db 109 HOYSKLPWT 117

RESULT 9
US-11-143-077-6
; Sequence 6, Application US/11/143077
; Publication No. US20060024295A1
; GENERAL INFORMATION:
; APPLICANT: Brunetta, Paul G.
; TITLE OF INVENTION: METHOD FOR TREATING LUPUS
; FILE REFERENCE: P2133R1
; CURRENT APPLICATION NUMBER: US/11/143,077
; CURRENT FILING DATE: 2005-06-02
; PRIOR APPLICATION NUMBER: US 60/577,235
; PRIOR FILING DATE: 2004-06-04
; PRIOR APPLICATION NUMBER: US 60/617,997
; PRIOR FILING DATE: 2004-10-11
; NUMBER OF SEQ ID NOS: 24
; SEQ ID NO 6
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized
US-11-143-077-6

Query Match 71.4%; Score 40; DB 7; Length 27;
Best Local Similarity 75.0%; Pred. No. 0.28;
Matches 6; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

QY 2 QYSKLPWT 9
Db 20 QYNSLPWT 27

; Publication No. US20060058512A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUMANA, YOSHIHISA
; TITLE OF INVENTION: METHOD FOR TREATING SJOGERN'S SYNDROME
; FILE REFERENCE: P2149R1
; CURRENT APPLICATION NUMBER: US/11/187,364
; CURRENT FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US 60/590,302
; PRIOR FILING DATE: 2004-07-22
; NUMBER OF SEQ ID NOS: 36
; SEQ ID NO 6
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized
US-11-187-364-6

Query Match 71.4%; Score 40; DB 7; Length 27;
Best Local Similarity 75.0%; Pred. No. 0.28;
Matches 6; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

QY 2 QYSKLPWT 9
Db 20 QYNSLPWT 27

RESULT 11
US-11-154-337-5
; Sequence 5, Application US/11/154337
; Publication No. US20060013819A1
; GENERAL INFORMATION:
; APPLICANT: KELSEY, STEPHEN M.
; TITLE OF INVENTION: THERAPY OF PLATINUM-RESISTANT CANCER
; FILE REFERENCE: P2146R1
; CURRENT APPLICATION NUMBER: US/11/154,337
; CURRENT FILING DATE: 2005-06-15
; PRIOR APPLICATION NUMBER: US 60/580,333
; PRIOR FILING DATE: 2004-06-16
; NUMBER OF SEQ ID NOS: 17
; SEQ ID NO 5
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-11-154-337-5

Query Match 71.4%; Score 40; DB 7; Length 107;
Best Local Similarity 75.0%; Pred. No. 1;
Matches 6; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

QY 2 QYSKLPWT 9
Db 90 QYNSLPWT 97

RESULT 12
US-11-182-908-5
; Sequence 5, Application US/11/182908
; Publication No. US20060018899A1
; GENERAL INFORMATION:
; APPLICANT: KAO, YUNG-HSIANG
; APPLICANT: VANDERLAAN, MARTIN
; TITLE OF INVENTION: HER2 ANTIBODY COMPOSITIONS
; FILE REFERENCE: P2105R1
; CURRENT APPLICATION NUMBER: US/11/182,908
; CURRENT FILING DATE: 2005-07-15
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; PRIOR APPLICATION NUMBER: US 60/590,202  
; PRIOR FILING DATE: 2004-07-22  
; NUMBER OF SEQ ID NOS: 24  
; SEQ ID NO 5  
; LENGTH: 107  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: sequence is synthesized  
US-11-182-908-5

Query Match 71.4%; Score 40; DB 7; Length 107;  
Best Local Similarity 75.0%; Pred. No. 1;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYSKLPWT 9  
||: ||||  
Db 90 QYNSLPWT 97

RESULT 13  
US-11-102-120-5  
; Sequence 5, Application US/11102120  
; Publication No. US20060034840A1  
; GENERAL INFORMATION:  
; APPLICANT: AGUS, David B.  
; TITLE OF INVENTION: ErbB Antagonists for Pain Therapy  
; FILE REFERENCE: 39766-0138 US  
; CURRENT APPLICATION NUMBER: US/11/102,120  
; CURRENT FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: US 60/561,076  
; PRIOR FILING DATE: 2004-04-08  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5  
; LENGTH: 107  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Consensus human framework for the humanized  
; OTHER INFORMATION: antibody hum KI (variable light)  
US-11-102-120-5

Query Match 71.4%; Score 40; DB 7; Length 107;  
Best Local Similarity 75.0%; Pred. No. 1;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYSKLPWT 9  
||: ||||  
Db 90 QYNSLPWT 97

RESULT 14  
US-11-223-361-5  
; Sequence 5, Application US/11223361  
; Publication No. US20060034842A1  
; GENERAL INFORMATION:  
; APPLICANT: Adams, Camellia W.  
; APPLICANT: Presta, Leonard G.  
; APPLICANT: Slivkowski, Mark X.  
; TITLE OF INVENTION: Humanized Anti-ErbB2 Antibodies and Treatment with  
; FILE REFERENCE: P1467R2  
; CURRENT APPLICATION NUMBER: US/11/223,361  
; CURRENT FILING DATE: 2005-09-09  
; PRIOR APPLICATION NUMBER: US/09/602,812  
; PRIOR FILING DATE: 2000-06-23  
; PRIOR APPLICATION NUMBER: US 60/141,316  
; PRIOR FILING DATE: 1999-06-25  
; NUMBER OF SEQ ID NOS: 13  
; SEQ ID NO 5  
; LENGTH: 107  
; TYPE: PRT

; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: light chain consensus sequence  
US-11-223-361-5

Query Match 71.4%; Score 40; DB 7; Length 107;  
Best Local Similarity 75.0%; Pred. No. 1;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYSKLPWT 9  
||: ||||  
Db 90 QYNSLPWT 97

RESULT 15  
US-10-665-658-3  
; Sequence 3, Application US/10665658  
; Publication No. US20050276801A1  
; GENERAL INFORMATION:  
; APPLICANT: Jardieu, Paula M.  
; APPLICANT: Presta, Leonard G.  
; TITLE OF INVENTION: Humanized Anti-CD11a Antibodies  
; NUMBER OF SEQUENCES: 71  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/665,658  
; FILING DATE: 19-Sep-2003  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/031971  
; FILING DATE: 27-NOV-1996  
; APPLICATION NUMBER: 08/974899  
; FILING DATE: 20-NOV-1997  
; APPLICATION NUMBER: 09/420745  
; FILING DATE: 20-OCT-1999  
; APPLICATION NUMBER: 09/975798  
; FILING DATE: 28-FEB-2001  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Tan, Lee K.  
; REGISTRATION NUMBER: 39,447  
; REFERENCE/DOCKET NUMBER: P1014R1C1D1C1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-4462  
; TELEFAX: 650/952-3881  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 108 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
US-10-665-658-3

Query Match 71.4%; Score 40; DB 6; Length 108;  
Best Local Similarity 75.0%; Pred. No. 1;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYSKLPWT 9  
||: ||||  
Db 90 QYNSLPWT 97

RESULT 16

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US-11-120-338-3
; Sequence 3, Application US/11120338
; Publication No. US20050271658A1
; GENERAL INFORMATION:
; APPLICANT: BRUNETTA, PAUL G.
; APPLICANT: GREWAL, IQBAL S.
; APPLICANT: WALICKE, PATRICIA A.
; TITLE OF INVENTION: PREVENTING AUTOIMMUNE DISEASE
; FILE REFERENCE: P2079R2
; CURRENT APPLICATION NUMBER: US/11/120,338
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: US 60/568,460
; PRIOR FILING DATE: 2004-05-05
; NUMBER OF SEQ ID NOS: 25
; SEQ ID NO 3
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-11-120-338-3

Query Match          71.4%; Score 40; DB 7; Length 108;
Best Local Similarity 75.0%; Pred. No. 1;
Matches 6; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

QY      2 QYSKLPWT 9
Db      90 QYNSLPWT 97

RESULT 17
US-11-106-820-3
; Sequence 3, Application US/11106820
; Publication No. US2006002930A1
; GENERAL INFORMATION:
; APPLICANT: BRUNETTA, PAUL G
; APPLICANT: SEWELL, KATHRYN L.
; TITLE OF INVENTION: Treatment of Disorders
; FILE REFERENCE: P2102R1
; CURRENT APPLICATION NUMBER: US/11/106,820
; CURRENT FILING DATE: 2005-04-15
; PRIOR APPLICATION NUMBER: US 60/563,227
; PRIOR FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: US 60/565,098
; PRIOR FILING DATE: 2004-04-22
; NUMBER OF SEQ ID NOS: 45
; SEQ ID NO 3
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-106-820-3

Query Match          71.4%; Score 40; DB 7; Length 108;
Best Local Similarity 75.0%; Pred. No. 1;
Matches 6; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

QY      2 QYSKLPWT 9
Db      90 QYNSLPWT 97

RESULT 18
US-11-143-077-3
; Sequence 3, Application US/11143077
; Publication No. US20060024295A1
; GENERAL INFORMATION:
; APPLICANT: Brunetta, Paul G.
; TITLE OF INVENTION: METHOD FOR TREATING LUPUS
; FILE REFERENCE: P2133R1
; CURRENT APPLICATION NUMBER: US/11/143,077
; CURRENT FILING DATE: 2005-06-02
; PRIOR APPLICATION NUMBER: US 60/577,235
; PRIOR FILING DATE: 2003-12-16

US-11-190-364-3
; Sequence 3, Application US/11190364
; Publication No. US20060024300A1
; GENERAL INFORMATION:
; APPLICANT: Adams ET AL.
; TITLE OF INVENTION: Immunoglobulin Variants and Uses Thereof
; FILE REFERENCE: P1990R3C1P1
; CURRENT APPLICATION NUMBER: US/11/190,364
; CURRENT FILING DATE: 2005-07-26
; PRIOR APPLICATION NUMBER: US 60/434,115
; PRIOR FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: US 60/526,163
; PRIOR FILING DATE: 2003-12-01
; PRIOR APPLICATION NUMBER: PCT/US03/40426
; PRIOR FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: US 11/147,780
; PRIOR FILING DATE: 2005-06-07
; NUMBER OF SEQ ID NOS: 38
; SEQ ID NO 3
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized
US-11-190-364-3

Query Match          71.4%; Score 40; DB 7; Length 108;
Best Local Similarity 75.0%; Pred. No. 1;
Matches 6; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

QY      2 QYSKLPWT 9
Db      90 QYNSLPWT 97

RESULT 19
US-11-190-364-3
; Sequence 3, Application US/11190364
; Publication No. US20060024300A1
; GENERAL INFORMATION:
; APPLICANT: Adams ET AL.
; TITLE OF INVENTION: Immunoglobulin Variants and Uses Thereof
; FILE REFERENCE: P1990R3C1P1
; CURRENT APPLICATION NUMBER: US/11/190,364
; CURRENT FILING DATE: 2005-07-26
; PRIOR APPLICATION NUMBER: US 60/434,115
; PRIOR FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: US 60/526,163
; PRIOR FILING DATE: 2003-12-01
; PRIOR APPLICATION NUMBER: PCT/US03/40426
; PRIOR FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: US 11/147,780
; PRIOR FILING DATE: 2005-06-07
; NUMBER OF SEQ ID NOS: 38
; SEQ ID NO 3
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized
US-11-190-364-3

Query Match          71.4%; Score 40; DB 7; Length 108;
Best Local Similarity 75.0%; Pred. No. 1;
Matches 6; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

QY      2 QYSKLPWT 9
Db      90 QYNSLPWT 97

RESULT 20
US-11-147-780-3
; Sequence 3, Application US/11147780
; Publication No. US20060034835A1
; GENERAL INFORMATION:
; APPLICANT: Adams ET AL.
; TITLE OF INVENTION: Immunoglobulin Variants and Uses Thereof
; FILE REFERENCE: P1990R3C1
; CURRENT APPLICATION NUMBER: US/11/147,780
; CURRENT FILING DATE: 2005-06-07
; PRIOR APPLICATION NUMBER: US 60/434,115
; PRIOR FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: US 60/526,163
; PRIOR FILING DATE: 2003-12-01
; PRIOR APPLICATION NUMBER: PCT/US03/40426
; PRIOR FILING DATE: 2003-12-16
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; NUMBER OF SEQ ID NOS: 38
; SEQ ID NO 3
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized
US-11-147-780-3

Query Match 71.4%; Score 40; DB 7; Length 108;
Best Local Similarity 75.0%; Pred. No. 1;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYSKLPWT 9
||: ||||
Db 90 QYNSLPWT 97

RESULT 21
US-11-143-386-3
; Sequence 3, Application US/11143386
; Publication No. US20060051345A1
; GENERAL INFORMATION:
; APPLICANT: FROHNA, PAUL A.
; TITLE OF INVENTION: METHOD FOR TREATING MULTIPLE SCLEROSIS
; FILE REFERENCE: P2134R1
; CURRENT APPLICATION NUMBER: US/11/143,386
; CURRENT FILING DATE: 2005-06-02
; PRIOR APPLICATION NUMBER: US 60/576,993
; PRIOR FILING DATE: 2004-06-04
; NUMBER OF SEQ ID NOS: 25
; SEQ ID NO 3
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized.
US-11-143-386-3

Query Match 71.4%; Score 40; DB 7; Length 108;
Best Local Similarity 75.0%; Pred. No. 1;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYSKLPWT 9
||: ||||
Db 90 QYNSLPWT 97

RESULT 22
US-11-187-364-3
; Sequence 3, Application US/11187364
; Publication No. US20060062787A1
; GENERAL INFORMATION:
; APPLICANT: Hitraya, Elena
; TITLE OF INVENTION: METHOD FOR TREATING SJOGREN'S SYNDROME
; FILE REFERENCE: P2149R1
; CURRENT APPLICATION NUMBER: US/11/187,364
; CURRENT FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US 60/590,302
; PRIOR FILING DATE: 2004-07-22
; NUMBER OF SEQ ID NOS: 36
; SEQ ID NO 3
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-187-364-3

Query Match 71.4%; Score 40; DB 7; Length 108;
Best Local Similarity 75.0%; Pred. No. 1;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYSKLPWT 9
||: ||||
Db 90 QYNSLPWT 97

RESULT 23
US-10-981-356A-5
; Sequence 5, Application US/10981356A
; Publication No. US20060015952A1
; GENERAL INFORMATION:
; APPLICANT: FILVAROFF, ELLEN H.
; TITLE OF INVENTION: SCREENING ASSAYS AND METHODS OF TUMOR TREATMENT
; FILE REFERENCE: P2068R1
; CURRENT APPLICATION NUMBER: US/10/981,356A
; CURRENT FILING DATE: 2004-11-04
; PRIOR APPLICATION NUMBER: US 60/520,398
; PRIOR FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US 60/557,951
; PRIOR FILING DATE: 2004-03-31
; NUMBER OF SEQ ID NOS: 45
; SEQ ID NO 5
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized
US-10-981-356A-5

Query Match 71.4%; Score 40; DB 6; Length 109;
Best Local Similarity 75.0%; Pred. No. 1.1;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYSKLPWT 9
||: ||||
Db 90 QYNSLPWT 97

RESULT 24
US-11-096-046-5
; Sequence 5, Application US/11096046
; Publication No. US20050276802A1
; GENERAL INFORMATION:
; APPLICANT: ADAMS, CAMELLIA W.
; APPLICANT: FERRARA, NAPOLEONE
; APPLICANT: FILVAROFF, ELLEN H.
; APPLICANT: MAO, WEIGUANG
; APPLICANT: PRESTA, LEONARD G.
; APPLICANT: TEJADA, MAX L.
; TITLE OF INVENTION: Humanized Anti-TGF-Beta Antibodies
; FILE REFERENCE: P1954R1US
; CURRENT APPLICATION NUMBER: US/11/096,046
; CURRENT FILING DATE: 2005-03-31
; PRIOR APPLICATION NUMBER: US 60/558,290
; PRIOR FILING DATE: 2004-03-31
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 5
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-11-096-046-5

Query Match 71.4%; Score 40; DB 7; Length 109;
Best Local Similarity 75.0%; Pred. No. 1.1;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYSKLPWT 9
||: ||||
Db 90 QYNSLPWT 97

RESULT 25
US-11-208-422-7
; Sequence 7, Application US/11208422
```

; Publication No. US20060067930A1

; GENERAL INFORMATION:

; APPLICANT: Adams, Camellia W.

; APPLICANT: Lien, Samantha

; APPLICANT: Lowman, Henry B.

; APPLICANT: Marvin, Jonathan S.

; APPLICANT: Meng, Yu-Ju G.

; TITLE OF INVENTION: POLYPEPTIDE VARIANTS WITH ALTERED EFFECTOR FUNCTION

; FILE REFERENCE: P2158R1

; CURRENT APPLICATION NUMBER: US/11/208,422

; CURRENT FILING DATE: 2005-08-19

; PRIOR APPLICATION NUMBER: US 60/603,057

; PRIOR FILING DATE: 2004-08-19

; NUMBER OF SEQ ID NOS: 54

; SEQ ID NO 7

; LENGTH: 108

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Sequence is synthesized

US-11-208-422-7

Query Match 69.6%; Score 39; DB 7; Length 108;

Best Local Similarity 75.0%; Pred. No. 1.6;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYSKLPWT 9

||| :|||

Db 90 QYSTVPWT 97

RESULT 26

US-11-208-422-9

; Sequence 9, Application US/11208422

; Publication No. US20060067930A1

; GENERAL INFORMATION:

; APPLICANT: Adams, Camellia W.

; APPLICANT: Lien, Samantha

; APPLICANT: Lowman, Henry B.

; APPLICANT: Marvin, Jonathan S.

; APPLICANT: Meng, Yu-Ju G.

; TITLE OF INVENTION: POLYPEPTIDE VARIANTS WITH ALTERED EFFECTOR FUNCTION

; FILE REFERENCE: P2158R1

; CURRENT APPLICATION NUMBER: US/11/208,422

; CURRENT FILING DATE: 2005-08-19

; PRIOR APPLICATION NUMBER: US 60/603,057

; PRIOR FILING DATE: 2004-08-19

; NUMBER OF SEQ ID NOS: 54

; SEQ ID NO 9

; LENGTH: 108

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Sequence is synthesized

US-11-208-422-9

Query Match 69.6%; Score 39; DB 7; Length 108;

Best Local Similarity 75.0%; Pred. No. 1.6;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYSKLPWT 9

||| :|||

Db 90 QYSTVPWT 97

RESULT 27

US-11-208-422-11

; Sequence 11, Application US/11208422

; Publication No. US20060067930A1

; GENERAL INFORMATION:

; APPLICANT: Adams, Camellia W.

; APPLICANT: Lien, Samantha

; APPLICANT: Lowman, Henry B.

; APPLICANT: Marvin, Jonathan S.

; APPLICANT: Meng, Yu-Ju G.

; TITLE OF INVENTION: POLYPEPTIDE VARIANTS WITH ALTERED EFFECTOR FUNCTION

; FILE REFERENCE: P2158R1

; CURRENT APPLICATION NUMBER: US/11/208,422

; CURRENT FILING DATE: 2005-08-19

; PRIOR APPLICATION NUMBER: US 60/603,057

; PRIOR FILING DATE: 2004-08-19

; NUMBER OF SEQ ID NOS: 54

; SEQ ID NO 11

; LENGTH: 108

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Sequence is synthesized

US-11-208-422-11

Query Match 69.6%; Score 39; DB 7; Length 108;

Best Local Similarity 75.0%; Pred. No. 1.6;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYSKLPWT 9

||| :|||

Db 90 QYSTVPWT 97

RESULT 28

US-10-648-816-1

; Sequence 1, Application US/10648816

; Publication No. US20050244405A1

; GENERAL INFORMATION:

; APPLICANT: Van Bruggen, Nicholas

; APPLICANT: Ferrara, Napoleone

; TITLE OF INVENTION: Vascular Endothelial Cell Growth Factor Antagonists

; FILE REFERENCE: P1717D1

; CURRENT APPLICATION NUMBER: US/10/648,816

; CURRENT FILING DATE: 2003-08-26

; PRIOR APPLICATION NUMBER: US/09/718,694

; PRIOR FILING DATE: 2000-11-21

; PRIOR APPLICATION NUMBER: US 09/218,481

; PRIOR FILING DATE: 1998-12-22

; NUMBER OF SEQ ID NOS: 16

; SEQ ID NO 1

; LENGTH: 110

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-648-816-1

Query Match 69.6%; Score 39; DB 6; Length 110;

Best Local Similarity 75.0%; Pred. No. 1.7;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYSKLPWT 9

||| :|||

Db 90 QYSTVPWT 97

RESULT 29

US-10-648-816-2

; Sequence 2, Application US/10648816

; Publication No. US20050244405A1

; GENERAL INFORMATION:

; APPLICANT: Van Bruggen, Nicholas

; APPLICANT: Ferrara, Napoleone

; TITLE OF INVENTION: Vascular Endothelial Cell Growth Factor Antagonists

; FILE REFERENCE: P1717D1

; CURRENT APPLICATION NUMBER: US/10/648,816

; CURRENT FILING DATE: 2003-08-26

; PRIOR APPLICATION NUMBER: US/09/718,694

; PRIOR FILING DATE: 2000-11-21

; PRIOR APPLICATION NUMBER: US 09/218,481

; PRIOR FILING DATE: 1998-12-22  
; NUMBER OF SEQ ID NOS: 16  
; SEQ ID NO 2  
; LENGTH: 110  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-648-816-2

Query Match 69.6%; Score 39; DB 6; Length 110;  
Best Local Similarity 75.0%; Pred. No. 1.7;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYSKLPWT 9  
|||:||||  
Db 90 QYSTVPWT 97

RESULT 30  
US-10-648-816-3  
; Sequence 3, Application US/10648816  
; Publication No. US20050244405A1  
; GENERAL INFORMATION:  
; APPLICANT: Van Bruggen, Nicholas  
; TITLE OF INVENTION: Vascular Endothelial Cell Growth Factor Antagonists  
; FILE REFERENCE: P1717D1  
; CURRENT APPLICATION NUMBER: US/10/648,816  
; CURRENT FILING DATE: 2003-08-26  
; PRIOR APPLICATION NUMBER: US/09/718,694  
; PRIOR FILING DATE: 2000-11-21  
; PRIOR APPLICATION NUMBER: US 09/218,481  
; PRIOR FILING DATE: 1998-12-22  
; NUMBER OF SEQ ID NOS: 16  
; SEQ ID NO 3  
; LENGTH: 110  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-648-816-3

Query Match 69.6%; Score 39; DB 6; Length 110;  
Best Local Similarity 75.0%; Pred. No. 1.7;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYSKLPWT 9  
|||:||||  
Db 90 QYSTVPWT 97

RESULT 31  
US-10-648-816-4  
; Sequence 4, Application US/10648816  
; Publication No. US20050244405A1  
; GENERAL INFORMATION:  
; APPLICANT: Van Bruggen, Nicholas  
; TITLE OF INVENTION: Vascular Endothelial Cell Growth Factor Antagonists  
; FILE REFERENCE: P1717D1  
; CURRENT APPLICATION NUMBER: US/10/648,816  
; CURRENT FILING DATE: 2003-08-26  
; PRIOR APPLICATION NUMBER: US/09/718,694  
; PRIOR FILING DATE: 2000-11-21  
; PRIOR APPLICATION NUMBER: US 09/218,481  
; PRIOR FILING DATE: 1998-12-22  
; NUMBER OF SEQ ID NOS: 16  
; SEQ ID NO 4  
; LENGTH: 110  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-648-816-4

Query Match 69.6%; Score 39; DB 6; Length 110;

Best Local Similarity 75.0%; Pred. No. 1.7;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYSKLPWT 9  
|||:||||  
Db 90 QYSTVPWT 97

RESULT 32  
US-10-648-816-5  
; Sequence 5, Application US/10648816  
; Publication No. US20050244405A1  
; GENERAL INFORMATION:  
; APPLICANT: Van Bruggen, Nicholas  
; TITLE OF INVENTION: Vascular Endothelial Cell Growth Factor Antagonists  
; FILE REFERENCE: P1717D1  
; CURRENT APPLICATION NUMBER: US/10/648,816  
; CURRENT FILING DATE: 2003-08-26  
; PRIOR APPLICATION NUMBER: US/09/718,694  
; PRIOR FILING DATE: 2000-11-21  
; PRIOR APPLICATION NUMBER: US 09/218,481  
; PRIOR FILING DATE: 1998-12-22  
; NUMBER OF SEQ ID NOS: 16  
; SEQ ID NO 5  
; LENGTH: 110  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-648-816-5

Query Match 69.6%; Score 39; DB 6; Length 110;  
Best Local Similarity 75.0%; Pred. No. 1.7;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYSKLPWT 9  
|||:||||  
Db 90 QYSTVPWT 97

RESULT 33  
US-10-648-816-6  
; Sequence 6, Application US/10648816  
; Publication No. US20050244405A1  
; GENERAL INFORMATION:  
; APPLICANT: Van Bruggen, Nicholas  
; TITLE OF INVENTION: Vascular Endothelial Cell Growth Factor Antagonists  
; FILE REFERENCE: P1717D1  
; CURRENT APPLICATION NUMBER: US/10/648,816  
; CURRENT FILING DATE: 2003-08-26  
; PRIOR APPLICATION NUMBER: US/09/718,694  
; PRIOR FILING DATE: 2000-11-21  
; PRIOR APPLICATION NUMBER: US 09/218,481  
; PRIOR FILING DATE: 1998-12-22  
; NUMBER OF SEQ ID NOS: 16  
; SEQ ID NO 6  
; LENGTH: 110  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-648-816-6

Query Match 69.6%; Score 39; DB 6; Length 110;  
Best Local Similarity 75.0%; Pred. No. 1.7;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYSKLPWT 9  
|||:||||  
Db 90 QYSTVPWT 97

RESULT 34

```
US-10-648-816-7
; Sequence 7, Application US/10648816
; Publication No. US20050244405A1
; GENERAL INFORMATION:
; APPLICANT: Van Bruggen, Nicholas
; TITLE OF INVENTION: Vascular Endothelial Cell Growth Factor Antagonists
; TITLE OF INVENTION: and Uses Thereof
; FILE REFERENCE: P1717D1
; CURRENT APPLICATION NUMBER: US/10/648,816
; CURRENT FILING DATE: 2003-08-26
; PRIOR APPLICATION NUMBER: US/09/718,694
; PRIOR FILING DATE: 2000-11-21
; PRIOR APPLICATION NUMBER: US 09/218,481
; PRIOR FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 16
; SEQ ID NO 7
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-648-816-7

Query Match 69.6%; Score 39; DB 6; Length 110;
Best Local Similarity 75.0%; Pred. No. 1.7;
Matches 6; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

QY 2 QYSKLPWT 9
|||:|
Db 90 QYSTVPWT 97

RESULT 35
US-10-648-816-8
; Sequence 8, Application US/10648816
; Publication No. US20050244405A1
; GENERAL INFORMATION:
; APPLICANT: Van Bruggen, Nicholas
; TITLE OF INVENTION: Vascular Endothelial Cell Growth Factor Antagonists
; TITLE OF INVENTION: and Uses Thereof
; FILE REFERENCE: P1717D1
; CURRENT APPLICATION NUMBER: US/10/648,816
; CURRENT FILING DATE: 2003-08-26
; PRIOR APPLICATION NUMBER: US/09/718,694
; PRIOR FILING DATE: 2000-11-21
; PRIOR APPLICATION NUMBER: US 09/218,481
; PRIOR FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 16
; SEQ ID NO 8
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-648-816-8

Query Match 69.6%; Score 39; DB 6; Length 110;
Best Local Similarity 75.0%; Pred. No. 1.7;
Matches 6; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

QY 2 QYSKLPWT 9
|||:|
Db 90 QYSTVPWT 97

RESULT 36
US-10-524-647-16
; Sequence 16, Application US/10524647
; Publication No. US20050281909A1
; GENERAL INFORMATION:
; APPLICANT: Flachmann, Ralf
; APPLICANT: Sauer, Matt
; APPLICANT: Schopfer, Christel R.
; APPLICANT: Klebsattel, Martin
; APPLICANT: Pfeiffer, Angelika-Maria

US-10-648-816-7
; APPLICANT: Luck, Thomas
; APPLICANT: Voeste, Dirk
; TITLE OF INVENTION: Use of astaxanthin-containing plants or parts of plants of the
; TITLE OF INVENTION: genus Tagetes as feedstuffs
; FILE REFERENCE: 13173-00004-US
; CURRENT APPLICATION NUMBER: US/10/524,647
; CURRENT FILING DATE: 2005-02-17
; PRIOR APPLICATION NUMBER: PCT/EP2003/009109
; PRIOR FILING DATE: 2003-08-18
; PRIOR APPLICATION NUMBER: DE 102 38 980.2
; PRIOR FILING DATE: 2002-08-20
; PRIOR APPLICATION NUMBER: DE 102 38 978.0
; PRIOR FILING DATE: 2002-08-20
; PRIOR APPLICATION NUMBER: DE 102 38 979.9
; PRIOR FILING DATE: 2002-08-20
; PRIOR APPLICATION NUMBER: DE 102 53 112.9
; PRIOR FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: DE 102 58 971.2
; PRIOR FILING DATE: 2002-12-16
; NUMBER OF SEQ ID NOS: 142
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 16
; LENGTH: 258
; TYPE: PRT
; ORGANISM: Nostoc sp.
US-10-524-647-16

Query Match 69.6%; Score 39; DB 6; Length 258;
Best Local Similarity 62.5%; Pred. No. 3.7;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 HQYKLPW 8
|:|:|
Db 240 HEYPQLPW 247

RESULT 37
US-10-524-972-16
; Sequence 16, Application US/10524972
; Publication No. US20060031963A1
; GENERAL INFORMATION:
; APPLICANT: Schopfer, Christel R.
; APPLICANT: Flachmann, Ralf
; APPLICANT: Herbers, Karin
; APPLICANT: Kunze, Irene
; APPLICANT: Sauer, Matt
; APPLICANT: Klebsattel, Martin
; TITLE OF INVENTION: Method for the production of Astaxanthin in flowers of plants
; FILE REFERENCE: 13173-00007-US
; CURRENT APPLICATION NUMBER: US/10/524,972
; CURRENT FILING DATE: 2005-02-18
; PRIOR APPLICATION NUMBER: PCT/EP2003/009102
; PRIOR FILING DATE: 2003-08-18
; PRIOR APPLICATION NUMBER: DE 102 38 980.2
; PRIOR FILING DATE: 2002-08-20
; PRIOR APPLICATION NUMBER: DE 102 38 978.0
; PRIOR FILING DATE: 2002-08-20
; PRIOR APPLICATION NUMBER: DE 102 38 979.9
; PRIOR FILING DATE: 2002-08-20
; PRIOR APPLICATION NUMBER: DE 102 53 112.9
; PRIOR FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: DE 102 58 971.2
; PRIOR FILING DATE: 2002-12-16
; NUMBER OF SEQ ID NOS: 172
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 16
; LENGTH: 258
; TYPE: PRT
; ORGANISM: Nostoc sp.
US-10-524-972-16

Query Match 69.6%; Score 39; DB 6; Length 258;
Best Local Similarity 62.5%; Pred. No. 3.7;
```

Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HQYSKLPW 8  
|:|:|  
Db 240 HEYPQLPW 247

## RESULT 38

US-10-504-389A-53  
; Sequence 53, Application US/10504389A  
; Publication No. US20060045876A1

## GENERAL INFORMATION:

; APPLICANT: Renner, Christoph  
; APPLICANT: Scott, Andrew  
; TITLE OF INVENTION: FUSION PROTEINS OF HUMANIZED G250 SPECIFIC  
; FILE REFERENCE: LUD 5821  
; CURRENT FILING DATE: 2004-08-10  
; PRIOR APPLICATION NUMBER: US/10/504,389A  
; PRIOR FILING DATE: 2002-02-12  
; NUMBER OF SEQ ID NOS: 56  
; SEQ ID NO 53  
; LENGTH: 132  
; TYPE: PRT  
; ORGANISM: Mus musculus  
; FEATURE:  
; OTHER INFORMATION: amino acid sequence for murine G250 light chain variable region

US-10-504-389A-53  
Query Match 67.9%; Score 38; DB 6; Length 132;  
Best Local Similarity 75.0%; Pred. No. 3.1;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 QYSKLPWT 9  
|:|:|  
Db 114 QYSNYPWT 121

## RESULT 39

US-11-232-269-4  
; Sequence 4, Application US/11232269  
; Publication No. US20060063248A1

## GENERAL INFORMATION:

; APPLICANT: Lockridge, Oksana  
; APPLICANT: Watkins, Jeffrey  
; TITLE OF INVENTION: Butyrylcholinesterase Variants and Methods of Use  
; FILE REFERENCE: X16699A  
; CURRENT APPLICATION NUMBER: US/11/232,269  
; CURRENT FILING DATE: 2005-09-21  
; PRIOR APPLICATION NUMBER: US 09/748,739  
; PRIOR FILING DATE: 2000-12-26  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 4  
; LENGTH: 574  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Synthetic construct  
; FEATURE:  
; NAME/KEY: MISC\_FEATURE  
; LOCATION: (1)..(574)  
; OTHER INFORMATION: S287G variant

## US-11-232-269-4

Query Match 67.9%; Score 38; DB 7; Length 574;  
Best Local Similarity 75.0%; Pred. No. 12;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HQYSKLPW 8  
|:|:|  
Db 423 HRSSKLPW 430

## RESULT 40

US-11-232-269-6  
; Sequence 6, Application US/11232269  
; Publication No. US20060063248A1

## GENERAL INFORMATION:

; APPLICANT: Lockridge, Oksana  
; APPLICANT: Watkins, Jeffrey  
; TITLE OF INVENTION: Butyrylcholinesterase Variants and Methods of Use  
; FILE REFERENCE: X16699A  
; CURRENT APPLICATION NUMBER: US/11/232,269  
; CURRENT FILING DATE: 2005-09-21  
; PRIOR APPLICATION NUMBER: US 09/748,739  
; PRIOR FILING DATE: 2000-12-26  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 6  
; LENGTH: 574  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Synthetic construct  
; FEATURE:  
; NAME/KEY: MISC\_FEATURE  
; LOCATION: (1)..(574)  
; OTHER INFORMATION: P285Q variant

## US-11-232-269-6

Query Match 67.9%; Score 38; DB 7; Length 574;  
Best Local Similarity 75.0%; Pred. No. 12;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HQYSKLPW 8  
|:|:|  
Db 423 HRSSKLPW 430

## RESULT 41

US-11-232-269-8  
; Sequence 8, Application US/11232269  
; Publication No. US20060063248A1

## GENERAL INFORMATION:

; APPLICANT: Lockridge, Oksana  
; APPLICANT: Watkins, Jeffrey  
; TITLE OF INVENTION: Butyrylcholinesterase Variants and Methods of Use  
; FILE REFERENCE: X16699A  
; CURRENT APPLICATION NUMBER: US/11/232,269  
; CURRENT FILING DATE: 2005-09-21  
; PRIOR APPLICATION NUMBER: US 09/748,739  
; PRIOR FILING DATE: 2000-12-26  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 8  
; LENGTH: 574  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Synthetic construct  
; FEATURE:  
; NAME/KEY: MISC\_FEATURE  
; LOCATION: (1)..(574)  
; OTHER INFORMATION: P285S variant

## US-11-232-269-8

Query Match 67.9%; Score 38; DB 7; Length 574;  
Best Local Similarity 75.0%; Pred. No. 12;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HQYSKLPW 8  
|:|:|  
Db 423 HRSSKLPW 430

RESULT 42  
US-11-232-269-17  
; Sequence 17, Application US/11232269  
; Publication No. US20060063248A1  
; GENERAL INFORMATION:  
; APPLICANT: Lockridge, Oksana  
; APPLICANT: Watkins, Jeffry  
; TITLE OF INVENTION: Butyrylcholinesterase Variants and Methods of Use  
; FILE REFERENCE: X16699A  
; CURRENT APPLICATION NUMBER: US/11/232,269  
; CURRENT FILING DATE: 2005-09-21  
; PRIOR APPLICATION NUMBER: US 09/748,739  
; PRIOR FILING DATE: 2000-12-26  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 17  
; LENGTH: 574  
; TYPE: PRT  
; ORGANISM: homo sapiens  
; FEATURE:  
; NAME/KEY: MISC FEATURE  
; LOCATION: (1)..(574)  
; OTHER INFORMATION: Human wt butyrylcholinesterase  
US-11-232-269-17

Query Match 67.9%; Score 38; DB 7; Length 574;  
Best Local Similarity 75.0%; Pred. No. 12;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYSKLPW 8  
|: |||||  
DB 423 HRSSKLPW 430

RESULT 43  
US-11-232-269-18  
; Sequence 18, Application US/11232269  
; Publication No. US20060063248A1  
; GENERAL INFORMATION:  
; APPLICANT: Lockridge, Oksana  
; APPLICANT: Watkins, Jeffry  
; TITLE OF INVENTION: Butyrylcholinesterase Variants and Methods of Use  
; FILE REFERENCE: X16699A  
; CURRENT APPLICATION NUMBER: US/11/232,269  
; CURRENT FILING DATE: 2005-09-21  
; PRIOR APPLICATION NUMBER: US 09/748,739  
; PRIOR FILING DATE: 2000-12-26  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 18  
; LENGTH: 574  
; TYPE: PRT  
; ORGANISM: homo sapiens  
; FEATURE:  
; NAME/KEY: MISC FEATURE  
; LOCATION: (1)..(574)  
; OTHER INFORMATION: Human A variant butyrylcholinesterase  
US-11-232-269-18

Query Match 67.9%; Score 38; DB 7; Length 574;  
Best Local Similarity 75.0%; Pred. No. 12;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYSKLPW 8  
|: |||||  
DB 423 HRSSKLPW 430

RESULT 44  
US-11-232-269-19  
; Sequence 19, Application US/11232269  
; Publication No. US20060063248A1

; GENERAL INFORMATION:  
; APPLICANT: Lockridge, Oksana  
; APPLICANT: Watkins, Jeffry  
; TITLE OF INVENTION: Butyrylcholinesterase Variants and Methods of Use  
; FILE REFERENCE: X16699A  
; CURRENT APPLICATION NUMBER: US/11/232,269  
; CURRENT FILING DATE: 2005-09-21  
; PRIOR APPLICATION NUMBER: US 09/748,739  
; PRIOR FILING DATE: 2000-12-26  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 19  
; LENGTH: 574  
; TYPE: PRT  
; ORGANISM: homo sapiens  
; FEATURE:  
; NAME/KEY: MISC FEATURE  
; LOCATION: (1)..(574)  
; OTHER INFORMATION: Human J variant butyrylcholinesterase  
US-11-232-269-19

Query Match 67.9%; Score 38; DB 7; Length 574;  
Best Local Similarity 75.0%; Pred. No. 12;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYSKLPW 8  
|: |||||  
DB 423 HRSSKLPW 430

RESULT 45  
US-11-232-269-20  
; Sequence 20, Application US/11232269  
; Publication No. US20060063248A1  
; GENERAL INFORMATION:  
; APPLICANT: Lockridge, Oksana  
; APPLICANT: Watkins, Jeffry  
; TITLE OF INVENTION: Butyrylcholinesterase Variants and Methods of Use  
; FILE REFERENCE: X16699A  
; CURRENT APPLICATION NUMBER: US/11/232,269  
; CURRENT FILING DATE: 2005-09-21  
; PRIOR APPLICATION NUMBER: US 09/748,739  
; PRIOR FILING DATE: 2000-12-26  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 20  
; LENGTH: 574  
; TYPE: PRT  
; ORGANISM: homo sapiens  
; FEATURE:  
; NAME/KEY: MISC FEATURE  
; LOCATION: (1)..(574)  
; OTHER INFORMATION: Human K variant butyrylcholinesterase  
US-11-232-269-20

Query Match 67.9%; Score 38; DB 7; Length 574;  
Best Local Similarity 75.0%; Pred. No. 12;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYSKLPW 8  
|: |||||  
DB 423 HRSSKLPW 430

RESULT 46  
US-11-232-269-23  
; Sequence 23, Application US/11232269  
; Publication No. US20060063248A1  
; GENERAL INFORMATION:  
; APPLICANT: Lockridge, Oksana  
; APPLICANT: Watkins, Jeffry  
; TITLE OF INVENTION: Butyrylcholinesterase Variants and Methods of Use  
; FILE REFERENCE: X16699A



```
; CURRENT APPLICATION NUMBER: US/11/232,269
; CURRENT FILING DATE: 2005-09-21
; PRIOR APPLICATION NUMBER: US 09/748,739
; PRIOR FILING DATE: 2000-12-26
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 23
; LENGTH: 574
; TYPE: PRT
; ORGANISM: Rattus sp.
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(574)
; OTHER INFORMATION: Rat butyrylcholinesterase
US-11-232-269-23

Query Match      67.9%; Score 38; DB 7; Length 574;
Best Local Similarity 75.0%; Pred. No. 12;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYSKLPW 8
Db 423 HRSSKLPW 430

RESULT 47
US-11-232-269-2
; Sequence 2, Application US/11/232,269
; Publication No. US20060063248A1
; GENERAL INFORMATION:
; APPLICANT: Lockridge, Oksana
; APPLICANT: Watkins, Jeffry
; TITLE OF INVENTION: Butyrylcholinesterase Variants and Methods of Use
; FILE REFERENCE: X16699A
; CURRENT APPLICATION NUMBER: US/11/232,269
; CURRENT FILING DATE: 2005-09-21
; PRIOR APPLICATION NUMBER: US 09/748,739
; PRIOR FILING DATE: 2000-12-26
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2
; LENGTH: 602
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic construct
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(602)
; OTHER INFORMATION: A328W variant
US-11-232-269-2

Query Match      67.9%; Score 38; DB 7; Length 602;
Best Local Similarity 75.0%; Pred. No. 13;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYSKLPW 8
Db 451 HRSSKLPW 458

RESULT 48
US-11-096-568A-24813
; Sequence 24813, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
```

```
; SEQ ID NO 24813
; LENGTH: 288
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(288)
; OTHER INFORMATION: Ceres Seq. ID no. 12455028
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (236)..(236)
; OTHER INFORMATION: Xaa is any aa, unknown or other
US-11-096-568A-24813

Query Match      64.3%; Score 36; DB 7; Length 288;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 SKLPWT 9
Db 7 SKLPWT 12

RESULT 49
US-11-087-099-7921
; Sequence 7921, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 7921
; LENGTH: 439
; TYPE: PRT
; ORGANISM: Methanosarcina acetivorans C2A
US-11-087-099-7921

Query Match      64.3%; Score 36; DB 7; Length 439;
Best Local Similarity 66.7%; Pred. No. 23;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 HOYSKLPWT 9
Db 320 HOKLKPWT 328

RESULT 50
US-10-506-454-834
; Sequence 834, Application US/10506454
; Publication No. US20060068386A1
; GENERAL INFORMATION:
; APPLICANT: Slesarev, Alexi I
; APPLICANT: Mezheva, Katja V
; APPLICANT: Polushin, Nikolai N
; APPLICANT: Shcherbinina, Olga V
; APPLICANT: Shakhova, Vera V
; APPLICANT: Malykh, Andrei G
; APPLICANT: Koz'yavkin, Sergei A
; TITLE OF INVENTION: The Complete Genome and Protein Sequences of the Hyperthermophile
; TITLE OF INVENTION: Methanopyrus Kandleri AV19 and Monophyly of Archaeal Methanogens
; FILE REFERENCE: FID001
; CURRENT APPLICATION NUMBER: US/10/506,454
; CURRENT FILING DATE: 2004-08-31
; PRIOR APPLICATION NUMBER: PCT/US03/06664
; PRIOR FILING DATE: 2003-03-04
; PRIOR APPLICATION NUMBER: 60/361,742
; PRIOR FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 1722
; SOFTWARE: PatentIn version 3.2
```

```
; SEQ ID NO 834
; LENGTH: 500
; TYPE: PRT
; ORGANISM: Methanopyrus kandleri
US-10-506-454-834

Query Match      64.3%; Score 36; DB 6; Length 500;
Best Local Similarity 62.5%; Pred. No. 26;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 HOYSKLPW 8
      | : | : |
Db      209 HKMSRLPW 216
```

Search completed: April 6, 2006, 09:22:56  
Job time : 14.1525 secs

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GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: April 6, 2006, 08:47:08 ; Search time 26.6031 Seconds  
(without alignments)  
1965.416 Million cell updates/sec

Title: US-10-089-500-9  
Perfect score: 624  
Sequence: 1 EVQLVESGDFVQPGSLRV.....KLGTYVFDISWGQITLLTVSS 119

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A Geneseq 21.\*  
1: Geneseqp1980s.\*  
2: Geneseqp1990s.\*  
3: Geneseqp2000s.\*  
4: Geneseqp2001s.\*  
5: Geneseqp2002s.\*  
6: Geneseqp2003as.\*  
7: Geneseqp2003bs.\*  
8: Geneseqp2004s.\*  
9: Geneseqp2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	624	100.0	119	4 AAB81985	Aab81985 Gangliosi
2	624	100.0	119	6 ABU11010	Abu11010 Modified
3	624	100.0	119	9 ADZ57821	Adz57821 Gangliosi
4	624	100.0	582	4 AAB81987	Aab81987 Gangliosi
5	585	93.8	119	9 ADZ57818	Adz57818 Gangliosi
6	579	92.8	119	4 AAB81989	Aab81989 Gangliosi
7	579	92.8	119	6 ABU11012	Abu11012 Modified
8	579	92.8	119	9 ADZ57816	Adz57816 Gangliosi
9	579	92.8	130	2 AAB33256	Aar33256 Rat immun
10	579	92.8	130	2 AAR53341	Aar53341 KM641 L C
11	579	92.8	130	2 AAY28369	Aay28369 PKM641 HA
12	579	92.8	130	3 AAB01627	Aab01627 Murine im
13	579	92.8	138	4 AAB81977	Aab81977 Gangliosi
14	579	92.8	138	6 ABU11002	Abu11002 Modified
15	579	92.8	582	4 AAB81991	Aab81991 Gangliosi
16	502	80.4	274	8 AD025153	Ado25153 Melanoma
17	499	80.0	118	9 ADZ08201	Adz08201 IGF-speci
18	499	80.0	119	5 AAB28851	Aae28851 Human con
19	498	79.8	119	4 AAB62088	Aab62088 Human Vh
20	498	79.8	119	4 AAB60401	Aab60401 Consensus
21	498	79.8	119	4 AAB61586	Aab61586 Human var
22	498	79.8	119	5 AAU74541	Aau74541 Human sub
23	498	79.8	119	8 AD871455	Ad871455 Human ant
24	498	79.8	119	8 ADJ88009	Adj88009 Human var

25	498	79.8	119	8 ADN12055	Adn12055 Variable
26	498	79.8	119	8 ADP43329	Adp43329 Human mon
27	498	79.8	119	8 ADP79575	Adp79575 Human hea
28	498	79.8	119	9 ADW21311	Adw21311 Human hea
29	498	79.8	120	9 AEA41074	Aea41074 Germline
30	493.5	79.1	224	6 ABR01511	Abro1511 Human ant
31	492.5	78.9	126	6 ADA89891	Ada89891 MS-Roche
32	492.5	78.9	137	9 ADZ08220	Adz08220 IGF-speci
33	492	78.8	119	8 ADO36357	Ado36357 Intracell
34	492	78.8	119	8 ADQ75230	Adq75230 Immunoglo
35	492	78.8	121	7 ADL91330	Adl91330 VH chain
36	492	78.8	313	4 AAU14320	Aau14320 Human nov
37	491.5	78.8	251	8 ADI58099	Adi58099 Reg IV-gp
38	490.5	78.6	118	7 ADJ95639	Adj95639 Insulin-1
39	490.5	78.6	118	9 ADZ08158	Adz08158 IGF-speci
40	490.5	78.6	137	9 ADZ08159	Adz08159 IGF-speci
41	490	78.5	119	8 ADR47408	Adr47408 Heavy cha
42	490	78.5	129	9 AEA53384	Aea53384 Novel hum
43	489.5	78.4	126	6 ADA89974	Ada89974 Anti-Abet
44	489	78.4	119	2 AAR95216	Aar95216 Human foe
45	489	78.4	143	6 ADA43059	Ada43059 Human ant

ALIGNMENTS

RESULT 1  
AAB81985  
ID AAB81985 standard; protein; 119 AA.  
XX  
AC AAB81985;  
XX  
DT 03-JUL-2001 (first entry)  
XX  
DE Ganglioside GD3 specific antibody related protein SEQ ID NO: 9.  
XX  
KW Ganglioside; GD3; complementarity determining region; CDR; antibody;  
KW cancer.  
XX  
OS Synthetic.  
XX  
PN WO200123432-A1.  
XX  
PD 05-APR-2001.  
XX  
PF 29-SEP-2000; 2000WO-JP006774.  
XX  
PR 30-SEP-1999; 99JP-00278291.  
PR 06-APR-2000; 2000JP-00105088.  
XX  
(KYOW ) KYOWA HAKKO KOGYO KK.  
XX  
Hanai N, Shitara K, Nakamura K, Niwa R;  
WPI; 2001-266143/27.  
XX  
New human type complementation-determining region-transplanted antibody  
PT and derivatives against ganglioside GD3, useful in diagnosis and therapy  
of e.g. tumors, with low antigenicity, little side effects but potent  
activity in cancer.  
XX  
Claim 20; Page 142-143; 183pp; Japanese.  
PS  
The present invention describes a monoclonal antibody which can react  
specifically with ganglioside GD3. The antibody and its derivatives are  
CC useful in the diagnosis and therapy of tumours, particularly cancer  
diagnosis. The present sequence is a protein used in the exemplification  
of the invention  
CC  
SQ Sequence 119 AA;  
Query Match 100.0%; Score 624; DB 4; Length 119;  
Best Local Similarity 100.0%; Pred. No. 9.8e-50;

Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVLVESGDFVQPGSLRVSCAASGFAFSHYAMSWVRQAPGKLEWVAYISSGSGTTY 60  
 |||||  
 Db 1 EVLVESGDFVQPGSLRVSCAASGFAFSHYAMSWVRQAPGKLEWVAYISSGSGTTY 60  
 |||||

QY 61 SDSVKGRTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLTGYTFDSWGQGLTLTVSS 119  
 |||||  
 Db 61 SDSVKGRTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLTGYTFDSWGQGLTLTVSS 119  
 |||||

RESULT 2  
 ABU1010  
 ID ABU1010 standard; protein; 119 AA.  
 XX  
 AC ABU1010;  
 XX  
 DT 04-FEB-2003 (first entry)  
 XX  
 DE Modified ganglioside GD3 antibody associated protein #3.  
 XX  
 KW Ganglioside GD3; anti-ganglioside GD3 antibody; tumour; melanoma.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200278739-A1.  
 XX  
 PD 10-OCT-2002.  
 XX  
 PF 29-MAR-2002; 2002WO-JP003170.  
 XX  
 PR 29-MAR-2001; 2001JP-00097483.  
 XX  
 PA (KYOW ) KYOWA HAKKO KOGYO KK.  
 XX  
 PI Shitara K, Niwa R, Kanazawa J, Asada M;  
 XX  
 DR WPI; 2003-067410/06.  
 XX

PT Drugs containing genetically-modified antibody against ganglioside GD3,  
 its fragment, immunocompetent cell activators or/and antitumor agents in  
 PT combination, applicable in treating malignant tumor like melanoma.  
 XX  
 PS Claim 8; Page 99; 121pp; Japanese.  
 XX

CC The invention describes drugs contain a genetically-modified antibody  
 against ganglioside GD3 or its fragment and at least 1 of a substance  
 CC capable of activating immunocompetent cells and a substance having an  
 CC antitumor activity in combination. The drugs can be used to treat tumour  
 CC like melanoma and can provide a treatment with enhanced therapeutic  
 CC effect and little side-reactions, particularly to relieve problems of  
 CC side-effects during the conventional single administration. This sequence  
 CC represents a protein associated with the anti- ganglioside GD3 antibody  
 XX  
 SQ Sequence 119 AA;

Query Match 100.0%; Score 624; DB 6; Length 119;  
 Best Local Similarity 100.0%; Pred. No. 9.8e-50;  
 Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVLVESGDFVQPGSLRVSCAASGFAFSHYAMSWVRQAPGKLEWVAYISSGSGTTY 60  
 |||||  
 Db 1 EVLVESGDFVQPGSLRVSCAASGFAFSHYAMSWVRQAPGKLEWVAYISSGSGTTY 60  
 |||||

QY 61 SDSVKGRTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLTGYTFDSWGQGLTLTVSS 119  
 |||||  
 Db 61 SDSVKGRTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLTGYTFDSWGQGLTLTVSS 119  
 |||||

RESULT 3  
 ADZ57821  
 ID ADZ57821 standard; protein; 119 AA.  
 XX  
 AC ADZ57821;

AC ADZ57821;  
 XX  
 DT 30-JUN-2005 (first entry)  
 XX  
 DE Ganglioside GD3 binding antibody associated protein SEQ ID NO 25.  
 XX  
 KW cytostatic; antibody engineering; cancer; neoplasm; ganglioside; GD3;  
 KW pharmaceutical.  
 XX  
 OS Synthetic.  
 XX  
 PN WO2005035577-A1.  
 XX  
 PD 21-APR-2005.  
 XX  
 PF 08-OCT-2004; 2004WO-JP015314.  
 XX  
 PR 08-OCT-2003; 2003JP-00350161.  
 XX  
 PA (KYOW ) KYOWA HAKKO KOGYO KK.  
 XX  
 PI Iida S, Satoh M, Urakubo M, Wakitani M, Uchida K, Niwa R;  
 PI Shitara K;  
 XX  
 DR WPI; 2005-346195/35.  
 XX

PT Antibody composition for treating ganglioside GD3 associated disease e.g.  
 cancer, comprises genetically modified antibody molecule, which  
 PT specifically binds to ganglioside GD3 and has N-glycoside-binding sugar  
 PT chain in its Fc domain.  
 XX  
 PS Claim 24; SEQ ID NO 25; 124pp; Japanese.  
 XX

CC The invention describes an antibody composition (I), comprising a  
 CC genetically modified antibody molecule which specifically binds to  
 CC ganglioside GD3 and has an N-glycoside-binding complex sugar chain in its  
 CC Fc domain, where the N-glycoside-binding complex sugar chain is a sugar  
 CC chain having no fucose attached to N-acetylglucosamine at the reducing  
 CC end of the sugar chain. Also described are: a transformant (II) capable  
 CC of producing (I), obtained by introducing DNA that encodes the antibody  
 CC molecule which specifically binds with ganglioside GD3, to a host cell;  
 CC producing (I), involving cultivating (I) in a culture medium, such that  
 CC Cl (sic) is produced and accumulated in the culture, extracting and  
 CC purifying Cl from the culture medium; a pharmaceutical (III) containing  
 CC Cl as an active ingredient; and a therapeutic agent (A1) for ganglioside  
 CC GD3 associated disease, comprising Cl as an active ingredient. (I) is  
 CC useful for treating GD3 associated disease, which involves administering  
 CC (I), where the GD3 associated disease is cancer. (A1) is also useful for  
 CC treating GD3 associated disease. (II) is useful for producing (I). (I) is  
 CC useful for manufacturing a therapeutic agent for GD3 associated disease.  
 CC This sequence represents a ganglioside GD3 binding antibody associated  
 CC protein.  
 XX  
 SQ Sequence 119 AA;

Query Match 100.0%; Score 624; DB 9; Length 119;  
 Best Local Similarity 100.0%; Pred. No. 9.8e-50;  
 Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVLVESGDFVQPGSLRVSCAASGFAFSHYAMSWVRQAPGKLEWVAYISSGSGTTY 60  
 |||||  
 Db 1 EVLVESGDFVQPGSLRVSCAASGFAFSHYAMSWVRQAPGKLEWVAYISSGSGTTY 60  
 |||||

QY 61 SDSVKGRTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLTGYTFDSWGQGLTLTVSS 119  
 |||||  
 Db 61 SDSVKGRTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLTGYTFDSWGQGLTLTVSS 119  
 |||||

RESULT 4  
 AAB81987  
 ID AAB81987 standard; protein; 582 AA.  
 XX  
 AC AAB81987;

```
XX 03-JUL-2001 (first entry)
XX
XX Ganglioside GD3 specific antibody related protein SEQ ID NO: 53.
DE
XX Ganglioside; GD3; complementarity determining region; CDR; antibody;
KW
XX Ganglioside; GD3; complementarity determining region; CDR; antibody;
KW
XX Synthetic.
XX
XX WO200123432-A1.
PN
XX
XX 05-APR-2001.
PD
XX
XX 29-SEP-2000; 2000WO-JP006774.
PF
XX
XX 30-SEP-1999; 99JP-00278291.
PR
XX 06-APR-2000; 2000JP-00105088.
PR
XX
XX (KYOW ) KYOWA HAKKO KOGYO KK.
PA
XX Hanai N, Shitara K, Nakamura K, Niwa R;
PI
XX WPI; 2001-266143/27.
XX
XX New human type complementation-determining region-transplanted antibody
PT and derivatives against ganglioside GD3, useful in diagnosis and therapy
PT of e.g. tumors, with low antigenicity, little side effects but potent
PT activity in cancer.
XX
XX Claim 41; Page 168-172; 183pp; Japanese.
PS
XX
XX The present invention describes a monoclonal antibody which can react
CC specifically with ganglioside GD3. The antibody and its derivatives are
CC useful in the diagnosis and therapy of tumors, particularly cancer
CC diagnosis. The present sequence is a protein used in the exemplification
CC of the invention
XX
XX Sequence 582 AA;
SQ
Query Match 100.0%; Score 624; DB 4; Length 582;
Best Local Similarity 100.0%; Pred. No. 5,2e-49;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EVQLVESGGDFVQPGGSLRVSCAASGFAFSHYAMSWVRQAPGKLEWVAYISSGSGTTY 60
DB 1 EVQLVESGGDFVQPGGSLRVSCAASGFAFSHYAMSWVRQAPGKLEWVAYISSGSGTTY 60
QY 61 SDSVKGRFTISRDNKNTLYLQMRSLRAEDSAVFCTRVKLTGYTFDSWGQGTLLTVSS 119
DB 61 SDSVKGRFTISRDNKNTLYLQMRSLRAEDSAVFCTRVKLTGYTFDSWGQGTLLTVSS 119
RESULT 5
ADZ57818
ID ADZ57818 standard; protein; 119 AA.
XX
XX ADZ57818;
AC
XX
XX 30-JUN-2005 (first entry)
DT
XX
XX Ganglioside GD3 binding antibody associated protein SEQ ID NO 22.
DE
XX cytotatic; antibody engineering; cancer; neoplasm; ganglioside; GD3;
KW pharmaceutical.
KW
XX Synthetic.
XX
XX WO2005035577-A1.
PN
XX
XX 21-APR-2005.
PD
XX
XX 08-OCT-2004; 2004WO-JP015314.
PF
XX
XX 03-JUL-2001 (first entry)
XX
XX Ganglioside GD3 specific antibody related protein SEQ ID NO: 55.
DE
XX Ganglioside; GD3; complementarity determining region; CDR; antibody;
KW cancer.
KW
XX Mus musculus.
XX
XX WO200123432-A1.
PN
XX
XX 05-APR-2001.
PD
XX
XX 29-SEP-2000; 2000WO-JP006774.
PF
XX
XX 08-OCT-2003; 2003JP-00350161.
XX
XX (KYOW ) KYOWA HAKKO KOGYO KK.
XX
XX Iida S, Satoh M, Urakubo M, Wakitani M, Uchida K, Niwa R;
PI Shitara K;
XX
XX WPI; 2005-346195/35.
XX
XX Antibody composition for treating ganglioside GD3 associated disease e.g.
PT cancer, comprises genetically modified antibody molecule, which
PT specifically binds to ganglioside GD3 and has N-glycoside-binding sugar
PT chain in its Fc domain.
XX
XX Claim 19; SEQ ID NO 22; 124pp; Japanese.
PS
XX
XX The invention describes an antibody composition (I), comprising a
CC genetically modified antibody molecule which specifically binds to
CC ganglioside GD3 and has an N-glycoside-binding complex sugar chain in its
CC Fc domain, where the N-glycoside-binding complex sugar chain is a sugar
CC chain having no fucose attached to N-acetylglucosamine at the reducing
CC end of the sugar chain. Also described are: a transformant (II) capable
CC of producing (I), obtained by introducing DNA that encodes the antibody
CC molecule which specifically binds with ganglioside GD3, to a host cell;
CC producing (I), involving cultivating (I) in a culture medium, such that
CC Cl (sic) is produced and accumulated in the culture, extracting and
CC purifying Cl from the culture medium; a pharmaceutical (III) containing
CC Cl as an active ingredient; and a therapeutic agent (A1) for ganglioside
CC GD3 associated disease, comprising Cl as an active ingredient. (I) is
CC useful for treating GD3 associated disease, which involves administering
CC (I), where the GD3 associated disease is cancer. (A1) is also useful for
CC treating GD3 associated disease. (II) is useful for producing (I). (I) is
CC useful for manufacturing a therapeutic agent for GD3 associated disease.
CC This sequence represents a ganglioside GD3 binding antibody associated
CC protein.
XX
XX Sequence 119 AA;
SQ
Query Match 93.8%; Score 585; DB 9; Length 119;
Best Local Similarity 92.4%; Pred. No. 3,8e-46;
Matches 110; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
QY 1 EVQLVESGGDFVQPGGSLRVSCAASGFAFSHYAMSWVRQAPGKLEWVAYISSGSGTTY 60
DB 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSHYAMSWVRQAPGKLEWVAYISSGSGTTY 60
QY 61 SDSVKGRFTISRDNKNTLYLQMRSLRAEDSAVFCTRVKLTGYTFDSWGQGTLLTVSS 119
DB 61 SDSVKGRFTISRDNKNTLYLQMRSLRAEDTAIVYICARVKLTGYTFDSWGQGTLLTVSS 119
RESULT 6
AAB81989
ID AAB81989 standard; protein; 119 AA.
XX
XX AAB81989;
AC
XX
XX 03-JUL-2001 (first entry)
DT
XX
XX Ganglioside GD3 specific antibody related protein SEQ ID NO: 55.
DE
XX Ganglioside; GD3; complementarity determining region; CDR; antibody;
KW cancer.
KW
XX Mus musculus.
XX
XX WO200123432-A1.
PN
XX
XX 05-APR-2001.
PD
XX
XX 29-SEP-2000; 2000WO-JP006774.
PF
XX
```

PR 30-SEP-1999; 99JP-00278291.  
PR 06-APR-2000; 2000JP-00105088.  
XX  
PA (KYOW ) KYOWA HAKKO KOGYO KK.  
XX  
PI Hanai N, Shitara K, Nakamura K, Niwa R;  
XX WPI; 2001-266143/27.  
XX  
XX New human type complementation-determining region-transplanted antibody  
PT and derivatives against ganglioside GD3, useful in diagnosis and therapy  
PT of e.g. tumors, with low antigenicity, little side effects but potent  
PT activity in cancer.  
XX  
XX Claim 10; Page 173-174; 183pp; Japanese.  
PS  
PS The present invention describes a monoclonal antibody which can react  
CC specifically with ganglioside GD3. The antibody and its derivatives are  
CC useful in the diagnosis and therapy of tumors, particularly cancer  
CC diagnosis. The present sequence is a protein used in the exemplification  
CC of the invention  
XX  
XX Sequence 119 AA;  
SQ

Query Match 92.8%; Score 579; DB 4; Length 119;  
Best Local Similarity 91.6%; Pred. No. 1.4e-45;  
Matches 109; Conservative 5; Mismatches 5; Indels 0; Gaps 0;  
QY 1 EVLVESGGDFVQPGSLRVSCAAGFAFASHYAMSWVRQAPKGLEWVAYISSGSGTTY 60  
DB 1 EVTLVESGGDFVKPGGSLKVSACAGFAFASHYAMSWVRQTPAKRLEWVAYISSGSGTTY 60  
QY 61 SDSVKGRFTISRDNKNTLYLQMSLRSEDNAVYFCTRVKLGTYTFDSWGQGTTLTVSS 119  
DB 61 SDSVKGRFTISRDNKNTLYLQMSLRSEDSAMYFCTRVKLGTYTFDSWGQGTTLTVSS 119  
RESULT 8  
ADZ57816  
ID ADZ57816 standard; protein; 119 AA.  
XX  
AC ADZ57816;  
XX  
DT 30-JUN-2005 (first entry)  
DE Ganglioside GD3 binding antibody associated protein SEQ ID NO 20.  
XX  
KW cytostatic; antibody engineering; cancer; neoplasm; ganglioside; GD3;  
KW pharmaceutical.  
XX  
OS Mus musculus.  
XX  
PN WO2005035577-A1.  
XX  
PD 21-APR-2005.  
XX  
PF 08-OCT-2004; 2004WO-JP015314.  
XX  
PR 08-OCT-2003; 2003JP-00350161.  
XX  
PA (KYOW ) KYOWA HAKKO KOGYO KK.  
XX  
PI Iida S, Satoh M, Urakubo M, Wakitani M, Uchida K, Niwa R;  
PI Shitara K;  
XX  
XX WPI; 2005-346195/35.  
XX  
XX Antibody composition for treating ganglioside GD3 associated disease e.g.  
PT cancer, comprises genetically modified antibody molecule, which  
PT specifically binds to ganglioside GD3 and has N-glycoside-binding sugar  
PT chain in its FC domain.  
XX  
PS Claim 13; SEQ ID NO 20; 124pp; Japanese.  
XX  
XX The invention describes an antibody composition (I), comprising a  
CC genetically modified antibody molecule which specifically binds to  
CC ganglioside GD3 and has an N-glycoside-binding complex sugar chain in its  
CC FC domain, where the N-glycoside-binding complex sugar chain is a sugar  
CC chain having no fucose attached to N-acetylglucosamine at the reducing  
CC end of the sugar chain. Also described are: a transformant (II) capable  
CC of producing (I), obtained by introducing DNA that encodes the antibody  
CC molecule which specifically binds with ganglioside GD3, to a host cell;  
CC producing (I), involving cultivating (I) in a culture medium, such that  
CC CI (sic) is produced and accumulated in the culture, extracting and  
CC purifying CI from the culture medium; a pharmaceutical (III) containing  
CC CI as an active ingredient; and a therapeutic agent (A1) for ganglioside  
CC GD3 associated disease, comprising CI as an active ingredient. (I) is  
CC useful for treating GD3 associated disease, which involves administering

Query Match 92.8%; Score 579; DB 4; Length 119;  
Best Local Similarity 91.6%; Pred. No. 1.4e-45;  
Matches 109; Conservative 5; Mismatches 5; Indels 0; Gaps 0;  
QY 1 EVLVESGGDFVQPGSLRVSCAAGFAFASHYAMSWVRQAPKGLEWVAYISSGSGTTY 60  
DB 1 EVTLVESGGDFVKPGGSLKVSACAGFAFASHYAMSWVRQTPAKRLEWVAYISSGSGTTY 60  
QY 61 SDSVKGRFTISRDNKNTLYLQMSLRSEDNAVYFCTRVKLGTYTFDSWGQGTTLTVSS 119  
DB 61 SDSVKGRFTISRDNKNTLYLQMSLRSEDSAMYFCTRVKLGTYTFDSWGQGTTLTVSS 119  
RESULT 7  
ABU11012  
ID ABU11012 standard; protein; 119 AA.  
XX  
AC ABU11012;  
XX  
DT 04-FEB-2003 (first entry)  
DE Modified ganglioside GD3 antibody associated protein #5.  
XX  
KW Ganglioside GD3; anti-ganglioside GD3 antibody; tumour; melanoma.  
XX  
OS Mus musculus.  
XX  
PN WO200278739-A1.  
XX  
PD 10-OCT-2002.  
XX  
PF 29-MAR-2002; 2002WO-JP003170.  
XX  
PR 29-MAR-2001; 2001JP-00097483.  
XX  
XX (KYOW ) KYOWA HAKKO KOGYO KK.  
XX  
PI Shitara K, Niwa R, Kanazawa J, Asada M;  
PI WPI; 2003-067410/06.  
XX  
XX Drugs containing genetically-modified antibody against ganglioside GD3,  
PT its fragment, immunocompetent cell activators or/and antitumor agents in  
PT combination, applicable in treating malignant tumor like melanoma.  
XX  
XX Claim 7; Page 112-113; 121pp; Japanese.  
PS  
PS The invention describes drugs contain a genetically-modified antibody  
CC against ganglioside GD3 or its fragment and at least 1 of a substance

CC (I), where the GD3 associated diseases is cancer. (A1) is also useful for  
 CC treating GD3 associated disease. (II) is useful for producing (I) (I) is  
 CC useful for manufacturing a therapeutic agent for GD3 associated disease.  
 CC This sequence represents a ganglioside GD3 binding antibody associated  
 CC protein.  
 XX  
 SQ Sequence 119 AA;

Query Match 92.8%; Score 579; DB 9; Length 119;  
 Best Local Similarity 91.6%; Pred. No. 1.4e-45;  
 Matches 109; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 EVLVESGGDFVQPGSLRVSCAASGFAPSHYAMSWVRQAPKGLWVAYISSGSGTTY 60  
 DB 1 EVTLVESGGDFVQPGSLRVSCAASGFAPSHYAMSWVRQTPAKRLWVAYISSGSGTTY 60  
 QY 61 SDSVKGRFTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLGTYYPDSWGQGTLLTVSS 119  
 DB 61 SDSVKGRFTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLGTYYPDSWGQGTLLTVSS 119

RESULT 9  
 AAR33256  
 ID AAR33256 standard; protein; 130 AA.  
 XX  
 AC AAR33256;

DT 25-MAR-2003 (revised)  
 DT 12-JUL-1993 (first entry)  
 XX  
 XX Rat immunoglobulin H chain variable region of pKM641HA3.

XX Promoter; variable; region; rat; immunoglobulin; heavy; H; chain;  
 KW humanised; chimeric; antibody; expression vector.  
 XX  
 XX Rattus rattus.

XX Key Location/Qualifiers  
 FH Peptide 1..10  
 FT /note= "Signal peptide"  
 FT Protein 11..130  
 FT /note= "Mature protein"

XX EP533199-A2.  
 XX  
 XX 24-MAR-1993.  
 XX  
 XX 18-SEP-1992; 92EP-00116026.  
 XX  
 XX 18-SEP-1991; 91JP-00238375.  
 XX  
 XX (KYOW ) KYOWA HAKKO KOGYO CO LTD.

XX Shitara K, Hanai N, Hasegawa M, Miyaji H, Kuwana Y;  
 XX  
 XX WPI; 1993-095510/12.  
 DR N-PSDB; AAQ33257.

XX Humanised chimeric antibody prodn. against ganglioside GD3 - for treating  
 PT cancers, such as melanoma, neuroblastoma, etc.  
 XX  
 XX Claim 6; Page 29-30; 63pp; English.

XX The sequences given in AAR33256-57 represent rat heavy and light chain  
 CC variable regions respectively. The DNA sequences encoding these proteins  
 CC were used in the construction of humanised chimeric antibody expression  
 CC vectors. In these humanised antibodies none of the amino acids of the non  
 CC -human animal Ab variable region have been changed. (Updated on 25-MAR-  
 CC 2003 to correct PN field.)  
 XX  
 SQ Sequence 130 AA;

Query Match 92.8%; Score 579; DB 2; Length 130;

Best Local Similarity 91.6%; Pred. No. 1.5e-45;  
 Matches 109; Conservative 5; Mismatches 5; Indels 0; Gaps 0;  
 QY 1 EVLVESGGDFVQPGSLRVSCAASGFAPSHYAMSWVRQAPKGLWVAYISSGSGTTY 60  
 DB 11 EVTLVESGGDFVQPGSLRVSCAASGFAPSHYAMSWVRQTPAKRLWVAYISSGSGTTY 70  
 QY 61 SDSVKGRFTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLGTYYPDSWGQGTLLTVSS 119  
 DB 71 SDSVKGRFTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLGTYYPDSWGQGTLLTVSS 129

RESULT 10  
 AAR53341  
 ID AAR53341 standard; protein; 130 AA.  
 XX  
 AC AAR53341;

DT 18-NOV-1994 (first entry)  
 XX  
 XX KM641 L chain variable region.

XX Monoclonal antibody; Ab; ganglioside GM2; chimera; chimeric antibody;  
 KW expression vector; heavy; light; chain; hypervariable region; CDR;  
 KW constant region; hybridoma; Ig; immunoglobulin; promoter; enhancer.  
 XX  
 OS Mus musculus.

XX Key Location/Qualifiers  
 FH Peptide 1..10  
 FT /label= sig\_peptide

XX AU9346181-A.  
 XX 17-MAR-1994.

XX 07-SEP-1993; 93AU-00046181.  
 XX  
 XX 07-SEP-1992; 92JP-00238452.  
 XX  
 XX (KYOW ) KYOWA HAKKO KOGYO KK.

XX Nakamura K, Koike M, Shitara K, Hanai N, Kuwana Y, Hasegawa M;  
 XX  
 XX WPI; 1994-126857/16.  
 DR N-PSDB; AAQ45439.

XX Humanised antibody specific for ganglioside GM2 - used for producing a  
 PT cytotoxic effect on cancers such as melanoma, neuroblastoma and glioma.  
 XX  
 XX Example 2; Page 116-117; 191pp; English.

XX Example 2 describes the construction of the vector pChi641HA1 for  
 CC chimeric human antibody H chain expression. mRNA from mouse anti-GD3  
 CC monoclonal Ab KM641-producing cells was isolated and KM641 H and L chain  
 CC cDNAs isolated. The base sequences of the Ig variable regions in KM641 H  
 CC chain cDNA (pKM641HA3) and KM641 L chain cDNA (pKM641LA2) are given in  
 CC AAQ45438-39. A KM641-derived chimeric human Ab H chain expression vector  
 CC was constructed by joining the H chain variable region gene from  
 CC pKM641HA3 to a vector for chimeric human Ab H chain expression using the  
 CC synthetic DNAs given in AAQ63439 and AAQ63440

XX Sequence 130 AA;

Query Match 92.8%; Score 579; DB 2; Length 130;  
 Best Local Similarity 91.6%; Pred. No. 1.5e-45;  
 Matches 109; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 EVLVESGGDFVQPGSLRVSCAASGFAPSHYAMSWVRQAPKGLWVAYISSGSGTTY 60  
 DB 11 EVTLVESGGDFVQPGSLRVSCAASGFAPSHYAMSWVRQTPAKRLWVAYISSGSGTTY 70  
 QY 61 SDSVKGRFTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLGTYYPDSWGQGTLLTVSS 119





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XX PD 05-APR-2001.
XX PF 29-SEP-2000; 2000WO-JP006774.
XX PR 30-SEP-1999; 99JP-00278291.
XX PR 06-APR-2000; 2000JP-00105088.
XX XX (KYOW ) KYOWA HAKKO KOGYO KK.
XX PA Hanai N, Shitara K, Nakamura K, Niwa R;
XX PI WPI; 2001-266143/27.
XX DR
XX XX
XX PT New human type complementation-determining region-transplanted antibody.
XX PT and derivatives against ganglioside GD3, useful in diagnosis and therapy
XX of e.g. tumors, with low antigenicity, little side effects but potent
XX activity in cancer.
XX PS Example 1; Page 138-139; 183pp; Japanese.
XX CC The present invention describes a monoclonal antibody which can react
XX specifically with ganglioside GD3. The antibody and its derivatives are
XX useful in the diagnosis and therapy of tumors, particularly cancer
XX diagnosis. The present sequence is a protein used in the exemplification
XX of the invention
XX SQ Sequence 138 AA;

Query Match 92.8%; Score 579; DB 4; Length 138;
Best Local Similarity 91.6%; Pred. No. 1.6e-45;
Matches 109; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 EVQLVESGGDFVQPGGSLRVSCAASGFAFASHYAMSVVRQAPKGLEWVAYISSGGSGTYY 60
DB 20 EVTLVESGGDFVQPGGSLRVSCAASGFAFASHYAMSVVRQAPKGLEWVAYISSGGSGTYY 79
QY 61 SDSVKGRFTISRDNKNTLYLQMRSLRAEDSAVFCTRVKLGTYYPDSWGQGTLLTVSS 119
DB 80 SDSVKGRFTISRDNKNTLYLQMRSLRAEDSAVFCTRVKLGTYYPDSWGQGTLLTVSS 138

RESULT 14
ABU11002
ID ABU11002 standard; protein; 138 AA.
XX AC ABU11002;
XX DT 04-FEB-2003 (first entry)
XX DE Modified ganglioside GD3 antibody associated protein #1.
XX KW Ganglioside GD3; anti-ganglioside GD3 antibody; tumour; melanoma.
XX OS Mus musculus.
XX PN WO200278739-A1.
XX PD 10-OCT-2002.
XX PF 29-MAR-2002; 2002WO-JP003170.
XX PR 29-MAR-2001; 2001JP-00097483.
XX XX (KYOW ) KYOWA HAKKO KOGYO KK.
XX PA Shitara K, Niwa R, Kanazawa J, Asada M;
XX PI WPI; 2003-067410/06.
XX DR
XX PT Drugs containing genetically-modified antibody against ganglioside GD3,
XX its fragment, immunocompetent cell activators or/and antitumor agents in
XX combination, applicable in treating malignant tumor like melanoma.

XX PS Example 3; Page 97; 121pp; Japanese.
XX CC The invention describes drugs contain a genetically-modified antibody
XX against ganglioside GD3 or its fragment and at least 1 of a substance
XX capable of activating immunocompetent cells and a substance having an
XX antitumor activity in combination. The drugs can be used to treat tumour
XX like melanoma and can provide a treatment with enhanced therapeutic
XX effect and little side-reactions, particularly to relieve problems of
XX side-effects during the conventional single administration. This sequence
XX represents a protein associated with the anti- ganglioside GD3 antibody
XX SQ Sequence 138 AA;

Query Match 92.8%; Score 579; DB 6; Length 138;
Best Local Similarity 91.6%; Pred. No. 1.6e-45;
Matches 109; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 EVQLVESGGDFVQPGGSLRVSCAASGFAFASHYAMSVVRQAPKGLEWVAYISSGGSGTYY 60
DB 20 EVTLVESGGDFVQPGGSLRVSCAASGFAFASHYAMSVVRQAPKGLEWVAYISSGGSGTYY 79
QY 61 SDSVKGRFTISRDNKNTLYLQMRSLRAEDSAVFCTRVKLGTYYPDSWGQGTLLTVSS 119
DB 80 SDSVKGRFTISRDNKNTLYLQMRSLRAEDSAVFCTRVKLGTYYPDSWGQGTLLTVSS 138

RESULT 15
AAB81991
ID AAB81991 standard; protein; 582 AA.
XX AC AAB81991;
XX DT 03-JUL-2001 (first entry)
XX DE Ganglioside GD3 specific antibody related protein SEQ ID NO: 57.
XX KW Ganglioside; GD3; complementarity determining region; CDR; antibody;
XX cancer.
XX OS Synthetic.
XX PN WO200123432-A1.
XX PD 05-APR-2001.
XX PF 29-SEP-2000; 2000WO-JP006774.
XX PR 30-SEP-1999; 99JP-00278291.
XX PR 06-APR-2000; 2000JP-00105088.
XX PA (KYOW ) KYOWA HAKKO KOGYO KK.
XX PI Hanai N, Shitara K, Nakamura K, Niwa R;
XX DR WPI; 2001-266143/27.
XX XX
XX PT New human type complementation-determining region-transplanted antibody
XX and derivatives against ganglioside GD3, useful in diagnosis and therapy
XX of e.g. tumors, with low antigenicity, little side effects but potent
XX activity in cancer.
XX PS Claim 39; Page 175-179; 183pp; Japanese.
XX CC The present invention describes a monoclonal antibody which can react
XX specifically with ganglioside GD3. The antibody and its derivatives are
XX useful in the diagnosis and therapy of tumors, particularly cancer
XX diagnosis. The present sequence is a protein used in the exemplification
XX of the invention
XX SQ Sequence 582 AA;

Query Match 92.8%; Score 579; DB 4; Length 582;
```

Best Local Similarity 91.6%; Pred. No. 7.3e-45;  
Matches 109; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Qy	1	EVOLVEGGDFVOPGGSLRVSCAAGFAFSHYAMSWVRQAPGKLEWVAYISSGGSGTYT	60
		:     :     :     :     :     :     :     :     :	
Db	1	EVTLVESGGDFVKPGGSLKVSACAAGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYT	60
		:     :     :     :     :     :     :     :	
Qy	61	SDSVKGRFTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLGTYTFDSWGQGTLLTVSS	119
		:     :     :     :     :     :     :     :	
Db	61	SDSVKGRFTISRDNKNTLYLQMRSLRSEDSAMYFCTRVKLGTYTFDSWGQGTLLTVSS	119
		:     :     :     :     :     :     :     :	

Search completed: April 6, 2006, 08:50:42  
Job time : 28.6031 secs

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: April 6, 2006, 08:49:11 ; Search time 6.09924 Seconds  
(without alignments)  
1877.250 Million cell updates/sec

Title: US-10-089-500-9  
Perfect score: 624  
Sequence: 1 EVQLVESGGDFVQPGGSLRV.....KLGTYYFDSWGQGLTLTVSS 119

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 80:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	501	80.3	119	2 S31107	Ig heavy chain - h
2	501	80.3	138	2 S31666	Ig heavy chain v r
3	486	77.9	119	2 D36005	Ig heavy chain v r
4	484	77.6	119	2 S31108	Ig heavy chain - h
5	483	77.4	140	2 S31686	Ig heavy chain v r
6	482.5	77.3	140	2 S70442	Ig heavy chain pre
7	480	76.9	123	2 S31114	Ig heavy chain - h
8	479	76.8	125	2 S30531	Ig heavy chain v r
9	477.5	76.5	124	2 S20782	Ig heavy chain v r
10	477.5	76.5	128	2 S26790	Ig heavy chain v r
11	474	76.0	119	2 C36005	Ig heavy chain v r
12	474	76.0	135	2 S31598	Ig heavy chain v r
13	474	76.0	140	2 S31588	Ig heavy chain v r
14	473.5	75.9	120	2 S48798	Ig heavy chain v r
15	471	75.5	160	2 S05271	Ig heavy chain pre
16	470.5	75.4	118	2 S31105	Ig heavy chain (su
17	470.5	75.4	135	2 I31778	Ig variable region
18	470	75.3	119	2 F36005	Ig heavy chain v r
19	469.5	75.2	120	2 S44111	Ig heavy chain v-D
20	469	75.2	127	2 S38489	Ig heavy chain - h
21	466.5	74.8	122	2 PC2398	anti-tetanus toxin
22	466	74.7	121	2 G36005	Ig heavy chain v r
23	466	74.7	132	2 S31603	Ig heavy chain v r
24	466	74.7	143	2 S23624	Ig heavy chain v r
25	465	74.5	134	2 S31679	Ig heavy chain v r
26	464.5	74.4	139	2 S31674	Ig heavy chain v r
27	464	74.4	121	2 I55673	Ig heavy chain - h
28	464	74.4	121	2 S19666	Ig heavy chain v r
29	464	74.4	134	2 S31699	Ig heavy chain v r

30	463.5	74.3	114	2 S31120	Ig heavy chain - h
31	463.5	74.3	147	2 I37780	Ig variable region
32	462.5	74.1	128	2 S26786	Ig heavy chain v r
33	462	74.0	139	2 I37781	Ig variable region
34	461.5	74.0	136	2 S31587	Ig heavy chain v r
35	461.5	74.0	137	2 S78054	Ig heavy chain pre
36	459.5	73.6	114	2 S46390	Ig heavy chain v r
37	459	73.6	140	2 A30532	Ig heavy chain pre
38	458.5	73.5	141	2 S31669	Ig heavy chain v r
39	457.5	73.3	122	2 E36005	Ig heavy chain v r
40	457	73.2	123	2 S26794	Ig heavy chain v r
41	455	72.9	119	2 B34353	anti-peptide Fab'
42	454.5	72.8	120	2 S31112	Ig heavy chain - h
43	453.5	72.7	118	2 S31116	Ig heavy chain - h
44	453.5	72.7	122	2 S20772	Ig heavy chain v r
45	453.5	72.7	133	2 S31510	Ig heavy chain - h

ALIGNMENTS

RESULT 1

S31107  
Ig heavy chain - human  
C:Species: Homo sapiens (man)  
C:Date: 02-Dec-1993 #sequence\_revision 26-May-1995 #text\_change 17-Mar-1999  
C:Accession: S31107  
R:Raphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman Eur. J. Immunol. 22, 247-251, 1992  
A:Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complement A:Reference number: S31104; MUID:92111633; PMID:1730252  
A:Accession: S31107  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-119 <RAA>  
A:Cross-references: UNIPARC:UPI0000176DC7; EMBL:X62955  
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match	80.3%	Score 501;	DB 2;	Length 119;
Best Local Similarity	79.8%;	Pred. No. 3.4e-38;		
Matches	95;	Conservative	8;	Mismatches 16;
		Indels	0;	Gaps 0;
QY	1	EVQLVESGGDFVQPGGSLRVCAASGFAFASHYAMSVVRQAPGKGLEWVAYISSGSGSTYY	60	
Db	1	EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMSVVRQAPGKGLEWVSAISSGSGSTYY	60	
QY	61	SDSVKGRFTISRDNSKNTLYLQMNSLRAEDSAVYFCTRVKLTGYFDPSWGQGLTLTVSS	119	
Db	61	ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVVYCAKDPGASVYFDYWGQGLTLTVSS	119	

RESULT 2

S31666  
Ig heavy chain V region - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999  
C:Accession: S31666  
R:Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C. submitted to the EMBL Data Library, June 1992  
A:Description: Mechanisms that generate human immunoglobulin diversity operate from the A:Reference number: S31585  
A:Accession: S31666  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-138 <CUI>  
A:Cross-references: UNIPARC:UPI0000116474; EMBL:Z14202; NID:g30963; PIDN:CAA78571.1; PID C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:34-117/Domain: immunoglobulin homology <IMM>





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RESULT 11
C36005
Ig heavy chain V region (30pl) - human
C/Species: Homo sapiens (man)
C/Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 16-Aug-1996
C/Accession: C36005
R/Schroeder Jr., H.W.; Wang, J.Y.
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
A/Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene
A/Reference number: A36005; MUID:90349571; PMID:2117273
A/Accession: C36005
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-119 <SCH>
A/Cross-references: UNIPARC:UPI0000176C27; GB:M18513
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 76.0%; Score 474; DB 2; Length 119;
Best Local Similarity 77.3%; Pred. No. 9.2e-36;
Matches 92; Conservative 8; Mismatches 19; Indels 0; Gaps 0;

Qy 1 EVQLVESGGGVQPGGSLRVSCAASGAFSPSHYAMSWVRQAPGKGLEWYATISSGSGSTYY 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 EVQLVESGGGVQPGGSLRVSCAASGTFSSYAMSWVRQAPGKGLEWYATISSGSGSTYY 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 61 SDSVKGRFTISRDNKNTLYLQMSLRRAEDSAVFCTRVKLTGYFPDSWGOGTLLTVSS 119
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 ADSVKGRFTISRDNKNTLYLQMSLRRAEDTAVYCAKDGWGSDFYWGOGTLTVTSS 119
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 12
S31598
Ig heavy chain V region - human
C/Species: Homo sapiens (man)
C/Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C/Accession: S31598
R/Cuisinier, A.M.; Gauthier, L.; Boublil, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A/Description: Mechanisms that generate human immunoglobulin diversity operate from the
A/Reference number: S31585
A/Accession: S31598
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-135 <CU1>
A/Cross-references: UNIPARC:UPI0000116457; EMBL:Z14170; NID:g31001; PIDN:CAA78539.1; PII:
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F:31-114/Domain: immunoglobulin homology <IMM>

Query Match 76.0%; Score 474; DB 2; Length 135;
Best Local Similarity 75.6%; Pred. No. 1e-35;
Matches 90; Conservative 9; Mismatches 20; Indels 0; Gaps 0;

Qy 1 EVQLVESGGGVQPGGSLRVSCAASGAFSPSHYAMSWVRQAPGKGLEWYATISSGSGTYY 60
Db 17 QVQLVESGGGVQPGGSLRVSCAASGTFSSYGMHVRQAPGKGLEWYAFIRYDGSNKYY 76
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 61 SDSVKGRFTISRDNKNTLYLQMSLRRAEDSAVFCTRVKLTGYFPDSWGOGTLLTVSS 119
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 77 ADSVKGRFTISRDNKNTLYLQMSLRRAEDTAVYCAKISWEVSERFDYWGOGTLTVTSS 135
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 13
S31588
Ig heavy chain V region - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C/Accession: S31588
R/Cuisinier, A.M.; Gauthier, L.; Boublil, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992

```

A;Description: Mechanisms that generate human immunoglobulin diversity operate from the

A;Reference number: S31585

A;Accession: S31588

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-140 <CUI>

A;Cross-references: UNIPARC:UPI0000116472; EMBL:Z14200; NID:g30957; PIDN:CAA78569.1; PID

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 76.0%; Score 474; DB 2; Length 140;

Best Local Similarity 76.9%; Pred. No. 1.1e-35;

Matches 93; Conservative 9; Mismatches 17; Indels 2; Gaps 2;

Qy 1 EVQLVESGGDFVQPGGSLRVSCAAGFAFASHYAMSVWROAPGKGLEWVAIVSSGGSTYY 60

Db 20 EVQLLESQGGVLPQGGSLRVSCAAGFTFSSYAMSVWROAPGKGLEWVAISGGSTYY 79

Qy 61 SDSVKGRFTISRDNKNTLYLQMRSLRAEDSAVYFCTR-VKLGT-YFDSWGQGLTLTVS 118

Db 80 ADSVKGRFTISRDNKNTLYLQMRSLRAEDTAVYYCAKQHDYSNYIYFDYWGQGLTLTVS 139

Qy 119 S 119

Db 140 S 140

RESULT 14

S48798

Ig heavy chain V region (anti-Sm, VH3/Dxp4/JH4b) - human

C;Species: Homo sapiens (man)

C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 23-Jul-1999

C;Accession: S48798

R;Mahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D.

submitted to the EMBL Data Library, October 1994

A;Description: Molecular characterization of natural human anti-Sm autoantibodies.

A;Reference number: S48797

A;Accession: S48798

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-120 <MAH>

A;Cross-references: UNIPARC:UPI0000116701; EMBL:Z46382; NID:g562324; PIDN:CAA6521.1; PI

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 75.9%; Score 473.5; DB 2; Length 120;

Best Local Similarity 76.7%; Pred. No. 1e-35;

Matches 92; Conservative 10; Mismatches 17; Indels 1; Gaps 1;

Qy 1 EVQLVESGGDFVQPGGSLRVSCAAGFAFASHYAMSVWROAPGKGLEWVAIVSSGGSTYY 60

Db 1 EVQLLESQGGVLPQGGSLRVSCAAGFTFSSYAMSVWROAPGKGLEWVAISGGSTYY 60

Qy 61 SDSVKGRFTISRDNKNTLYLQMRSLRAEDSAVYFCTR-VK-LCTYYFDSWGQGLTLTVS 119

Db 61 ADSVKGRFTISRDNKNTLYLQMRSLRAEDTAVYYCAKQGRFWSGYKDYWGQGLTLTVS 120

RESULT 15

S05271

Ig heavy chain precursor - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 31-Dec-2004

C;Accession: S05271; S04602

R;Kishimoto, T.

submitted to the EMBL Data Library, March 1989

A;Reference number: S05270

A;Accession: S05271

A;Molecule type: mRNA

A;Residues: 1-160 <KIS1>

A;Cross-references: UNIPROT:O96BB9; UNIPARC:UPI0000176B50; EMBL:X14584



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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 6, 2006, 08:48:06 ; Search time 36.855 Seconds

(without alignments)  
2278.061 Million cell updates/sec

**Title:** US-10-089-500-9

Perfect score: 624

Sequence: 1 EVQLVESGGDFVQPGGSLRV.....KLGTYYFDSWGQGLLTVSS 119

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs. 705528306 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Minimum	DB	seq	length:	0
Maximum	DB	seq	length:	2000000000

Post-processing: Minimum Match 0%

Post processing: Minimum Match 0%  
Maximum Match 100%

Maximum MATCH 100%  
Listing first 45 summaries

Database : UniProt 05.80:\*

```
1: uniprot_sprot:*
```

2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	
1	469	75.2	121	2	Q9UL71_HUMAN	Q9ul71 homo sapien	
2	463.5	74.3	459	2	Q569F4_HUMAN	Q569f4 homo sapien	
3	456	73.1	464	2	Q6MZU6_HUMAN	Q6mzu6 homo sapien	
4	456	73.1	470	2	Q6PUYA_HUMAN	Q6pu1a4 homo sapien	
5	455.5	73.0	613	2	Q8WUK1_HUMAN	Q8wuk1 homo sapien	
6	455	72.9	113	2	Q9UL90_HUMAN	Q9ul90 homo sapien	
7	455	72.9	597	2	Q96HB9_HUMAN	Q96hb9 homo sapien	
8	454	72.8	478	2	Q6P181_HUMAN	Q6p181 homo sapien	
9	451.5	72.4	118	2	Q9UL91_HUMAN	Q9ul91 homo sapien	
10	451.5	72.4	606	2	Q6GMY2_HUMAN	Q6gmy2 homo sapien	
11	451	72.3	240	2	Q65YC9_HUMAN	Q65yc9 homo sapien	
12	450	72.1	479	2	Q5POK9_RAT	Q5pok9 rattus norv	
13	449.5	72.0	119	2	Q5FP18_MOUSE	Q5fp18 mus musculus	
14	448.5	71.9	118	2	Q9UL72_HUMAN	Q9ul72 homo sapien	
15	448.5	71.9	475	2	Q6MZQ6_HUMAN	Q6mzq6 homo sapien	
16	447	71.6	493	2	Q6GMX2_HUMAN	Q6gm26 homo sapien	
17	446	71.5	119	2	Q920E7_MOUSE	Q920e7 mus musculus	
18	446	71.5	479	2	Q5BK12_RAT	Q5bk12 rattus norv	
19	443.5	71.1	473	2	Q6MZV7_HUMAN	Q6mzv7 homo sapien	
20	443	71.0	116	2	Q9UL93_HUMAN	Q9ul93 homo sapien	
21	442.5	70.9	465	2	Q6P6C4_HUMAN	Q6p6c4 homo sapien	
22	441	70.7	255	2	Q6KB05_MOUSE	Q6kb05 mus musculus	
23	438.5	70.3	122	2	Q9UL84_HUMAN	Q9ul84 homo sapien	
24	438.5	70.3	487	2	Q99KA4_MOUSE	Q99ka4 mus musculus	
25	437.5	70.1	122	1	HV3G_HUMAN	Q91768 homo sapien	
26	437.5	70.1	465	2	Q510J0_RAT	Q510j0 rattus norv	
27	437.5	70.1	494	2	Q95K68_HUMAN	Q95k68 homo sapien	
28	435.5	69.8	147	2	Q9Y509_HUMAN	Q9y509 homo sapien	
29	433.5	69.5	473	2	Q91Z05_MOUSE	Q91z05 mus musculus	
30	433	69.4	479	2	Q91WP5_MOUSE	Q91wp5 mus musculus	
31	431.5	69.2	112	2	Q9HCC1_HUMAN	Q9hcc1 homo sapien	

[illegible]

## ALIGNMENTS

```

RESULT 1
ID Q9UL71_HUMAN PRELIMINARY; PRT; 121 AA.
AC Q9UL71;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homi
OC Homo
OX NCBI_TaxID=9606;
[1]
RN NUCLEOTIDE SEQUENCE.
RP PubMed=9827139; PubMed=9614934; DOI=10.1006/cclin.1998.4531;
RX Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RE fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998) .
DR EMBL; AF035043; AAD56279.1; -; mRNA.
DR HSSP; P01852; 1NFD.
DR SMR; Q9UL71; 1-121.
DR Ensembl; ENSG00000130076; Homo sapiens.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 1..
DR PROSITE; PS50835; IG-LIKE; 1.
FT NON TER 1
FT NON TER 121
SQ SEQUENCE 121 AA; 13154 MW; 2F045CCFA5D50736 CRC64;

```

Query Match	75.2%	Score 469;	DB 2;	Length 121;
Best Local Similarity	74.4%	Pred. No. 3e-41;		
Matches	90;	Conservative 11;	Mismatches 18;	Indels 2; Gaps 1;

  

1	EVOLVESGGDFVQPGSLVSCAASGPFASFHYAMSWVRQAPCKGLEWVAVYISGSGSTYY	60
1	EVOLVESGGVVPQGSRLRFCAASGTFDGYAMHWVRQAPCKGLEWVSLISGGGSTYY	60
61	SDSVKGRFTISRDNSKNTLYLQMRSLRAEDSNVYFCTRVKLTYY--FDSWGQGTLLTVS	118
61	ADSVKGRFTISRDNSKNSLYLQMSLRADETALYCAKGVTTTYDRPDINGOGTMTVTS	120

RESULT 2  
Q569F4 HUMAN  
ID Q569F4 HUMAN PRELIMINARY;  
PRT; 469 AA.



```
RC TISSUE=Primary B-Cells;
RG NIH MGC Project;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC018747; AAH18747.1; -, mRNA.
DR HSSP; P01861; 1ADQ.
DR SMR; Q6PJA4; 20-470.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
SQ SEQUENCE 470 AA; 51716 MW; 7B49556A11FD7D99 CRC64;

Query Match 73.1%; Score 456; DB 2; Length 470;
Best Local Similarity 74.4%; Pred. No. 3.3e-39;
Matches 90; Conservative 7; Mismatch 22; Indels 2; Gaps 1;

QY 1 EVQLVESGGDFVQPGSGSLRVSCAAGFATFSYAMSVWRQAPGKLEWVAYISSGGSGTY 60
DB 20 EVQLVESGGGLVQPGSLRLSCVSGFTFSSTWMSWRQAPGKLEWVANIQDGSERY 79
QY 61 SDPSVGRFTISRDNKNTLYLQWRLRAEDSAVYFCYTRVKLGTY--YFDSWQGGTLTYS 118
DB 80 VDSVGRFTISRDNKAKNSLYLQWNSLRADETAVYCYCARDGSSWYRDFPWCQGLTIVTS 139
QY 119 S 119
DB 140 S 140

RESULT 5
ID Q8WUK1 HUMAN PRELIMINARY; PRT; 613 AA.
AC Q8WUK1;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE IGHM protein.
GN Name=IGHM;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toehlyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A.C., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalka U., Smallos D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RN NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RG NIH MGC Project;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
[3]
RN NUCLEOTIDE SEQUENCE.
RP PubMed=2117273;
RX Schroeder H.W. Jr, Wang J.Y.;
RA "Preferential utilization of conserved immunoglobulin heavy chain
RT variable gene segments during human fetal life.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:6146-6150(1990).
[4]
RN NUCLEOTIDE SEQUENCE.
RP PubMed=1383695; DOI=10.1016/0161-5890(92)90173-U;
RX Cuisinier A.M., Fumoux F., Fougereau M., Tonnelie C.;
RA "IGM kappa/lambda EBV human B cell clone: an early step of
RT differentiation of fetal B cells or a distinct B lineage?";
RL Mol. Immunol. 29:1363-1373(1992).
[5]
RN NUCLEOTIDE SEQUENCE.
RP PubMed=1730252;
RX Raaphorst F.M., Timmers E., Kenter M.J., Van Tol M.J., Vossen J.M.,
RA Schuurman R.K.;
RA "Restricted utilization of germ-line VH3 genes and short diverse third
RT complementarity-determining regions (CDR3) in human fetal B lymphocyte
RL immunoglobulin heavy chain rearrangements.";
RL Eur. J. Immunol. 22:247-251(1992).
[6]
RN NUCLEOTIDE SEQUENCE.
RP PubMed=1904154;
RX Neale G.A., Kitchingman G.R.;
RA "mRNA transcripts initiating within the human immunoglobulin mu heavy
RT chain enhancer region contain a non-translatable exon and are
RT extremely heterogeneous at the 5' end.";
RL Nucleic Acids Res. 19:2427-2433(1991).
[7]
RN NUCLEOTIDE SEQUENCE.
RP PubMed=2840480; DOI=10.1084/jem.168.1.229;
RX Bird J., Galili N., Link M., Stites D., Sklar J.;
RA "Continuing rearrangement but absence of somatic hypermutation in
RT immunoglobulin genes of human B cell precursor leukemia.";
RL J. Exp. Med. 168:229-245(1988).
[8]
RN NUCLEOTIDE SEQUENCE.
RP PubMed=2538551; DOI=10.1084/jem.169.4.1391;
RX Nickerson K.G., Berman J., Glickman E., Chess L., Alt F.W.;
RA "Early human IGH gene assembly in Epstein-Barr virus-transformed fetal
RT B cell lines. Preferential utilization of the most JH-proximal D
segment (DQ52) and two unusual VH-related rearrangements.";
RL J. Exp. Med. 169:1391-1403(1989).
[9]
RN NUCLEOTIDE SEQUENCE.
RP MEDLINE=93301610; PubMed=8315388; DOI=10.1084/jem.178.1.331;
RX Hillson J.L., Karr N.S., Opplinger I.R., Mannik M., Sasso E.H.;
RA "The structural basis of germline-encoded VH3 immunoglobulin binding
RT to staphylococcal protein A.";
RL J. Exp. Med. 178:331-336(1993).
DR EMBL; BC020240; AAH20240.1; -, mRNA.
DR PIR; F36005; F36005.
DR PIR; G36005; G36005.
DR PIR; PH1642; PH1642.
DR PIR; PH1643; PH1643.
DR PIR; PH1645; PH1645.
DR PIR; PH1646; PH1646.
DR PIR; PL0098; PL0098.
DR PIR; PL0120; PL0120.
DR PIR; S15590; S15590.
DR PIR; S31116; S31116.
DR PIR; S31119; S31119.
DR PIR; S70442; S70442.
DR HSSP; P01861; 1ADQ.
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DR SMR; Q8WUK1; 20-242.
DR Ensembl; ENSG00000130076; Homo sapiens.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; C1-set; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG_LIKE; 5.
DR PROSITE; PS0290; IG_MHC; UNKNOWN_3.
KW Immunoglobulin domain.
SQ SEQUENCE 613 AA; 67296 MW; 60C7F5950671E315 CRC64;

Query Match 73.0%; Score 455.5; DB 2; Length 613;
Best Local Similarity 75.0%; Pred. No. 5.1e-39;
Matches 90; Conservative 8; Mismatches 21; Indels 1; Gaps 1;

QY 1 EVQLVESGGDFVQPGGSLRVSCAASGFAFASHYAMSVWRQAPGKGLWVAIVSSGSGTTY 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 20 QVQLVESGGGVVQPGGSLRLSCAASGFTFSYGMHWVRQAPGKGLWVAIVSYDGSNKY 79
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 SDSVKGRFTISRDNKNTLYLQMSLRADSAVYFCTR-VKLGTYFDSSWGQGLTLTVSS 119
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 80 ADSVKGRFTISRDNKNTLYLQMSLRADTAIVYCAKDSGVEFDIWGQGLTLTVSS 139
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 6
Q9UL90 HUMAN
ID Q9UL90 HUMAN PRELIMINARY; PRT; 113 AA.
AC Q9UL90.
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2004 (TrEMBLrel. 26, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
(Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berny S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
   fetus."
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=1730252;
RA Raaphorst F.M., Timmers E., Kenter M.J., Van Tol M.J., Vossen J.M.,
RA Schuurman R.K.;
RT "Restricted utilization of germ-line VH3 genes and short diverse third
   complementarity-determining regions (CDR3) in human fetal B lymphocyte
   immunoglobulin heavy chain rearrangements."
RL Eur. J. Immunol. 22:247-251(1992).
DR EMBL; AF035024; AAD56260.1; -; mRNA.
DR PIR; S78486; S78486.
DR HSSP; P01772; 2FB4.
DR SMR; Q9UL90; 1-113.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 113
SQ SEQUENCE 113 AA; 12437 MW; ED57FDD19086D07F CRC64;

Query Match 72.9%; Score 455; DB 2; Length 113;
Best Local Similarity 74.8%; Pred. No. 8.2e-40;
Matches 89; Conservative 8; Mismatches 16; Indels 6; Gaps 1;

QY 1 EVQLVESGGDFVQPGGSLRVSCAASGFAFASHYAMSVWRQAPGKGLWVAIVSSGSGTTY 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 EVQLVESGGGVVQPGGSLRLSCAASGFTFSYGMHWVRQAPGKGLWVAIVSYDGSNKY 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 SDSVKGRFTISRDNKNTLYLQMSLRADSAVYFCTR-VKLGTYFDSSWGQGLTLTVSS 119
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 ADSVKGRFTISRDNKNTLYLQMSLRADTAIVYCAKDSGVEFDIWGQGLTLTVSS 113
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 7
Q96BB9 HUMAN
ID Q96BB9 HUMAN PRELIMINARY; PRT; 597 AA.
AC Q96BB9.
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE IGHM protein.
GN Name=IGHM;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ussin T.B., Toshiyuki S., Carninci P., Frange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
   and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=2500644;
RA Kishimoto T., Okajima H., Okumoto T., Taniguchi M.;
RT "Nucleotide sequences of the cDNAs encoding the V-regions of H- and L-
   chains of a human monoclonal antibody with broad reactivity to
   malignant tumor cells."
RL Nucleic Acids Res. 17:4385-0(1989).
DR EMBL; BC015760; AAH15760.1; -; mRNA.
DR PIR; S05271; S05271.
DR PIR; S24260; S24260.
DR HSSP; P01861; IADQ.
DR Ensembl; ENSG00000130076; Homo sapiens.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; C1-set; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG_LIKE; 5.
DR PROSITE; PS0290; IG_MHC; UNKNOWN_3.
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KW Immunoglobulin domain.  
SQ SEQUENCE 597 AA; 65039 MW; 4FCA3AD8ECE263D9 CRC64;  
Query Match 72.9%; Score 455; DB 2; Length 597;  
Best Local Similarity 72.0%; Pred. No. 5.6e-39;  
Matches 90; Conservative 12; Mismatches 17; Indels 6; Gaps 2;  
QY 1 EVQLVESGGDFVQPGGSLRVSQAAGFAFASHYAMSVWRQAPGKGLWVAYISSGGSGTYY 60  
DB 20 EVQLVESGGGLVQPGGSLRLSCAASGFSFSSVAMNVRQAPGKGLWVAISGSGGTYY 79  
QY 61 SDSVKGRTISRDNKNTLYLQMSLRADSAVYFCTR-----VKLGTY-YFDSMGQGL 114  
DB 80 ADSVKGRTISRDNKNTLYLQMSLRADSAVYFCTR-----VKLGTY-YFDSMGQGL 139  
QY 115 LTVSS 119  
DB 140 VTVSS 144  
RESULT 8  
Q6PI81 HUMAN  
ID Q6PI81\_HUMAN PRELIMINARY; PRT; 478 AA.  
AC Q6PI81;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE IGHM protein.  
GN Name=IGHM;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Primary B-Cells;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smallos D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences."  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Primary B-Cells;  
RG NIH MGC Project;  
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC041037; AAH41037.1; -, mRNA.  
DR HSSP; P01861; 1ADO.  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig.cl.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_V.  
DR Pfam; PF07654; C1-set; 3.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IGC1; 3.

DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS0835; IG LIKE; 4.  
DR PROSITE; PS0290; IG\_MHC; UNKNOWN 2.  
SQ SEQUENCE 478 AA; 52667 MW; 17BED38D917970D6 CRC64;  
Query Match 72.8%; Score 454; DB 2; Length 478;  
Best Local Similarity 71.3%; Pred. No. 5.5e-39;  
Matches 92; Conservative 7; Mismatches 20; Indels 10; Gaps 2;  
QY 1 EVQLVESGGDFVQPGGSLRVSQAAGFAFASHYAMSVWRQAPGKGLWVAYISSGGSGTYY 60  
DB 20 EVQLVESGGGLVQPGGSLRLSCAASGFTFSSVMSVWRQAPGKGLWVANIQDSEKYY 79  
QY 61 SDSVKGRTISRDNKNTLYLQMSLRADSAVYFCTR-----VKLGTYF--DSWG 110  
DB 80 VDSVKGRTISRDNKNTLYLQMSLRADSAVYFCTR-----VKLGTYF--DSWG 139  
QY 111 QGTLTVSS 119  
DB 140 KGTTVTVSS 148  
RESULT 9  
Q9UL91 HUMAN  
ID Q9UL91\_HUMAN PRELIMINARY; PRT; 118 AA.  
AC Q9UL91;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Myosin-reactive immunoglobulin heavy chain variable region  
DE (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;  
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,  
RA Young D.C.;  
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
RT fetus."  
RL Clin. Immunol. Immunopathol. 87:184-192 (1998).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RX PubMed=1660528;  
RA Manheimer-Lory A., Katz J.B., Pillinger M., Grossein C., Smith A.,  
RA Diamond B.;  
RT "Molecular characteristics of antibodies bearing an anti-DNA-  
RT associated idiotype."  
RL J. Exp. Med. 174:1639-1652 (1991).  
RN [3]  
RP PROTEIN SEQUENCE.  
RX PubMed=1555592;  
RA Makiya R., Stigbrand T.;  
RT "Placental alkaline phosphatase has a binding site for the human  
RT immunoglobulin-G Fc portion."  
RL Eur. J. Biochem. 205:341-345 (1992).  
DR EMBL; AF035023; AAD56259.1; -, mRNA.  
DR PIR; PH0875; PH0875.  
DR PIR; S21205; S21205.  
DR PIR; S30531; S30531.  
DR HSSP; P01783; 1IGC.  
DR SMR; Q9UL91; 1-117.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_V.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS0835; IG LIKE; 1.  
FT NON\_TER 1  
FT NON\_TER 118  
SQ SEQUENCE 118 AA; 12843 MW; D0633949F2AC149D CRC64;

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Query Match      72.4%; Score 451.5; DB 2; Length 118;
Best Local Similarity 74.6%; Pred. No. 26-39;
Matches 88; Conservative 12; Mismatches 17; Indels 1; Gaps 1;

QY 1 EVOLVESGDFVQPGSLRVSCAASGAFSHYAMSVVRQAPGKLEWVAYISSGSGTYY 60
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 EVOLVESGGLVQPGSLRLSCAASGFTFSSYMNVRQAPGKLEWVSYISTITIYY 60
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 SDSVKGRTTISRDNKNTLYLQMSLRASDAVYFCTRVKLTGYFDSNGQGTLLTVSS 118
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 ADSVKGRTTISRDNKNTLYLQMSLRASDAVYFCTRVKLTGYFDSNGQGTLLTVSS 117

RESULT 10
Q6GMV2 HUMAN PRELIMINARY; PRT; 606 AA.
AC Q6GMV2;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DE IGHM protein.
GN Name=IGHM;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toehlyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kattaman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RG NIH MGC Project;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073758; AAH73758.1; -; mRNA.
DR SMR; Q6GMV2; 20-256.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003587; IG-cl.
DR InterPro; IPR003006; IG.MHC.
DR InterPro; IPR003596; IG.V.
DR Pfam; PF07654; C1-set; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 4.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PSS0835; IG.LIKE; 5.
DR PROSITE; PSS0290; IG.MHC; UNKNOWN 3.
SQ SEQUENCE 606 AA; 66185 MW; B6B38B51114E4C55 CRC64;

Query Match      72.4%; Score 451.5; DB 2; Length 606;
Best Local Similarity 67.2%; Pred. No. 1.3e-38;
Matches 90; Conservative 12; Mismatches 17; Indels 15; Gaps 2;

QY 1 EVOLVESGDFVQPGSLRVSCAASGAFSHYAMSVVRQAPGKLEWVAYISSGSGTYY 60
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 EVOLVESGGLVQPGSLRLSCAASGFTFSSYMNVRQAPGKLEWVAVISYDGSNKYY 60
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 SDSVKGRTTISRDNKNTLYLQMSLRASDAVYFCTRVKLTGYFDSNGQGTLLTVSS 119
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 ADSVKGRTTISRDNKNTLYLQMSLRASDAVYFCTRVKLTGYFDSNGQGTLLTVSS 117

RESULT 12
QSPQK9 RAT PRELIMINARY; PRT; 479 AA.
AC QSPQK9;
DT 01-FEB-2005 (TReMBLrel. 29, Created)
DT 01-FEB-2005 (TReMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TReMBLrel. 29, Last annotation update)
DE Igha protein.
GN Name=Igha;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Rattus.

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OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung;
RX NIH MGC Project;
RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
RA EMBL; BC087137; AAH87137.1; -; mRNA.
RA GO; GO:0003823; P:antigen binding; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG v.
DR Pfam; PF07654; Cl-set; 2.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00407; IGV; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
SQ SEQUENCE 479 AA; 52354 MW; 1692EF3457BE686E CRC64;

Query Match 72.1%; Score 450; DB 2; Length 479;
Best Local Similarity 69.4%; Pred. No. 1.5e-38;
Matches 84; Conservative 17; Mismatches 18; Indels 2; Gaps 1;

QY 1 EVLVESGGDFVQPGSLRVSCAASGFASFHSHVMSWVRQAPKGLEWVAIYSSGGSGTY 60
DB 20 EVLVESGGGLVQPGSLRVSCAASGFASFHSHVMSWVRQAPKGLEWVAIYSSGGSGTY 79
QY 61 SDSVKGRTISRDNKNTLYLQMSLRADSVAVFCTRVK--LGTYFDPSWGQGLTLTVS 118
DB 80 PDSVKGRTISRDNKNTLYLQMSLRADSVAVFCTRVK--LGTYFDPSWGQGLTLTVS 139
QY 119 S 119
DB 140 S 140

RESULT 13
Q5F218 MOUSE
ID Q5F218 MOUSE PRELIMINARY; PRT; 119 AA.
AC Q5F218
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE Gamma heavy chain variable region (Fragment).
GN Name=IgG1 TS1 VH;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Query Match 72.1%; Score 450; DB 2; Length 479;
Best Local Similarity 69.4%; Pred. No. 1.5e-38;
Matches 84; Conservative 17; Mismatches 18; Indels 2; Gaps 1;

QY 1 EVLVESGGDFVQPGSLRVSCAASGFASFHSHVMSWVRQAPKGLEWVAIYSSGGSGTY 60
DB 20 EVLVESGGGLVQPGSLRVSCAASGFASFHSHVMSWVRQAPKGLEWVAIYSSGGSGTY 79
QY 61 SDSVKGRTISRDNKNTLYLQMSLRADSVAVFCTRVK--LGTYFDPSWGQGLTLTVS 118
DB 80 PDSVKGRTISRDNKNTLYLQMSLRADSVAVFCTRVK--LGTYFDPSWGQGLTLTVS 139
QY 119 S 119
DB 140 S 140

RESULT 14
Q9UL72 HUMAN
ID Q9UL72 HUMAN PRELIMINARY; PRT; 118 AA.
AC Q9UL72
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
RN [2]
RP PROTEIN SEQUENCE.
RX PubMed=1555592;
RA Makiya R., Stigbrand T.;
RT "Placental alkaline phosphatase has a binding site for the human immunoglobulin-G Fc portion.";
RL Eur. J. Biochem. 205:341-345(1992).
DR EMBL; AF035042; AAD56278.1; -; mRNA.
DR PIR; S21205; S21205.
DR HSSP; P01783; IIGC.
DR SMR; Q9UL72; 1-118.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG v.

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Search completed: April 6, 2006, 08:53:37  
Job time : 37.855 secs

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DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 118
SQ SEQUENCE 118 AA; 12872 MW; B4D1A5944B2D5CCA CRC64;

Query Match          71.9%; Score 448.5; DB 2; Length 118;
Best Local Similarity 74.8%; Pred. No. 4.1e-39;
Matches 89; Conservative 10; Mismatches 19; Indels 1; Gaps 1;

QY 1 EVQLVESGGDFVQPQGGSLRVSCAASGFAPFSHYAMSVWRQAPGKGLEWVAYISSGGSGTY 60
Db 1 EVQLVESGGDFVQPQGGSLRVSCAASGFAPFSHYAMSVWRQAPGKGLEWVAYISSGGSGTY 60
QY 61 SDSVKGRFTISRDNKNTLYLQWRLRAEDSAVYFCTRVKLTGYTFDSWGQGTLLTVSS 119
Db 60 ADSVKGRFTISRDNKNTLYLQWRLRAEDTAFYTCARDRFGFELFDYWGQGTLLTVSS 118

RESULT 15
Q6MZQ6 HUMAN
ID Q6MZQ6.HUMAN PRELIMINARY; PRT; 475 AA.
AC Q6MZQ6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein DKFZp686G11190.
GN Name=DKFZp686G11190;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Esophagus tumor;
RG The German CDNA Consortium;
RA Bahr A., Lauber J., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G.,
RA Han M., Wiemann S.;
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640947; CAE45972.1; -; mRNA.
DR HSSP; P01861; IADQ.
DR SMR; Q6MZQ6; 20-475.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_C1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 475 AA; 52043 MW; B7EAE255A26F4B8E CRC64;

Query Match          71.9%; Score 448.5; DB 2; Length 475;
Best Local Similarity 69.0%; Pred. No. 2.1e-38;
Matches 87; Conservative 13; Mismatches 19; Indels 7; Gaps 1;

QY 1 EVQLVESGGDFVQPQGGSLRVSCAASGFAPFSHYAMSVWRQAPGKGLEWVAYISSGGSGTY 60
Db 20 EVQLVESGGDFVQPQGGSLRVSCAASGFAPFSHYAMSVWRQAPGKGLEWVAYISSGGSGTY 79
QY 61 SDSVKGRFTISRDNKNTLYLQWRLRAEDSAVYFCTRVKLTGY-----YFDSWGQGT 113
Db 80 ADSVKGRFTISDGIINTNTLYLQWRLRAEDTAVYTCARDYRDYQVSPAYWTFDVGRT 139
QY 114 LLTVSS 119
Db 140 LVSVSA 145
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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 6, 2006, 08:50:25 ; Search time 7.39595 Seconds  
(without alignments)  
1330.063 Million cell updates/sec

Title: US-10-089-500-9  
Perfect score: 624  
Sequence: 1 EVLVESGDFVQPGSLRV.....KLGTYFDSWGQGLTLTVSS 119

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/ptodata/1/iaa/5\_COMB.pep.\*  
2: /cgn2\_6/ptodata/1/iaa/6\_COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/H\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/PTUS\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/RE\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfilese1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	579	92.8	130	2	US-09-325-322B-18
2	579	92.8	130	2	US-09-764-304-18
3	569	91.2	130	2	US-09-225-322B-8
4	569	91.2	130	2	US-09-764-304-8
5	498	79.8	119	2	US-09-648-067A-15
6	498	79.8	119	2	US-09-602-812A-6
7	495.5	79.4	120	1	US-07-934-373C-4
8	495.5	79.4	120	2	US-08-437-642B-4
9	495.5	79.4	120	2	US-08-146-206C-4
10	495.5	79.4	120	2	US-09-705-686-4
11	495.5	79.4	120	2	US-09-705-392A-4
12	495.5	79.4	120	2	US-09-705-398-4
13	489	78.4	119	1	US-08-331-398A-46
14	489	78.4	119	1	US-08-331-397B-46
15	489	78.4	119	1	US-08-759-804A-46
16	489	78.4	119	2	US-09-227-693-46
17	489	78.4	125	1	US-08-428-197-1
18	489	78.4	125	4	PCT-US93-10555-1
19	487.5	78.1	135	2	US-08-579-378A-20
20	487.5	78.1	433	4	PCT-US96-13152-4
21	485.5	77.8	122	1	US-07-934-373C-21
22	485.5	77.8	122	2	US-08-437-642B-21
23	485.5	77.8	122	2	US-08-146-206C-21
24	485.5	77.8	122	2	US-09-705-686-21
25	485.5	77.8	122	2	US-09-705-392A-21
26	485.5	77.8	122	2	US-09-705-398-21
27	485.5	77.8	122	4	PCT-US93-07832-21

28 485.5 77.8 263 2 US-09-069-821-3 Sequence 3, Appl1  
29 485.5 77.8 263 2 US-09-956-086-3 Sequence 3, Appl1  
30 485.5 77.8 263 2 US-09-956-087-3 Sequence 3, Appl1  
31 485.5 77.8 283 2 US-09-420-592A-6 Sequence 6, Appl1  
32 485.5 77.8 283 2 US-09-985-442-6 Sequence 6, Appl1  
33 485.5 77.8 283 2 US-09-983-580-6 Sequence 6, Appl1  
34 485 77.7 123 2 US-09-840-459-82 Sequence 82, Appl1  
35 485 77.7 123 2 US-09-497-625A-82 Sequence 82, Appl1  
36 483.5 77.5 140 2 US-08-983-607-32 Sequence 32, Appl1  
37 481 77.1 113 2 US-08-974-899-6 Sequence 6, Appl1  
38 481 77.1 113 2 US-09-795-798-6 Sequence 11, Appl1  
39 481 77.1 113 2 US-08-908-469-11 Sequence 38, Appl1  
40 480.5 77.0 120 2 US-09-025-769B-38 Sequence 38, Appl1  
41 480.5 77.0 120 2 US-09-025-769B-83 Sequence 63, Appl1  
42 480.5 77.0 120 2 US-09-490-070A-38 Sequence 63, Appl1  
43 480.5 77.0 120 2 US-09-490-070A-63 Sequence 38, Appl1  
44 480.5 77.0 120 2 US-09-490-153-38 Sequence 63, Appl1  
45 480.5 77.0 120 2 US-09-490-153-63 Sequence 63, Appl1

## ALIGNMENTS

RESULT 1

US-09-225-322B-18

; Sequence 18, Application US/09225322B

; Patent No. 6437098

; GENERAL INFORMATION:

; APPLICANT: SHITARA, KENYA

; APPLICANT: HANAI, NOBUO

; APPLICANT: HASEGAWA, MAMORU

; APPLICANT: MIYAJI, HIROMASA

; APPLICANT: KUMANA, YOSHIHISA

; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY

; FILE REFERENCE: 249-101

; CURRENT APPLICATION NUMBER: US/09/225,322B

; CURRENT FILING DATE: 1999-01-05

; PRIOR APPLICATION NUMBER: US 08/454,680

; PRIOR FILING DATE: 1995-05-31

; PRIOR APPLICATION NUMBER: US 08/408,133

; PRIOR FILING DATE: 1995-03-21

; PRIOR APPLICATION NUMBER: US 08/292,178

; PRIOR FILING DATE: 1994-08-17

; PRIOR APPLICATION NUMBER: US07/947,674

; PRIOR FILING DATE: 1992-09-17

; PRIOR APPLICATION NUMBER: JP 3-238375

; PRIOR FILING DATE: 1991-09-18

; NUMBER OF SEQ ID NOS: 19

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 18

; LENGTH: 130

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:CDNA KM-641

US-09-225-322B-18

Query Match 92.8%; Score 579; DB 2; Length 130;

Best Local Similarity 91.6%; Pred. No. 2,1e-51;

Matches 109; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 EVLVESGDFVQPGSLRVSCAASGFAPSHYAMSWVRQAPKGLWVAYISSGSGTYY 60

Db 11 EYTVESGDFVQPGSLRVSCAASGFAPSHYAMSWVRQTPAKRLWVAYISSGSGTYY 70

QY 61 SDSVKGRTTISDNSKNTLYLQMRSLRAEDSAVYFCTRVKLTGYFDSNGQGLTLTVSS 119

Db 71 SDSVKGRTTISDNTAKNTLYLQMRSLRSEDASVYFCTRVKLTGYFDSNGQGLTLTVSS 129

RESULT 2

US-09-764-304-18

; Sequence 18, Application US/09764304

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; Patent No. 6495666
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUWANA, YOSHIHISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/09/764,304
; CURRENT FILING DATE: 2001-01-19
; EARLIER APPLICATION NUMBER: 09/225,322
; EARLIER FILING DATE: 1999-01-05
; EARLIER APPLICATION NUMBER: US 08/454,680
; EARLIER FILING DATE: 1995-05-31
; EARLIER APPLICATION NUMBER: US 08/408,133
; EARLIER FILING DATE: 1995-03-21
; EARLIER APPLICATION NUMBER: US 08/292,178
; EARLIER FILING DATE: 1994-08-17
; EARLIER APPLICATION NUMBER: US07/947,674
; EARLIER FILING DATE: 1992-09-17
; EARLIER APPLICATION NUMBER: JP 3-238375
; EARLIER FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: cDNA KM-641
US-09-764-304-18

Query Match          92.8%; Score 579; DB 2; Length 130;
Best Local Similarity 91.6%; Pred. No. 2.1e-51;
Matches 109; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 EVLVESGGDFVOPGSLRVSCAASGFAFASHYAMSWVRQAPGKLEWVAYISSGGSGTYY 60
Db 11 EVTLVESGGDFVKPGSLKVSACASGFAFASHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 70

QY 61 SDSVKGRFTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLGTYFFDSWGQGTLLTVSS 119
Db 71 SDSVKGRFTISRDNKNTLYLQMRSLRSED SAMYFCTRVKLGTYFFDSWGQGTLLTVSS 129

RESULT 3
US-09-225-322B-8
; Sequence 8, Application US/09225322B
; Patent No. 6437098
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUWANA, YOSHIHISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/09/225,322B
; CURRENT FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: US 08/454,680
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
; PRIOR APPLICATION NUMBER: US07/947,674
; PRIOR FILING DATE: 1992-09-17
; PRIOR APPLICATION NUMBER: JP 3-238375
; PRIOR FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8

Query Match          92.8%; Score 579; DB 2; Length 130;
Best Local Similarity 91.6%; Pred. No. 2.1e-51;
Matches 109; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 EVLVESGGDFVOPGSLRVSCAASGFAFASHYAMSWVRQAPGKLEWVAYISSGGSGTYY 60
Db 11 EVTLVESGGDFVKPGSLKVSACASGFAFASHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 70

QY 61 SDSVKGRFTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLGTYFFDSWGQGTLLTVSS 119
Db 71 SDSVKGRFTISRDNKNTLYLQMRSLRSED SAMYFCTRVKLGTYFFDSWGQGTLLTVSS 129

RESULT 4
US-09-764-304-8
; Sequence 8, Application US/09764304
; Patent No. 6495666
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUWANA, YOSHIHISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/09/764,304
; CURRENT FILING DATE: 2001-01-19
; EARLIER APPLICATION NUMBER: 09/225,322
; EARLIER FILING DATE: 1999-01-05
; EARLIER APPLICATION NUMBER: US 08/454,680
; EARLIER FILING DATE: 1995-05-31
; EARLIER APPLICATION NUMBER: US 08/408,133
; EARLIER FILING DATE: 1995-03-21
; EARLIER APPLICATION NUMBER: US 08/292,178
; EARLIER FILING DATE: 1994-08-17
; EARLIER APPLICATION NUMBER: US07/947,674
; EARLIER FILING DATE: 1992-09-17
; EARLIER APPLICATION NUMBER: JP 3-238375
; EARLIER FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: cDNA KM-641
US-09-764-304-8

Query Match          91.2%; Score 569; DB 2; Length 130;
Best Local Similarity 90.8%; Pred. No. 2.2e-50;
Matches 108; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 EVLVESGGDFVOPGSLRVSCAASGFAFASHYAMSWVRQAPGKLEWVAYISSGGSGTYY 60
Db 11 EVTLVESGGDFVKPGSLKVSACASGFAFASHYAMSWVRQTPAKRLEWVAGISSGGSGTYY 70

QY 61 SDSVKGRFTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLGTYFFDSWGQGTLLTVSS 119
Db 71 SDSVKGRFTISRDNKNTLYLQMRSLRSED SAMYFCTRVKLGTYFFDSWGQGTLLTVSS 129

RESULT 5
US-09-648-067A-15
; Sequence 15, Application US/09648067A
; Patent No. 6627196
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; GENERAL INFORMATION:
; APPLICANT: Baughman, Sharon A.
; APPLICANT: Shak Steven
; TITLE OF INVENTION: Dosages for Treatment with Anti-ErbB2 Antibodies
; FILE REFERENCE: P177SR1
; CURRENT APPLICATION NUMBER: US/09/648,067A
; CURRENT FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,018
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: US 60/213,822
; PRIOR FILING DATE: 2000-06-23
; NUMBER OF SEQ ID NOS: 15
; SEQ ID NO 15
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: VH consensus sequence
US-09-648-067A-15

Query Match          79.8%; Score 498; DB 2; Length 119;
Best Local Similarity 79.8%; Pred. No. 3.2e-43;
Matches 95; Conservative 8; Mismatches 16; Indels 0; Gaps 0;

QY 1 EVOLVESGGDFVQPGGSLRVSCAASGFAFSHYAMSWVRQAPGKLEWVAYISSGGSGTYY 60
Db 1 EVOLVESGGGLVQPGGSLRLSCLCAASGFTFSSYAMSWVRQAPGKLEWVAVISGDGGSTYY 60
QY 61 SDSVKGRFTISRDNKNTLYLQMSLRRAEDSAVYFCTRVKLGTYYPDSWGQGLTLTVSS 119
Db 61 ADSVKGRFTISRDNKNTLYLQMSLRRAEDTAVYYCARGVGSGLYDYGQGLTLTVSS 119

RESULT 6
US-09-602-812A-6
; Sequence 6, Application US/09602812A
; Patent No. 6949245
; GENERAL INFORMATION:
; APPLICANT: Adams, Camellia W.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Sliwkowski, Mark X.
; TITLE OF INVENTION: Humanized Anti-ErbB2 Antibodies and Treatment with
; FILE REFERENCE: P1467R2
; CURRENT APPLICATION NUMBER: US/09/602,812A
; CURRENT FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/141,316
; PRIOR FILING DATE: 1999-06-25
; NUMBER OF SEQ ID NOS: 13
; SEQ ID NO 6
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: heavy chain consensus sequence
US-09-602-812A-6

Query Match          79.8%; Score 498; DB 2; Length 119;
Best Local Similarity 79.8%; Pred. No. 3.2e-43;
Matches 95; Conservative 8; Mismatches 16; Indels 0; Gaps 0;

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Db 1 EVOLVESGGGLVQPGGSLRLSCLCAASGFTFSSYAMSWVRQAPGKLEWVAVISGDGGSTYY 60
QY 61 SDSVKGRFTISRDNKNTLYLQMSLRRAEDSAVYFCTRVKLGTYYPDSWGQGLTLTVSS 119
Db 61 ADSVKGRFTISRDNKNTLYLQMSLRRAEDTAVYYCARGVGSGLYDYGQGLTLTVSS 119

RESULT 7
US-07-934-373C-4
; Sequence 4, Application US/07934373C
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; Patent No. 5821317
; GENERAL INFORMATION:
; APPLICANT: Paul J. Carter
; APPLICANT: Leonard G. Presta
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/934,373C
; FILING DATE: 21-Aug-1992
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05126
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 120 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-07-934-373C-4

Query Match          79.4%; Score 495.5; DB 1; Length 120;
Best Local Similarity 80.8%; Pred. No. 5.8e-43;
Matches 97; Conservative 7; Mismatches 15; Indels 1; Gaps 1;

QY 1 EVOLVESGGDFVQPGGSLRVSCAASGFAFSHYAMSWVRQAPGKLEWVAYISSGGSGTYY 60
Db 1 EVOLVESGGGLVQPGGSLRLSCLCAASGFTFSSYAMSWVRQAPGKLEWVAVISGSDTYY 60
QY 61 SDSVKGRFTISRDNKNTLYLQMSLRRAEDSAVYFCTRVKLGTY-YFDSWGQGLTLTVSS 119
Db 61 ADSVKGRFTISRDNKNTLYLQMSLRRAEDTAVYYCARDRGAGVSYFDVWGQGLTLTVSS 120

RESULT 8
US-08-437-642B-4
; Sequence 4, Application US/08437642B
; Patent No. 6054297
; GENERAL INFORMATION:
; APPLICANT: Paul J. Carter
; APPLICANT: Leonard G. Presta
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
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;
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/437,642B
; FILING DATE: 09-May-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/934373
; FILING DATE: 21-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/146206
; FILING DATE: 17-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05126
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P2C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 120 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
;
US-08-437-642B-4

Query Match 79.4%; Score 495.5; DB 2; Length 120;
Best Local Similarity 80.8%; Pred. NO. 5.8e-43;
Matches 97; Conservative 7; Mismatches 15; Indels 1; Gaps 1;

QY 1 EVLVESGGDFVQPGSLRVSCAAGFAFASHYAMSVWRQAPGKLEWVAVISSGGSGTYY 60
DB 1 EVLVESGGGLVQPGSLRSLCAASGFTFSDYAMSVWRQAPGKLEWVAVISENGSDTYY 60
QY 61 SDSVKGRFTISRDNKNTLYLQMSLRADSAVYFCTRVKLGTY-YFDSWGQGTLLTVSS 119
DB 61 ADSVKGRFTISRDDSKNTLYLQMSLRADTAIVYCARDRGGAIVYFDVWGQGTLLTVSS 120

RESULT 9
US-08-146-206C-4
; Sequence 4, Application US/08146206C
; Patent No. 6407213
; GENERAL INFORMATION:
; APPLICANT: Carter, Paul J.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Method for Making Humanized Antibodies
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/146,206C
; FILING DATE: 17-NOV-1993
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709PID3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 120 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
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US-09-705-686-4
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Query Match      79.4%; Score 495.5; DB 2; Length 120;
Best Local Similarity 80.8%; Pred. No. 5.8e-43;
Matches 97; Conservative 7; Mismatches 15; Indels 1; Gaps 1;

QY 1 EVLVESGGDFVQPGSLRVSCAAGFAFASHYAMSVWRQAPGKLEWVAIYSSGGSGTTY 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 EVLVESGGGLVQPGSLRLSCLCAAGFTFSDYAMSVWRQAPGKLEWVAIYSSGGSDTY 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 61 SDSVKGRFTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLGTY-YFDSWGQGLTLTVSS 119
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 ADSVKGRFTISRDDSKNTLYLQMNLSRAEDTAVYYCARDRGGAVSFYDWMGQGLTLTVSS 120
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 11
US-09-705-392A-4
; Sequence 4, Application US/09705392A
; Patent No. 6719971
; GENERAL INFORMATION:
; APPLICANT: Carter, Paul J.
; Presta, Leonard G.
; TITLE OF INVENTION: Method for Making Humanized Antibodies
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/705,392A
; FILING DATE: 02-No. 6719971-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/146206
; FILING DATE: 17-NOV-1993
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P1D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 120 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-705-392A-4

Query Match      79.4%; Score 495.5; DB 2; Length 120;
Best Local Similarity 80.8%; Pred. No. 5.8e-43;
Matches 97; Conservative 7; Mismatches 15; Indels 1; Gaps 1;

QY 1 EVLVESGGDFVQPGSLRVSCAAGFAFASHYAMSVWRQAPGKLEWVAIYSSGGSGTTY 60
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Db 1 EVLVESGGGLVQPGSLRLSCLCAAGFTFSDYAMSVWRQAPGKLEWVAIYSSGGSDTY 60
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QY 61 SDSVKGRFTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLGTY-YFDSWGQGLTLTVSS 119
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RESULT 12
US-09-705-398-4
; Sequence 4, Application US/09705398A
; Patent No. 5608039
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira
; APPLICANT: Willingham, Mark
; APPLICANT: FitzGerald, David
; APPLICANT: Brinkmann, Ulrich
; APPLICANT: Pai, Lee
; TITLE OF INVENTION: Single Chain B3 Antibody Fusion Proteins
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Plaza
; CITY: San Francisco
```

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; Sequence 4, Application US/09705398
; Patent No. 6800738
; GENERAL INFORMATION:
; APPLICANT: Carter, Paul J.
; Presta, Leonard G.
; TITLE OF INVENTION: Method for Making Humanized Antibodies
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/705,398
; FILING DATE: 02-No. 6800738-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/146206
; FILING DATE: 17-NOV-1993
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P1D2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 120 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-705-398-4

Query Match      79.4%; Score 495.5; DB 2; Length 120;
Best Local Similarity 80.8%; Pred. No. 5.8e-43;
Matches 97; Conservative 7; Mismatches 15; Indels 1; Gaps 1;

QY 1 EVLVESGGDFVQPGSLRVSCAAGFAFASHYAMSVWRQAPGKLEWVAIYSSGGSGTTY 60
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Db 1 EVLVESGGGLVQPGSLRLSCLCAAGFTFSDYAMSVWRQAPGKLEWVAIYSSGGSDTY 60
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QY 61 SDSVKGRFTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLGTY-YFDSWGQGLTLTVSS 119
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RESULT 13
US-08-331-398A-46
; Sequence 46, Application US/08331398A
; Patent No. 5608039
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira
; APPLICANT: Willingham, Mark
; APPLICANT: FitzGerald, David
; APPLICANT: Brinkmann, Ulrich
; APPLICANT: Pai, Lee
; TITLE OF INVENTION: and Their Uses (as amended)
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Plaza
; CITY: San Francisco
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; FILING DATE: 03-DEC-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/331,398
; FILING DATE: 28-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/767,331
; FILING DATE: 30-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/596,289
; FILING DATE: 12-OCT-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen L.
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 015280-126140US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..119
; OTHER INFORMATION: /note= "Human fetal immunoglobulin
; OTHER INFORMATION: 56P1'CL Variable Heavy chain (V-H)"
US-08-759-804A-46

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Query Match      78.4%; Score 489; DB 1; Length 119;
Best Local Similarity 79.0%; Pred. No. 2.6e-42;
Matches 94; Conservative 7; Mismatches 18; Indels 0; Gaps 0;

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Db      1 QVELVESGGGVQPGKSLRLSCAASGFTFSYAMHWVRQAPGKLEWAVISYDGSNKYY 60

QY      61 SDSVKGRFTISRDNKNTLYLQMSLRRAEDSAVYFCTRVKLGTYFDWSWGQGLLTVSS 119
Db      61 ADSVKGRFTISRDNKNTLYLQMSLRRAEDTAVYFCARSARTYYFDYWGQGLTAVTSS 119

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Job time : 7.39695 secs

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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 6, 2006, 08:53:30 ; Search time 21.2824 Seconds  
(without alignments)  
2336.277 Million cell updates/sec

Title: US-10-089-500-9  
Perfect score: 624  
Sequence: 1 EVLVESGDFVQPGSLRV.....KLGTYFDSWGQTLTVSS 119

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA Main:  
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2: /cgn2\_6/prodata1/pubpaa/US08\_PUBCOMB.pep.\*  
3: /cgn2\_6/prodata1/pubpaa/US09\_PUBCOMB.pep.\*  
4: /cgn2\_6/prodata1/pubpaa/US10A\_PUBCOMB.pep.\*  
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6: /cgn2\_6/prodata1/pubpaa/US11\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	579	92.8	130	3	US-09-764-304-18
2	579	92.8	130	4	US-10-265-713-18
3	579	92.8	130	4	US-10-166-626-18
4	569	91.2	130	3	US-09-764-304-8
5	569	91.2	130	4	US-10-265-713-8
6	569	91.2	130	4	US-10-166-626-8
7	499	80.0	119	4	US-10-044-896-6
8	498	79.8	119	3	US-09-811-123-3
9	498	79.8	119	4	US-10-268-501-6
10	498	79.8	119	4	US-10-608-626-6
11	498	79.8	119	4	US-10-600-152-15
12	498	79.8	119	4	US-10-619-754-6
13	498	79.8	119	5	US-10-719-310-6
14	498	79.8	119	5	US-10-861-049-42
15	498	79.8	119	6	US-11-021-874-42
16	498	79.8	119	6	US-11-044-749-6
17	498	79.8	119	6	US-11-154-465-6
18	498	79.8	120	5	US-10-938-353-104
19	495.5	79.4	120	5	US-10-835-641-4
20	493.5	79.1	224	4	US-10-128-520-148
21	492.5	78.9	126	5	US-10-505-313-6
22	492	78.8	313	4	US-10-291-265-427
23	491.5	78.8	251	6	US-11-017-030-59
24	489.5	78.4	126	5	US-10-505-313-89
25	489	78.4	143	4	US-10-469-304-17
26	489	78.4	248	6	US-11-017-030-18
27	488.5	78.3	220	4	US-10-128-520-156

28	488.5	78.3	248	5	US-10-981-692-32	Sequence 32, Appl
29	488	78.2	136	5	US-10-910-901-24	Sequence 24, Appl
30	487.5	78.1	443	3	US-09-917-410-4	Sequence 4, Appl
31	487	78.0	121	4	US-10-275-046-78	Sequence 78, Appl
32	487	78.0	123	4	US-10-269-805-59	Sequence 59, Appl
33	487	78.0	247	3	US-09-880-748-1953	Sequence 1953, Ap
34	487	78.0	247	4	US-10-293-418-1953	Sequence 1953, Ap
35	486.5	78.0	136	3	US-09-837-306-184	Sequence 184, App
36	486.5	78.0	136	4	US-10-045-674-487	Sequence 487, App
37	486.5	78.0	367	4	US-10-045-674-453	Sequence 453, App
38	486.5	78.0	368	3	US-09-837-306-196	Sequence 196, App
39	485.5	77.8	122	5	US-10-835-641-21	Sequence 21, Appl
40	485.5	77.8	242	6	US-11-017-030-58	Sequence 58, Appl
41	485.5	77.8	263	3	US-09-956-086-3	Sequence 3, Appl
42	485.5	77.8	263	3	US-09-956-087-3	Sequence 3, Appl
43	485.5	77.8	283	3	US-09-983-580-6	Sequence 6, Appl
44	485.5	77.8	283	3	US-09-985-442-6	Sequence 6, Appl
45	485	77.7	123	3	US-09-840-459-82	Sequence 82, Appl

ALIGNMENTS

RESULT 1

US-09-764-304-18  
; Sequence 18, Application US/09764304  
; Patent No. US20020026036A1  
; GENERAL INFORMATION:  
; APPLICANT: SHITARA, KENYA  
; APPLICANT: HANAI, NOBUO  
; APPLICANT: HASEGAWA, MAMORU  
; APPLICANT: MIYAJI, HIROMASA  
; APPLICANT: KUWANA, YOSHIOHISA  
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY  
; FILE REFERENCE: 249-101  
; CURRENT APPLICATION NUMBER: US/09/764,304  
; CURRENT FILING DATE: 2001-01-19  
; EARLIER APPLICATION NUMBER: 09/225,322  
; EARLIER FILING DATE: 1999-01-05  
; EARLIER APPLICATION NUMBER: US 08/454,680  
; EARLIER FILING DATE: 1995-05-31  
; EARLIER APPLICATION NUMBER: US 08/408,133  
; EARLIER FILING DATE: 1995-03-21  
; EARLIER APPLICATION NUMBER: US 08/292,178  
; EARLIER FILING DATE: 1994-08-17  
; EARLIER APPLICATION NUMBER: US07/947,674  
; EARLIER FILING DATE: 1992-09-17  
; EARLIER APPLICATION NUMBER: JP 3-238375  
; EARLIER FILING DATE: 1991-09-18  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 18  
; LENGTH: 130  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: cDNA KM-641  
US-09-764-304-18

Query Match 92.8%; Score 579; DB 3; Length 130;  
Best Local Similarity 91.6%; Pred. No. 1.1e-44;  
Matches 109; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

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DB	11	EVLTVESGDFVKPGSLKVSACASGFAFSHYAMSVWRQTPAKRLEWVAYISSGSGTYY	70
QY	61	SDSVKGRFTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLGTYFYFDSWGQTLTVSS	119
DB	71	SDSVKGRFTISRDNKNTLYLQMRSLRSDSAVYFCTRVKLGTYFYFDSWGQTLTVSS	129

RESULT 2

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US-10-265-713-18
; Sequence 18, Application US/10265713
; Publication No. US20030095964A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KOWANA, YOSHIHISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/10/265,713
; CURRENT FILING DATE: 2002-10-08
; PRIOR APPLICATION NUMBER: US/09/225,322
; PRIOR FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: US 08/454,680
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
; PRIOR APPLICATION NUMBER: US07/947,674
; PRIOR FILING DATE: 1992-09-17
; PRIOR APPLICATION NUMBER: JP 3-238375
; PRIOR FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 18
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:cDNA KM-641
US-10-265-713-18
Query Match          92.8%; Score 579; DB 4; Length 130;
Best Local Similarity 91.6%; Pred. No. 1.1e-44;
Matches 109; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
QY 1 EVQLVESGGDFVQPGGSLRVSCAASGFAFASHYAMSVWRQAPGKGLEWYAYISGGSGTTY 60
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Db 11 EVTLVESGGDFVKPGGSLKVSAAAGFAFASHYAMSVWRQTAPAKLEWYAYISGGSGTTY 70
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 SDSVKGRTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLGTYTFDSWGQGTLLTVSS 119
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Db 71 SDSVKGRTISRDNKNTLYLQMRSLRSEDSAMYFCTRVKLGTYTFDSWGQGTLLTVSS 129
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RESULT 3
US-09-764-304-8
; Sequence 8, Application US/09764304
; Patent No. US20020026036A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KOWANA, YOSHIHISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/09/764,304
; CURRENT FILING DATE: 2001-01-19
; EARLIER APPLICATION NUMBER: 09/225,322
; EARLIER FILING DATE: 1999-01-05
; EARLIER APPLICATION NUMBER: US 08/454,680
; EARLIER FILING DATE: 1995-05-31
; EARLIER APPLICATION NUMBER: US 08/408,133
; EARLIER FILING DATE: 1995-03-21
; EARLIER APPLICATION NUMBER: US 08/292,178
; EARLIER FILING DATE: 1994-08-17
; EARLIER APPLICATION NUMBER: US07/947,674
; EARLIER FILING DATE: 1992-09-17
; EARLIER APPLICATION NUMBER: JP 3-238375
; EARLIER FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 8
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: cDNA KM-641
US-09-764-304-8
Query Match          91.2%; Score 569; DB 3; Length 130;
Best Local Similarity 90.8%; Pred. No. 9.1e-44;
Matches 108; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
QY 1 EVQLVESGGDFVQPGGSLRVSCAASGFAFASHYAMSVWRQAPGKGLEWYAYISGGSGTTY 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 11 EVTLVESGGDFVKPGGSLKVSAAAGFAFASHYAMSVWRQTAPAKLEWYAYISGGSGTTY 70
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 SDSVKGRTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLGTYTFDSWGQGTLLTVSS 119
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Db 71 SDSVKGRTISRDNKNTLYLQMRSLRSEDSAMYFCTRVKLGTYTFDSWGQGTLLTVSS 129
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; Sequence 18, Application US/10166626
; Publication No. US20030166876A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KOWANA, YOSHIHISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/10/166,626
; CURRENT FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: US/09/225,322B
; PRIOR FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: US 08/454,680
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
; PRIOR APPLICATION NUMBER: US07/947,674
; PRIOR FILING DATE: 1992-09-17
; PRIOR APPLICATION NUMBER: JP 3-238375
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RESULT 5
US-10-265-713-8
; Sequence 8, Application US/10265713
; Publication No. US20030095964A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUWANA, YOSHIIISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/10/265,713
; CURRENT FILING DATE: 2002-10-08
; PRIOR APPLICATION NUMBER: US/09/225,322
; PRIOR FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: US 08/454,680
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
; PRIOR APPLICATION NUMBER: US07/947,674
; PRIOR FILING DATE: 1992-09-17
; PRIOR APPLICATION NUMBER: JP 3-238375
; PRIOR FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: cDNA KM-641
US-10-265-713-8
Query Match          91.2%; Score 569; DB 4; Length 130;
Best Local Similarity 90.8%; Pred. No. 9.1e-44; Indels 0; Gaps 0;
Matches 108; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
QY 1 EVLVESGGDFVQPGSLRVSCAASGFAFASHYAMSVWRQAPGKLEWVAYISSGSGTYY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 11 EVTLVESGGDFVKPGSLKVSACAASGFAFASHYAMSVWRQTPAKRLEWVAGISSGSGTYY 70
QY 61 SDSVKGRFTISRDNKNTLYLQMSLRASDSAVYFCTRVKLGTYTFDSNGQGTLLTVSS 119
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 71 SDSVKGRFTISRDNKNTLYLQMSLRASDSAMYFCTRVKLGTYTFDSNGQGTLLTVSS 129
RESULT 6
US-10-044-896-6
; Sequence 6, Application US/10044896
; Publication No. US20030166228A1
; GENERAL INFORMATION:
; APPLICANT: Chantharapai, Anan
; APPLICANT: Kim, Jin K.
; APPLICANT: Stewart, Timothy
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: ANTI-INTERFERON-ALPHA ANTIBODIES
; FILE REFERENCE: GENENT. 074A
; CURRENT APPLICATION NUMBER: US/10/044,896
; CURRENT FILING DATE: 2002-01-09
; PRIOR APPLICATION NUMBER: 60/270775
; PRIOR FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-044-896-6
Query Match          80.0%; Score 499; DB 4; Length 119;
Best Local Similarity 80.7%; Pred. No. 1.8e-37; Indels 2; Gaps 1;
Matches 96; Conservative 8; Mismatches 13; Indels 2; Gaps 1;
QY 1 EVLVESGGDFVQPGSLRVSCAASGFAFASHYAMSVWRQAPGKLEWVAYISSGSGTYY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 EVLVESGGGLVQPGSLRLSCAASGFTFSSYAMSVWRQAPGKLEWAVISGSGTYY 60
QY 61 SDSVKGRFTISRDNKNTLYLQMSLRASDSAVYFCTRVKLGTYTFDSNGQGTLLTVSS 119
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 ADSVKGRFTISRDNKNTLYLQMSLRASDAVYVYCARGRVG--YYDYMGGQGTLLTVSS 117
RESULT 7
US-10-044-896-6
; Sequence 6, Application US/10044896
; Publication No. US20030166228A1
; GENERAL INFORMATION:
; APPLICANT: Chantharapai, Anan
; APPLICANT: Kim, Jin K.
; APPLICANT: Stewart, Timothy
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: ANTI-INTERFERON-ALPHA ANTIBODIES
; FILE REFERENCE: GENENT. 074A
; CURRENT APPLICATION NUMBER: US/10/044,896
; CURRENT FILING DATE: 2002-01-09
; PRIOR APPLICATION NUMBER: 60/270775
; PRIOR FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-044-896-6
Query Match          80.0%; Score 499; DB 4; Length 119;
Best Local Similarity 80.7%; Pred. No. 1.8e-37; Indels 2; Gaps 1;
Matches 96; Conservative 8; Mismatches 13; Indels 2; Gaps 1;
QY 1 EVLVESGGDFVQPGSLRVSCAASGFAFASHYAMSVWRQAPGKLEWVAYISSGSGTYY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 EVLVESGGGLVQPGSLRLSCAASGFTFSSYAMSVWRQAPGKLEWAVISGSGTYY 60
QY 61 SDSVKGRFTISRDNKNTLYLQMSLRASDSAVYFCTRVKLGTYTFDSNGQGTLLTVSS 119
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 ADSVKGRFTISRDNKNTLYLQMSLRASDAVYVYCARGRVG--YYDYMGGQGTLLTVSS 117
RESULT 8
US-09-811-123-3
; Sequence 3, Application US/09811123
; Patent No. US20020001587A1
; GENERAL INFORMATION:
; APPLICANT: Sharon Erickson
; APPLICANT: Ralph Schwall
; APPLICANT: Mark Sliwkowski
; TITLE OF INVENTION: METHODS OF TREATMENT USING ANTI-ERBB
; TITLE OF INVENTION: ANTIBODY-MAYTANSINOID CONJUGATES
; FILE REFERENCE: GENENT. 073A2
; CURRENT APPLICATION NUMBER: US/09/811,123
US-09-811-123-3
; Sequence 3, Application US/09811123
; Patent No. US20020001587A1
; GENERAL INFORMATION:
; APPLICANT: Sharon Erickson
; APPLICANT: Ralph Schwall
; APPLICANT: Mark Sliwkowski
; TITLE OF INVENTION: METHODS OF TREATMENT USING ANTI-ERBB
; TITLE OF INVENTION: ANTIBODY-MAYTANSINOID CONJUGATES
; FILE REFERENCE: GENENT. 073A2
; CURRENT APPLICATION NUMBER: US/09/811,123
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; CURRENT FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/238,327
; PRIOR FILING DATE: 2000-10-05
; PRIOR APPLICATION NUMBER: 09/602,530
; PRIOR FILING DATE: 2000-06-23
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized Antibody Sequence
US-09-811-123-3

Query Match          79.8%; Score 498; DB 3; Length 119;
Best Local Similarity 79.8%; Pred. No. 2.2e-37;
Matches 95; Conservative 8; Mismatches 16; Indels 0; Gaps 0;

QY 1 EVQLVESGGDFVQPGSLRVSCAASGFAPFASHYAMSWVRQAPGKGLEWVAIISGGSGTYY 60
   |||||
Db 1 EVQLVESGGGLVQPGSLRLSCAASGFTFSYAMSWVRQAPGKGLEWVAIISGGSGTYY 60
   |||||
QY 61 SDSVKGRFTISRDNKNTLYLQMRLSDRAEDSAVYFCTRVKLTGYTFDSWGQGTLLTVSS 119
   :|||
Db 61 ADSVKGRFTISRDNKNTLYLQMRLSDRAEDTAVYICARGRVGSLYDYWGQGTLLTVSS 119
   :|||

RESULT 9
US-10-268-501-6
; Sequence 6, Application US/10268501
; Publication No. US20030086924A1
; GENERAL INFORMATION:
; APPLICANT: Sliwkowski, Mark X.
; TITLE OF INVENTION: Treatment with Anti-ErbB2 Antibodies
; FILE REFERENCE: P1467R2P1
; CURRENT APPLICATION NUMBER: US/10/268,501
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 09/602,812
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/141,316
; PRIOR FILING DATE: 1999-06-25
; NUMBER OF SEQ ID NOS: 13
; SEQ ID NO 6
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: heavy chain consensus sequence
US-10-268-501-6

Query Match          79.8%; Score 498; DB 4; Length 119;
Best Local Similarity 79.8%; Pred. No. 2.2e-37;
Matches 95; Conservative 8; Mismatches 16; Indels 0; Gaps 0;

QY 1 EVQLVESGGDFVQPGSLRVSCAASGFAPFASHYAMSWVRQAPGKGLEWVAIISGGSGTYY 60
   |||||
Db 1 EVQLVESGGGLVQPGSLRLSCAASGFTFSYAMSWVRQAPGKGLEWVAIISGGSGTYY 60
   |||||
QY 61 SDSVKGRFTISRDNKNTLYLQMRLSDRAEDSAVYFCTRVKLTGYTFDSWGQGTLLTVSS 119
   :|||
Db 61 ADSVKGRFTISRDNKNTLYLQMRLSDRAEDTAVYICARGRVGSLYDYWGQGTLLTVSS 119
   :|||

RESULT 10
US-10-608-626-6
; Sequence 6, Application US/10608626
; Publication No. US20040013667A1
; GENERAL INFORMATION:
; APPLICANT: Kelsey, Stephen M.
; APPLICANT: Sliwkowski, Mark X.
; TITLE OF INVENTION: Treatment with Anti-ErbB2 Antibodies
; FILE REFERENCE: P1467R2P2
```

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; CURRENT APPLICATION NUMBER: US/10/608,626
; CURRENT FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: US 10/268,501
; PRIOR FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 09/602,812
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/141,316
; PRIOR FILING DATE: 1999-06-25
; NUMBER OF SEQ ID NOS: 13
; SEQ ID NO 6
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: heavy chain consensus sequence
US-10-608-626-6

Query Match          79.8%; Score 498; DB 4; Length 119;
Best Local Similarity 79.8%; Pred. No. 2.2e-37;
Matches 95; Conservative 8; Mismatches 16; Indels 0; Gaps 0;

QY 1 EVQLVESGGDFVQPGSLRVSCAASGFAPFASHYAMSWVRQAPGKGLEWVAIISGGSGTYY 60
   |||||
Db 1 EVQLVESGGGLVQPGSLRLSCAASGFTFSYAMSWVRQAPGKGLEWVAIISGGSGTYY 60
   |||||
QY 61 SDSVKGRFTISRDNKNTLYLQMRLSDRAEDSAVYFCTRVKLTGYTFDSWGQGTLLTVSS 119
   :|||
Db 61 ADSVKGRFTISRDNKNTLYLQMRLSDRAEDTAVYICARGRVGSLYDYWGQGTLLTVSS 119
   :|||

RESULT 11
US-10-600-152-15
; Sequence 15, Application US/10600152
; Publication No. US20040037824A1
; GENERAL INFORMATION:
; APPLICANT: Baughman, Sharon A.
; TITLE OF INVENTION: Dosages for Treatment with Anti-ErbB2 Antibodies
; FILE REFERENCE: P1775R1
; CURRENT APPLICATION NUMBER: US/10/600,152
; CURRENT FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: 09/648,067
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,018
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: US 60/213,822
; PRIOR FILING DATE: 2000-06-23
; NUMBER OF SEQ ID NOS: 15
; SEQ ID NO 15
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: VH consensus sequence
US-10-600-152-15

Query Match          79.8%; Score 498; DB 4; Length 119;
Best Local Similarity 79.8%; Pred. No. 2.2e-37;
Matches 95; Conservative 8; Mismatches 16; Indels 0; Gaps 0;

QY 1 EVQLVESGGDFVQPGSLRVSCAASGFAPFASHYAMSWVRQAPGKGLEWVAIISGGSGTYY 60
   |||||
Db 1 EVQLVESGGGLVQPGSLRLSCAASGFTFSYAMSWVRQAPGKGLEWVAIISGGSGTYY 60
   |||||
QY 61 SDSVKGRFTISRDNKNTLYLQMRLSDRAEDSAVYFCTRVKLTGYTFDSWGQGTLLTVSS 119
   :|||
Db 61 ADSVKGRFTISRDNKNTLYLQMRLSDRAEDTAVYICARGRVGSLYDYWGQGTLLTVSS 119
   :|||

RESULT 12
US-10-619-754-6
; Sequence 6, Application US/10619754
; Publication No. US20040106161A1
```

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; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Koll, Hans
; APPLICANT: Bossenmaier, Birgit
; APPLICANT: Muller, Hans-Joachim
; APPLICANT: Sliwkowski, Mark
; APPLICANT: Kelsey, Stephen
; TITLE OF INVENTION: Methods For Identifying Tumors That Are
; TITLE OF INVENTION: Responsive To Treatment With Anti-ErbB2 Antibodies
; FILE REFERENCE: 39766-0114A
; CURRENT APPLICATION NUMBER: US/10/619,754
; CURRENT FILING DATE: 2003-07-14
; PRIOR APPLICATION NUMBER: US 60/396,290
; PRIOR FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: US 60/480,043
; PRIOR FILING DATE: 2003-06-20
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Homosapiens
US-10-619-754-6

Query Match          79.8%; Score 498; DB 4; Length 119;
Best Local Similarity 79.8%; Pred. No. 2.2e-37;
Matches 95; Conservative 8; Mismatches 16; Indels 0; Gaps 0;

QY 1 EVLVESGGDFVQPGGSLRVSCAASGFAPSHYAMSVWRQAPGKLEWVAYISSGGSGTYY 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 EVLVESGGGLVQPGGSLRLSCAASGFTFSYAMSVWRQAPGKLEWVAVISGDGGSTYY 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 61 SDSVKGRFTISRDNKNTLYLQMSLRADSDAVYFCTRVKLGTYTFDSMQGTLTVSS 119
   :|||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||:
Db 61 ADSVKGRFTISRDNKNTLYLQMSLRADSDAVYFCTRVKLGTYTFDSMQGTLTVSS 119
   :|||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||:

RESULT 13
US-10-719-310-6
; Sequence 6, Application US/10719310
; Publication No. US20040258685A1
; GENERAL INFORMATION:
; APPLICANT: Brunetta, Paul G.
; APPLICANT: Sliwkowski, Mark X.
; TITLE OF INVENTION: THERAPY OF NON-MALIGNANT DISEASES OR DISORDERS WITH
; TITLE OF INVENTION: ANTI-ERBB2 ANTIBODIES
; FILE REFERENCE: P1979R1
; CURRENT APPLICATION NUMBER: US/10/719,310
; CURRENT FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: US 60/428,027
; PRIOR FILING DATE: 2002-11-21
; NUMBER OF SEQ ID NOS: 13
; SEQ ID NO 6
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-10-719-310-6

Query Match          79.8%; Score 498; DB 5; Length 119;
Best Local Similarity 79.8%; Pred. No. 2.2e-37;
Matches 95; Conservative 8; Mismatches 16; Indels 0; Gaps 0;

QY 1 EVLVESGGDFVQPGGSLRVSCAASGFAPSHYAMSVWRQAPGKLEWVAYISSGGSGTYY 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 EVLVESGGGLVQPGGSLRLSCAASGFTFSYAMSVWRQAPGKLEWVAVISGDGGSTYY 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 61 SDSVKGRFTISRDNKNTLYLQMSLRADSDAVYFCTRVKLGTYTFDSMQGTLTVSS 119
   :|||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||:
Db 61 ADSVKGRFTISRDNKNTLYLQMSLRADSDAVYFCTRVKLGTYTFDSMQGTLTVSS 119
   :|||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||:

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RESULT 14
US-10-861-049-42
; Sequence 42, Application US/10861049
; Publication No. US20050095243A1
; GENERAL INFORMATION:
; APPLICANT: Andrew Chan
; APPLICANT: Qian Gong
; APPLICANT: Flavius Martin
; TITLE OF INVENTION: COMBINATION THERAPY FOR B CELL DISORDERS
; FILE REFERENCE: P2040RIUS
; CURRENT APPLICATION NUMBER: US/10/861,049
; CURRENT FILING DATE: 2004-06-04
; PRIOR APPLICATION NUMBER: US 60/476,531
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/476,481
; PRIOR FILING DATE: 2003-06-05
; PRIOR APPLICATION NUMBER: US 60/476,414
; PRIOR FILING DATE: 2003-06-05
; NUMBER OF SEQ ID NOS: 145
; SEQ ID NO 42
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-861-049-42

Query Match          79.8%; Score 498; DB 5; Length 119;
Best Local Similarity 79.8%; Pred. No. 2.2e-37;
Matches 95; Conservative 8; Mismatches 16; Indels 0; Gaps 0;

QY 1 EVLVESGGDFVQPGGSLRVSCAASGFAPSHYAMSVWRQAPGKLEWVAYISSGGSGTYY 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 EVLVESGGGLVQPGGSLRLSCAASGFTFSYAMSVWRQAPGKLEWVAVISGDGGSTYY 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 61 SDSVKGRFTISRDNKNTLYLQMSLRADSDAVYFCTRVKLGTYTFDSMQGTLTVSS 119
   :|||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||:
Db 61 ADSVKGRFTISRDNKNTLYLQMSLRADSDAVYFCTRVKLGTYTFDSMQGTLTVSS 119
   :|||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||:

RESULT 15
US-11-021-874-42
; Sequence 42, Application US/11021874
; Publication No. US20050163775A1
; GENERAL INFORMATION:
; APPLICANT: Andrew Chan
; APPLICANT: Qian Gong
; APPLICANT: Flavius Martin
; TITLE OF INVENTION: COMBINATION THERAPY FOR B CELL DISORDERS
; FILE REFERENCE: P2040R1P1
; CURRENT APPLICATION NUMBER: US/11/021,874
; CURRENT FILING DATE: 2004-12-22
; PRIOR APPLICATION NUMBER: US 10/861,049
; PRIOR FILING DATE: 2004-06-04
; PRIOR APPLICATION NUMBER: US 60/476,531
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/476,481
; PRIOR FILING DATE: 2003-06-05
; PRIOR APPLICATION NUMBER: US 60/476,414
; PRIOR FILING DATE: 2003-06-05
; NUMBER OF SEQ ID NOS: 165
; SEQ ID NO 42
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-021-874-42

Query Match          79.8%; Score 498; DB 6; Length 119;
Best Local Similarity 79.8%; Pred. No. 2.2e-37;
Matches 95; Conservative 8; Mismatches 16; Indels 0; Gaps 0;

QY 1 EVLVESGGDFVQPGGSLRVSCAASGFAPSHYAMSVWRQAPGKLEWVAYISSGGSGTYY 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 EVLVESGGGLVQPGGSLRLSCAASGFTFSYAMSVWRQAPGKLEWVAVISGDGGSTYY 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: April 6, 2006, 08:53:51 ; Search time 4.15267 Seconds  
(without alignments)  
893.845 Million cell updates/sec

Title: US-10-089-500-9  
Perfect score: 624  
Sequence: 1 EVQLVESGDFVQPGSLRV.....KLGYTFDSWGQGLTLTVSS 119

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 184161 seqs, 31191982 residues

Total number of hits satisfying chosen parameters: 184161

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA New:\*  
1: /SDSS/ptodata/2/pubpaa/US08\_NEW\_PUB pep.\*  
2: /SDSS/ptodata/2/pubpaa/US06\_NEW\_PUB pep.\*  
3: /SDSS/ptodata/2/pubpaa/US07\_NEW\_PUB pep.\*  
4: /SDSS/ptodata/2/pubpaa/PCT\_NEW\_PUB pep.\*  
5: /SDSS/ptodata/2/pubpaa/US09\_NEW\_PUB pep.\*  
6: /SDSS/ptodata/2/pubpaa/US10\_NEW\_PUB pep.\*  
7: /SDSS/ptodata/2/pubpaa/US11\_NEW\_PUB pep.\*  
8: /SDSS/ptodata/2/pubpaa/US60\_NEW\_PUB pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	624	100.0	119	6	US-10-473-037-9
2	579	92.8	119	6	US-10-473-037-49
3	579	92.8	130	7	US-11-228-293-18
4	579	92.8	130	7	US-11-228-319-18
5	579	92.8	138	6	US-10-473-037-1
6	569	91.2	130	7	US-10-228-293-8
7	569	91.2	130	7	US-11-228-319-8
8	498	79.8	119	7	US-11-106-820-9
9	498	79.8	119	7	US-11-154-337-6
10	498	79.8	119	7	US-11-182-908-6
11	498	79.8	119	7	US-11-190-364-9
12	498	79.8	119	7	US-11-102-120-6
13	498	79.8	119	7	US-11-147-780-9
14	498	79.8	119	7	US-11-223-361-6
15	492	78.8	119	6	US-10-771-257-21
16	492	78.8	119	7	US-11-127-677-21
17	492	78.8	313	7	US-11-000-463-427
18	490	78.5	129	6	US-10-993-543-180
19	489.5	78.4	118	6	US-10-925-366A-208
20	489	78.4	119	7	US-11-120-338-9
21	489	78.4	119	7	US-11-143-077-9
22	489	78.4	119	7	US-11-143-386-9
23	489	78.4	119	7	US-11-187-364-9
24	487.5	78.1	116	7	US-11-125-837-38
25	487	78.0	123	6	US-10-982-440-59

26	487	78.0	123	7	US-11-049-536-238	Sequence 238, App
27	487	78.0	123	7	US-11-049-536-378	Sequence 378, App
28	487	78.0	123	7	US-11-049-536-398	Sequence 398, App
29	487	78.0	123	7	US-11-199-739-238	Sequence 378, App
30	487	78.0	123	7	US-11-199-739-378	Sequence 378, App
31	487	78.0	123	7	US-11-199-739-398	Sequence 398, App
32	487	78.0	247	7	US-11-054-515-1953	Sequence 1953, App
33	487	78.0	247	7	US-11-266-444-1953	Sequence 1953, App
34	486	77.9	117	7	US-11-049-536-642	Sequence 642, App
35	486	77.9	117	7	US-11-199-739-642	Sequence 642, App
36	486	77.9	123	7	US-11-102-512-56	Sequence 56, Appl
37	485	77.7	125	7	US-11-127-903-46	Sequence 46, Appl
38	485	77.7	248	7	US-11-054-515-1421	Sequence 1421, App
39	485	77.7	248	7	US-11-266-444-1421	Sequence 1421, App
40	484.5	77.6	118	7	US-11-049-536-338	Sequence 338, App
41	484.5	77.6	118	7	US-11-199-739-338	Sequence 338, App
42	484	77.6	117	6	US-10-981-356A-6	Sequence 6, Appl
43	484	77.6	117	7	US-11-096-046-6	Sequence 6, Appl
44	483.5	77.5	133	6	US-10-993-543-4	Sequence 4, Appl
45	483	77.4	119	7	US-11-049-536-370	Sequence 370, App

ALIGNMENTS

RESULT 1

US-10-473-037-9  
; Sequence 9, Application US/10473037  
; Publication No. US20050260206A1  
; GENERAL INFORMATION:  
; APPLICANT: KYOWA HAKKO KOGYO CO., LTD.  
; TITLE OF INVENTION: Agents for treatment of cancer using recombinant anti-GD3 antibody  
; TITLE OF INVENTION: the antibody fragments  
; FILE REFERENCE: 11374WO1  
; CURRENT APPLICATION NUMBER: US/10/473,037  
; CURRENT FILING DATE: 2003-09-26  
; PRIOR APPLICATION NUMBER: JP2001-097483  
; PRIOR FILING DATE: 2001-03-29  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 9  
; LENGTH: 119  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:synthetic protein  
US-10-473-037-9

Query Match	100.0%	Score 624;	DB 6;	Length 119;
Best Local Similarity	100.0%;	Pred. No. 1.3e-44;		
Matches 119;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	EVQLVESGDFVQPGSLRVSCAASGPAFASHYAMSVWRQAPGKGLIEWVAYISSGGSGTYY	60	
Db	1	EVQLVESGDFVQPGSLRVSCAASGPAFASHYAMSVWRQAPGKGLIEWVAYISSGGSGTYY	60	
QY	61	SDSVKGRFTISRDNSKNTLYLQMRSRLRAEDSAVYFCTRKVLGTYTFDSWGQGLTLTVSS	119	
Db	61	SDSVKGRFTISRDNSKNTLYLQMRSRLRAEDSAVYFCTRKVLGTYTFDSWGQGLTLTVSS	119	

RESULT 2

US-10-473-037-49  
; Sequence 49, Application US/10473037  
; Publication No. US20050260206A1  
; GENERAL INFORMATION:  
; APPLICANT: KYOWA HAKKO KOGYO CO., LTD.  
; TITLE OF INVENTION: Agents for treatment of cancer using recombinant anti-GD3 antibody  
; TITLE OF INVENTION: the antibody fragments  
; FILE REFERENCE: 11374WO1  
; CURRENT APPLICATION NUMBER: US/10/473,037  
; CURRENT FILING DATE: 2003-09-26  
; PRIOR APPLICATION NUMBER: JP2001-097483

; PRIOR FILING DATE: 2001-03-29  
 ; NUMBER OF SEQ ID NOS: 50  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 49  
 ; LENGTH: 119  
 ; TYPE: PRT  
 ; ORGANISM: Mus musculus  
 US-10-473-037-49

Query Match 92.8%; Score 579; DB 6; Length 119;  
 Best Local Similarity 91.6%; Pred. No. 6.1e-41;  
 Matches 109; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 EVLVESGGDFVQPGSLRVSCAASGFAPSHYAMSVWRQAPKGLWVAYISSGSGTTY 60

DB 1 EVTLVESGGDFVKPGSLRVSCAASGFAPSHYAMSVWRQTPAKRLEWVAYISSGSGTTY 60

QY 61 SDSVKGRTTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLGTYFFDSWGQGTLLTVSS 119

DB 61 SDSVKGRTTISRDNKNTLYLQMRSLRSED SAMYFCTRVKLGTYFFDSWGQGTLLTVSS 119

# RESULT 3

; Sequence 18, Application US/11228293  
 ; Publication No. US20060057139A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: SHITARA, KENYA  
 ; APPLICANT: HANAI, NOBUO  
 ; APPLICANT: HASEGAWA, MAMORU  
 ; APPLICANT: MIYAJI, HIROMASA  
 ; APPLICANT: KUWANA, YOSHIIISA  
 ; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY  
 ; FILE REFERENCE: 249-101  
 ; CURRENT APPLICATION NUMBER: US/11/228,293  
 ; PRIOR FILING DATE: 2005-09-19  
 ; PRIOR APPLICATION NUMBER: US/09/225,322  
 ; PRIOR FILING DATE: 1999-01-05  
 ; PRIOR APPLICATION NUMBER: US 08/454,680  
 ; PRIOR FILING DATE: 1995-05-31  
 ; PRIOR APPLICATION NUMBER: US 08/408,133  
 ; PRIOR FILING DATE: 1995-03-21  
 ; PRIOR APPLICATION NUMBER: US 08/292,178  
 ; PRIOR FILING DATE: 1994-08-17  
 ; PRIOR APPLICATION NUMBER: US07/947,674  
 ; PRIOR FILING DATE: 1992-09-17  
 ; PRIOR APPLICATION NUMBER: JP 3-238375  
 ; PRIOR FILING DATE: 1991-09-18  
 ; NUMBER OF SEQ ID NOS: 19  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 18  
 ; LENGTH: 130  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence:cDNA KM-641  
 US-11-228-293-18

Query Match 92.8%; Score 579; DB 6; Length 130;  
 Best Local Similarity 91.6%; Pred. No. 6.1e-41;  
 Matches 109; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 EVLVESGGDFVQPGSLRVSCAASGFAPSHYAMSVWRQAPKGLWVAYISSGSGTTY 60

DB 1 EVTLVESGGDFVKPGSLRVSCAASGFAPSHYAMSVWRQTPAKRLEWVAYISSGSGTTY 70

QY 61 SDSVKGRTTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLGTYFFDSWGQGTLLTVSS 119

DB 71 SDSVKGRTTISRDNKNTLYLQMRSLRSED SAMYFCTRVKLGTYFFDSWGQGTLLTVSS 129

RESULT 4

US-11-228-293-18

; Sequence 18, Application US/11228293  
 ; Publication No. US20060057139A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: SHITARA, KENYA  
 ; APPLICANT: HANAI, NOBUO  
 ; APPLICANT: HASEGAWA, MAMORU  
 ; APPLICANT: MIYAJI, HIROMASA  
 ; APPLICANT: KUWANA, YOSHIIISA  
 ; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY  
 ; FILE REFERENCE: 249-101  
 ; CURRENT APPLICATION NUMBER: US/11/228,293  
 ; PRIOR FILING DATE: 2005-09-19  
 ; PRIOR APPLICATION NUMBER: US/09/225,322  
 ; PRIOR FILING DATE: 1999-01-05  
 ; PRIOR APPLICATION NUMBER: US 08/454,680  
 ; PRIOR FILING DATE: 1995-05-31  
 ; PRIOR APPLICATION NUMBER: US 08/408,133  
 ; PRIOR FILING DATE: 1995-03-21  
 ; PRIOR APPLICATION NUMBER: US 08/292,178  
 ; PRIOR FILING DATE: 1994-08-17  
 ; PRIOR APPLICATION NUMBER: US07/947,674  
 ; PRIOR FILING DATE: 1992-09-17  
 ; PRIOR APPLICATION NUMBER: JP 3-238375  
 ; PRIOR FILING DATE: 1991-09-18  
 ; NUMBER OF SEQ ID NOS: 19  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 18  
 ; LENGTH: 130  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence:cDNA KM-641  
 US-11-228-293-18

Query Match 92.8%; Score 579; DB 7; Length 130;  
 Best Local Similarity 91.6%; Pred. No. 6.5e-41;  
 Matches 109; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 EVLVESGGDFVQPGSLRVSCAASGFAPSHYAMSVWRQAPKGLWVAYISSGSGTTY 60

DB 1 EVTLVESGGDFVKPGSLRVSCAASGFAPSHYAMSVWRQTPAKRLEWVAYISSGSGTTY 70

QY 61 SDSVKGRTTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLGTYFFDSWGQGTLLTVSS 119

DB 71 SDSVKGRTTISRDNKNTLYLQMRSLRSED SAMYFCTRVKLGTYFFDSWGQGTLLTVSS 129

# RESULT 4

US-11-228-319-18

; Sequence 18, Application US/11228319  
 ; Publication No. US20060058512A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: SHITARA, KENYA  
 ; APPLICANT: HANAI, NOBUO  
 ; APPLICANT: HASEGAWA, MAMORU  
 ; APPLICANT: MIYAJI, HIROMASA  
 ; APPLICANT: KUWANA, YOSHIIISA  
 ; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY  
 ; FILE REFERENCE: 249-101  
 ; CURRENT APPLICATION NUMBER: US/11/228,319  
 ; PRIOR FILING DATE: 2005-09-19  
 ; PRIOR APPLICATION NUMBER: US/09/225,322  
 ; PRIOR FILING DATE: 1999-01-05  
 ; PRIOR APPLICATION NUMBER: US 08/454,680  
 ; PRIOR FILING DATE: 1995-05-31  
 ; PRIOR APPLICATION NUMBER: US 08/408,133  
 ; PRIOR FILING DATE: 1995-03-21  
 ; PRIOR APPLICATION NUMBER: US 08/292,178  
 ; PRIOR FILING DATE: 1994-08-17  
 ; PRIOR APPLICATION NUMBER: US07/947,674  
 ; PRIOR FILING DATE: 1992-09-17  
 ; PRIOR APPLICATION NUMBER: JP 3-238375  
 ; PRIOR FILING DATE: 1991-09-18  
 ; NUMBER OF SEQ ID NOS: 19  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 18  
 ; LENGTH: 130  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence:cDNA KM-641  
 US-11-228-319-18

Query Match 92.8%; Score 579; DB 7; Length 130;  
 Best Local Similarity 91.6%; Pred. No. 6.5e-41;  
 Matches 109; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 EVLVESGGDFVQPGSLRVSCAASGFAPSHYAMSVWRQAPKGLWVAYISSGSGTTY 60

DB 1 EVTLVESGGDFVKPGSLRVSCAASGFAPSHYAMSVWRQTPAKRLEWVAYISSGSGTTY 70

QY 61 SDSVKGRTTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLGTYFFDSWGQGTLLTVSS 119

DB 71 SDSVKGRTTISRDNKNTLYLQMRSLRSED SAMYFCTRVKLGTYFFDSWGQGTLLTVSS 129

# RESULT 5

US-10-473-037-1  
 ; Sequence 1, Application US/10473037  
 ; Publication No. US20050260206A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: KYOWA HAKKO KOGYO CO., LTD.  
 ; TITLE OF INVENTION: Agents for treatment of cancer using recombinant anti-Gp3 antibody  
 ; TITLE OF INVENTION: the antibody fragments  
 ; FILE REFERENCE: 11374WO1  
 ; CURRENT APPLICATION NUMBER: US/10/473,037  
 ; CURRENT FILING DATE: 2003-09-26  
 ; PRIOR APPLICATION NUMBER: JP2001-097483  
 ; PRIOR FILING DATE: 2001-03-29  
 ; NUMBER OF SEQ ID NOS: 50  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 1  
 ; LENGTH: 138  
 ; TYPE: PRT  
 ; ORGANISM: Mus musculus  
 US-10-473-037-1

Query Match 92.8%; Score 579; DB 6; Length 138;  
 Best Local Similarity 91.6%; Pred. No. 6.9e-41;  
 Matches 109; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 EVLVESGGDFVQPGSLRVSCAASGFAPSHYAMSVWRQAPKGLWVAYISSGSGTTY 60



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Db 20 EVTLVESGGDFVKPGSLKVSAAAGFAFASHYAMSVWRTPAKRLWVAYISSGGSGTYY 79
QY 61 SDSVKGRFTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLGTYFYFDSWGQGTLLTVSS 119
Db 80 SDSVKGRFTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLGTYFYFDSWGQGTLLTVSS 138

RESULT 6
US-11-228-293-8
; Sequence 8, Application US/11228293
; Publication No. US20060057139A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUMANA, YOSHIHISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/11/228,293
; CURRENT FILING DATE: 2005-09-19
; PRIOR APPLICATION NUMBER: US/09/225,322
; PRIOR FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: US 08/454,680
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
; PRIOR APPLICATION NUMBER: US07/947,674
; PRIOR FILING DATE: 1992-09-17
; PRIOR APPLICATION NUMBER: JP 3-238375
; PRIOR FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: cDNA KM-641
US-11-228-293-8
Query Match 91.2%; Score 569; DB 7; Length 130;
Best Local Similarity 90.8%; Pred. No. 4.3e-40;
Matches 108; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
QY 1 EVTLVESGGDFVKPGSLKVSAAAGFAFASHYAMSVWRTPAKRLWVAYISSGGSGTYY 60
Db 11 EVTLVESGGDFVKPGSLKVSAAAGFAFASHYAMSVWRTPAKRLWVAYISSGGSGTYY 70
QY 61 SDSVKGRFTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLGTYFYFDSWGQGTLLTVSS 119
Db 71 SDSVKGRFTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLGTYFYFDSWGQGTLLTVSS 129

RESULT 7
US-11-228-319-8
; Sequence 8, Application US/11228319
; Publication No. US2006005812A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUMANA, YOSHIHISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/11/228,319
; CURRENT FILING DATE: 2005-09-19
; PRIOR APPLICATION NUMBER: US/09/225,322
; PRIOR FILING DATE: 1999-01-05
; OTHER INFORMATION: Description of Artificial Sequence: cDNA KM-641
US-11-228-293-8
Query Match 91.2%; Score 569; DB 7; Length 130;
Best Local Similarity 90.8%; Pred. No. 4.3e-40;
Matches 108; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
QY 1 EVTLVESGGDFVKPGSLKVSAAAGFAFASHYAMSVWRTPAKRLWVAYISSGGSGTYY 60
Db 11 EVTLVESGGDFVKPGSLKVSAAAGFAFASHYAMSVWRTPAKRLWVAYISSGGSGTYY 70
QY 61 SDSVKGRFTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLGTYFYFDSWGQGTLLTVSS 119
Db 71 SDSVKGRFTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLGTYFYFDSWGQGTLLTVSS 129

RESULT 8
US-11-106-820-9
; Sequence 9, Application US/11106820
; Publication No. US20060002930A1
; GENERAL INFORMATION:
; APPLICANT: BRUNETTA, PAUL G
; APPLICANT: SEWELL, KATHRYN L.
; TITLE OF INVENTION: Treatment of Disorders
; FILE REFERENCE: P2102R1
; CURRENT APPLICATION NUMBER: US/11/106,820
; CURRENT FILING DATE: 2005-04-15
; PRIOR APPLICATION NUMBER: US 60/563,227
; PRIOR FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: US 60/565,098
; PRIOR FILING DATE: 2004-04-22
; NUMBER OF SEQ ID NOS: 45
; SEQ ID NO 9
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-106-820-9
Query Match 79.8%; Score 498; DB 7; Length 119;
Best Local Similarity 79.8%; Pred. No. 2.5e-34;
Matches 95; Conservative 8; Mismatches 16; Indels 0; Gaps 0;
QY 1 EVTLVESGGDFVKPGSLKVSAAAGFAFASHYAMSVWRTPAKRLWVAYISSGGSGTYY 60
Db 1 EVTLVESGGGLVQPGGSLRLSCAASGFTFSYAMSVWRTPAKRLWVAYISSGGSGTYY 60
QY 61 SDSVKGRFTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLGTYFYFDSWGQGTLLTVSS 119
Db 61 ADSVKGRFTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLGTYFYFDSWGQGTLLTVSS 119

RESULT 9
US-11-154-337-6
; Sequence 6, Application US/11154337
; Publication No. US20060013819A1
; GENERAL INFORMATION:
```

```
; PRIOR APPLICATION NUMBER: US 08/454,680
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
; PRIOR APPLICATION NUMBER: US07/947,674
; PRIOR FILING DATE: 1992-09-17
; PRIOR APPLICATION NUMBER: JP 3-238375
; PRIOR FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: cDNA KM-641
US-11-228-319-8
Query Match 91.2%; Score 569; DB 7; Length 130;
Best Local Similarity 90.8%; Pred. No. 4.3e-40;
Matches 108; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
QY 1 EVTLVESGGDFVKPGSLKVSAAAGFAFASHYAMSVWRTPAKRLWVAYISSGGSGTYY 60
Db 11 EVTLVESGGDFVKPGSLKVSAAAGFAFASHYAMSVWRTPAKRLWVAYISSGGSGTYY 70
QY 61 SDSVKGRFTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLGTYFYFDSWGQGTLLTVSS 119
Db 71 SDSVKGRFTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLGTYFYFDSWGQGTLLTVSS 129

RESULT 8
US-11-106-820-9
; Sequence 9, Application US/11106820
; Publication No. US20060002930A1
; GENERAL INFORMATION:
; APPLICANT: BRUNETTA, PAUL G
; APPLICANT: SEWELL, KATHRYN L.
; TITLE OF INVENTION: Treatment of Disorders
; FILE REFERENCE: P2102R1
; CURRENT APPLICATION NUMBER: US/11/106,820
; CURRENT FILING DATE: 2005-04-15
; PRIOR APPLICATION NUMBER: US 60/563,227
; PRIOR FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: US 60/565,098
; PRIOR FILING DATE: 2004-04-22
; NUMBER OF SEQ ID NOS: 45
; SEQ ID NO 9
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-106-820-9
Query Match 79.8%; Score 498; DB 7; Length 119;
Best Local Similarity 79.8%; Pred. No. 2.5e-34;
Matches 95; Conservative 8; Mismatches 16; Indels 0; Gaps 0;
QY 1 EVTLVESGGDFVKPGSLKVSAAAGFAFASHYAMSVWRTPAKRLWVAYISSGGSGTYY 60
Db 1 EVTLVESGGGLVQPGGSLRLSCAASGFTFSYAMSVWRTPAKRLWVAYISSGGSGTYY 60
QY 61 SDSVKGRFTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLGTYFYFDSWGQGTLLTVSS 119
Db 61 ADSVKGRFTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLGTYFYFDSWGQGTLLTVSS 119

RESULT 9
US-11-154-337-6
; Sequence 6, Application US/11154337
; Publication No. US20060013819A1
; GENERAL INFORMATION:
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```
; APPLICANT: KELSEY, STEPHEN M.
; TITLE OF INVENTION: THERAPY OF PLATINUM-RESISTANT CANCER
; FILE REFERENCE: P2146R1
; CURRENT APPLICATION NUMBER: US/11/154,337
; CURRENT FILING DATE: 2005-06-15
; PRIOR APPLICATION NUMBER: US 60/580,333
; PRIOR FILING DATE: 2004-06-16
; NUMBER OF SEQ ID NOS: 17
; SEQ ID NO 6
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-11-154-337-6

Query Match          79.8%; Score 498; DB 7; Length 119;
Best Local Similarity 79.8%; Pred. No. 2.5e-34;
Matches 95; Conservative 8; Mismatches 16; Indels 0; Gaps 0;

QY 1 EVQLVESGGDFVPGGSLRVSCAASGFAPFASHYAMSWVRQAPKGLEWVAYISSGGSGTYY 60
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPKGLEWVAVISGDGGSTYY 60
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

QY 61 SDSVKGRFTISRDNKNTLYLQMSLRADSAVYFCTRVKLTGYTFDSWGQGTLLTVSS 119
    :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||
Db 61 ADSVKGRFTISRDNKNTLYLQMSLRADTAIVYCARGRVGSLYDYWGQGTLLTVSS 119
    :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||

RESULT 10
US-11-182-908-6
; Sequence 6, Application US/11182908
; Publication No. US2006001899A1
; GENERAL INFORMATION:
; APPLICANT: KAO, YUNG-HSIANG
; TITLE OF INVENTION: HER2 ANTIBODY COMPOSITIONS
; FILE REFERENCE: P2105R1
; CURRENT APPLICATION NUMBER: US/11/182,908
; CURRENT FILING DATE: 2005-07-15
; PRIOR APPLICATION NUMBER: US 60/590,202
; PRIOR FILING DATE: 2004-07-22
; NUMBER OF SEQ ID NOS: 24
; SEQ ID NO 6
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-11-182-908-6

Query Match          79.8%; Score 498; DB 7; Length 119;
Best Local Similarity 79.8%; Pred. No. 2.5e-34;
Matches 95; Conservative 8; Mismatches 16; Indels 0; Gaps 0;

QY 1 EVQLVESGGDFVPGGSLRVSCAASGFAPFASHYAMSWVRQAPKGLEWVAYISSGGSGTYY 60
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPKGLEWVAVISGDGGSTYY 60
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

QY 61 SDSVKGRFTISRDNKNTLYLQMSLRADSAVYFCTRVKLTGYTFDSWGQGTLLTVSS 119
    :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||
Db 61 ADSVKGRFTISRDNKNTLYLQMSLRADTAIVYCARGRVGSLYDYWGQGTLLTVSS 119
    :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||

RESULT 11
US-11-190-364-9
; Sequence 9, Application US/11190364
; Publication No. US20060024300A1
; GENERAL INFORMATION:
; APPLICANT: Adams ET AL.
; TITLE OF INVENTION: Immunoglobulin Variants and Uses Thereof
; FILE REFERENCE: P1990R3C1P1
; CURRENT APPLICATION NUMBER: US/11/190,364
; APPLICANT: KELSEY, STEPHEN M.
; TITLE OF INVENTION: THERAPY OF PLATINUM-RESISTANT CANCER
; FILE REFERENCE: P2146R1
; CURRENT APPLICATION NUMBER: US/11/154,337
; CURRENT FILING DATE: 2005-06-15
; PRIOR APPLICATION NUMBER: US 60/580,333
; PRIOR FILING DATE: 2004-06-16
; NUMBER OF SEQ ID NOS: 17
; SEQ ID NO 6
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-11-190-364-9

Query Match          79.8%; Score 498; DB 7; Length 119;
Best Local Similarity 79.8%; Pred. No. 2.5e-34;
Matches 95; Conservative 8; Mismatches 16; Indels 0; Gaps 0;

QY 1 EVQLVESGGDFVPGGSLRVSCAASGFAPFASHYAMSWVRQAPKGLEWVAYISSGGSGTYY 60
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPKGLEWVAVISGDGGSTYY 60
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

QY 61 SDSVKGRFTISRDNKNTLYLQMSLRADSAVYFCTRVKLTGYTFDSWGQGTLLTVSS 119
    :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||
Db 61 ADSVKGRFTISRDNKNTLYLQMSLRADTAIVYCARGRVGSLYDYWGQGTLLTVSS 119
    :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||

RESULT 12
US-11-102-120-6
; Sequence 6, Application US/11102120
; Publication No. US20060034840A1
; GENERAL INFORMATION:
; APPLICANT: AGUS, David B.
; TITLE OF INVENTION: ErbB Antagonists for Pain Therapy
; FILE REFERENCE: 39766-0138 US
; CURRENT APPLICATION NUMBER: US/11/102,120
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: US 60/561,076
; PRIOR FILING DATE: 2004-04-08
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Consensus human framework for the humanized
; OTHER INFORMATION: antibody hum III (variable heavy)
US-11-102-120-6

Query Match          79.8%; Score 498; DB 7; Length 119;
Best Local Similarity 79.8%; Pred. No. 2.5e-34;
Matches 95; Conservative 8; Mismatches 16; Indels 0; Gaps 0;

QY 1 EVQLVESGGDFVPGGSLRVSCAASGFAPFASHYAMSWVRQAPKGLEWVAYISSGGSGTYY 60
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPKGLEWVAVISGDGGSTYY 60
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

QY 61 SDSVKGRFTISRDNKNTLYLQMSLRADSAVYFCTRVKLTGYTFDSWGQGTLLTVSS 119
    :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||
Db 61 ADSVKGRFTISRDNKNTLYLQMSLRADTAIVYCARGRVGSLYDYWGQGTLLTVSS 119
    :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||

RESULT 13
US-11-147-780-9
; Sequence 9, Application US/11147780
; Publication No. US20060034835A1
; GENERAL INFORMATION:
; APPLICANT: Adams ET AL.
```

```
; TITLE OF INVENTION: Immunoglobulin Variants and Uses Thereof
; FILE REFERENCE: P1990R3C1
; CURRENT APPLICATION NUMBER: US/11/147,780
; CURRENT FILING DATE: 2005-06-07
; PRIOR APPLICATION NUMBER: US 60/434,115
; PRIOR FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: US 60/526,163
; PRIOR FILING DATE: 2003-12-01
; PRIOR APPLICATION NUMBER: PCT/US03/40426
; PRIOR FILING DATE: 2003-12-16
; NUMBER OF SEQ ID NOS: 38
; SEQ ID NO 9
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized
US-11-147-780-9

Query Match          79.8%; Score 498; DB 7; Length 119;
Best Local Similarity 79.8%; Pred. No. 2.5e-34;
Matches 95; Conservative 8; Mismatches 16; Indels 0; Gaps 0;

QY 1 EVLVESGGDFVQPGSLRVSCAASGFAPFSHYAMSWVRQAPGKLEWVAIISGGSGTTY 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 EVLVESGGGLVQPGGSLRLSCLASGFTFSSYAMSWVRQAPGKLEWVAISGGSGTTY 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 61 SDSVKGRFTISRDNKNTLYLQMSRLRAEDSAVYFCTRVKLGTYTFDSWGQGTLLTVSS 119
    :|||: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 ADSVKGRFTISRDNKNTLYLQMSRLRAEDTAVYVCARGVGSYLDYWGQGTLLTVSS 119
    :|||: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 14
US-11-223-361-6
; Sequence 6, Application US/11223361
; Publication No. US20060034842A1
; GENERAL INFORMATION:
; APPLICANT: Adams, Camellia W.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Sliwkowski, Mark X.
; TITLE OF INVENTION: Humanized Anti-ErbB2 Antibodies and Treatment with
; TITLE OF INVENTION: Anti-ErbB2 Antibodies
; FILE REFERENCE: P1467R2
; CURRENT APPLICATION NUMBER: US/11/223,361
; CURRENT FILING DATE: 2005-09-09
; PRIOR APPLICATION NUMBER: US/09/602,812
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/141,316
; PRIOR FILING DATE: 1999-06-25
; NUMBER OF SEQ ID NOS: 13
; SEQ ID NO 6
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: heavy chain consensus sequence
US-11-223-361-6

Query Match          79.8%; Score 498; DB 7; Length 119;
Best Local Similarity 79.8%; Pred. No. 2.5e-34;
Matches 95; Conservative 8; Mismatches 16; Indels 0; Gaps 0;

QY 1 EVLVESGGDFVQPGSLRVSCAASGFAPFSHYAMSWVRQAPGKLEWVAIISGGSGTTY 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 EVLVESGGGLVQPGGSLRLSCLASGFTFSSYAMSWVRQAPGKLEWVAISGGSGTTY 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 61 SDSVKGRFTISRDNKNTLYLQMSRLRAEDSAVYFCTRVKLGTYTFDSWGQGTLLTVSS 119
    :|||: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 ADSVKGRFTISRDNKNTLYLQMSRLRAEDTAVYVCARGVGSYLDYWGQGTLLTVSS 119
    :|||: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 15
US-10-771-257-21
```

```
; Sequence 21, Application US/10771257
; Publication No. US2005028864A1
; GENERAL INFORMATION:
; APPLICANT: Medical Research Council
; APPLICANT: SISSA - Scuola Superiore Internazionale di Studi Avanzati
; APPLICANT: Cattaneo, Antonino
; APPLICANT: Maritan, Amos
; APPLICANT: Visintin, Michela
; APPLICANT: Rabbitts, Terrence H
; APPLICANT: Settanni, Giovanni
; TITLE OF INVENTION: Intracellular antibodies
; FILE REFERENCE: 18396/2272
; CURRENT APPLICATION NUMBER: US/10/771,257
; CURRENT FILING DATE: 2004-02-03
; PRIOR APPLICATION NUMBER: PCT/GB02/03512
; PRIOR FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: GB 0119004.0
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: GB 0121577.1
; PRIOR FILING DATE: 2001-09-06
; PRIOR APPLICATION NUMBER: GB 0200928.0
; PRIOR FILING DATE: 2002-01-16
; PRIOR APPLICATION NUMBER: GB 0203569.9
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: IT RM2001A000633
; PRIOR FILING DATE: 2001-10-25
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 21
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-771-257-21

Query Match          78.8%; Score 492; DB 6; Length 119;
Best Local Similarity 78.2%; Pred. No. 7.6e-34;
Matches 93; Conservative 8; Mismatches 18; Indels 0; Gaps 0;

QY 1 EVLVESGGDFVQPGSLRVSCAASGFAPFSHYAMSWVRQAPGKLEWVAIISGGSGTTY 60
    :|||: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 QVLVESGGGLVQPGGSLRLSCLASGFTFSSYGMHWVRQAPGKLEWVAIFIRNDGSNEY 60
    :|||: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 61 SDSVKGRFTISRDNKNTLYLQMSRLRAEDSAVYFCTRVKLGTYTFDSWGQGTLLTVSS 119
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 VDSVKGRFTISRDNKNTLYLQMSRLRAEDTAVYVCARRRSWYIFDYWGQGTLLTVSS 119
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Search completed: April 6, 2006, 08:55:07
Job time : 4.15267 secs
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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 6, 2006, 08:47:08 ; Search time 24.1439 Seconds  
(without alignments)  
1965.416 Million cell updates/sec

Title: US-10-089-500-10

Perfect score: 574

Sequence: 1 DIQMTQSPSSLSASVGDRVT.....HQYSKLPWTFGGTKVEIKR 108

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: A\_Geneseq\_21.\*
- 2: geneseqp1980s.\*
- 3: geneseqp1990s.\*
- 4: geneseqp2000s.\*
- 5: geneseqp2001s.\*
- 6: geneseqp2002s.\*
- 7: geneseqp2003as.\*
- 8: geneseqp2003bs.\*
- 9: geneseqp2004s.\*
- 9: geneseqp2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	574	100.0	108	4	AAB81986
2	574	100.0	108	9	ADZ57820
3	571	99.5	128	4	AAB81996
4	570	99.3	128	4	AAB81993
5	564	98.3	108	9	ADZ57822
6	564	98.3	128	4	AAB81997
7	561	97.7	108	9	ADZ57819
8	561	97.7	128	4	AAB81995
9	558	97.2	128	4	AAB81994
10	558	97.2	128	4	AAB81992
11	557	97.0	108	6	ABU11011
12	548	95.5	108	4	AAB81988
13	548	95.5	108	9	ADZ57823
14	548	95.5	128	4	AAB81999
15	548	95.5	128	4	AAB81998
16	533	92.9	110	2	AAB70673
17	533	92.9	110	5	ABP61242
18	533	92.9	237	2	AAW70703
19	533	92.9	650	5	ABP61241
20	531	92.5	107	2	AAW86805
21	531	92.5	107	2	AAW70625
22	531	92.5	107	5	ABP61194
23	530	92.3	110	5	ABP61244
24	530	92.3	110	5	ABP61244

25	529	92.2	108	2	AAW70618	Anti-VEGF
26	529	92.2	108	5	ABP61187	Humanised
27	529	92.2	108	8	ADG31782	V(L) doma
28	529	92.2	108	8	ADG31768	V(L) doma
29	529	92.2	108	8	ADG31893	V(L) prot
30	529	92.2	108	9	ADX80647	Humanised
31	529	92.2	110	3	AAW80587	Humanised
32	529	92.2	110	3	ABP13376	F(ab)-12
33	529	92.2	237	8	ADQ90721	Anti-VEGF
34	527	91.8	107	2	AAW86804	Variable
35	527	91.8	107	5	ABP70623	Humanised
36	527	91.8	107	5	ABP61192	Humanised
37	526	91.6	108	8	ADG31770	V(L) doma
38	526	91.6	110	2	AAW70677	Anti-VEGF
39	526	91.6	110	2	AAW70687	Anti-VEGF
40	526	91.6	110	3	ABP13380	Anti-VEGF
41	526	91.6	110	5	ABP61256	Humanised
42	526	91.6	110	5	ABP61246	Humanised
43	526	91.6	214	7	ADC26154	Parent an
44	526	91.6	237	5	ABP81107	Anti-VEGF
45	526	91.6	237	5	ABP51952	Plasmid p

#### ALIGNMENTS

RESULT 1  
AAB81986  
ID AAB81986 standard; protein; 108 AA.  
XX  
AC AAB81986;  
XX  
DT 03-JUL-2001 (first entry)  
XX  
DE Ganglioside GD3 specific antibody related protein SEQ ID NO: 10.  
XX  
XX Ganglioside; GD3; complementarity determining region; CDR; antibody;  
XX Ganglioside; GD3; complementarity determining region; CDR; antibody;  
XX Cancer.  
XX  
XX Synthetic.  
XX  
XX WO200123432-A1.  
XX  
XX PD 05-APR-2001.  
XX  
XX PF 29-SEP-2000; 2000WO-JP006774.  
XX  
XX PR 30-SEP-1999; 95JP-00278291.  
XX PR 06-APR-2000; 2000JP-00105088.  
XX  
XX (KYOW ) KYOWA HAKKO KOGYO KK.  
XX  
XX Hanai N, Shitara K, Nakamura K, Niwa R;  
XX  
XX WPI; 2001-266143/27.  
XX  
XX New human type complementation-determining region-transplanted antibody  
XX PT and derivatives against ganglioside GD3, useful in diagnosis and therapy  
XX of e.g. tumors, with low antigenicity, little side effects but potent  
XX PT activity in cancer.  
XX  
XX Example 1; Page 143-144; 183pp; Japanese.  
XX  
XX The present invention describes a monoclonal antibody which can react  
XX specifically with ganglioside GD3. The antibody and its derivatives are  
XX useful in the diagnosis and therapy of tumors, particularly cancer  
XX diagnosis. The present sequence is a protein used in the exemplification  
XX of the invention  
XX  
XX SQ Sequence 108 AA;  
XX

Query Match 100.0%; Score 574; DB 4; Length 108;  
Best Local Similarity 100.0%; Pred. No. 1.5e-34;

Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY      1 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQKPGKAPKLLIFYSSNLHSGVPS 60
      |||
Db      1 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQKPGKAPKLLIFYSSNLHSGVPS 60
      |||
QY      61 RFSGGSGTDYTLTISSLPQDFATYYCHQYSKLPWTFGQGTKEIKR 108
      |||
Db      61 RFSGGSGTDYTLTISSLPQDFATYYCHQYSKLPWTFGQGTKEIKR 108
      |||

```

## RESULT 2

ADZ57820  
ID ADZ57820 standard; protein; 108 AA.

XX  
AC ADZ57820;

DT 30-JUN-2005 (first entry)

DE Ganglioside GD3 binding antibody associated protein SEQ ID NO 24.

XX cytostatic; antibody engineering; cancer; neoplasm; ganglioside; GD3;

KW pharmaceutical.

XX Synthetic.

XX WO2005035577-A1.

XX 21-APR-2005.

XX 08-OCT-2004; 2004WO-JP015314.

XX 08-OCT-2003; 2003JP-00350161.

XX (KYOW ) KYOWA HAKKO KOGYO KK.

XX Iida S, Satoh M, Urakubo M, Wakitani M, Uchida K, Niwa R;

PI Shitara K;

DR WPI; 2005-346195/35.

XX Antibody composition for treating ganglioside GD3 associated disease e.g. cancer, comprises genetically modified antibody molecule, which specifically binds to ganglioside GD3 and has N-glycoside-binding sugar chain in its Fc domain.

PS Claim 21; SEQ ID NO 24; 124pp; Japanese.

XX The invention describes an antibody composition (I), comprising a genetically modified antibody molecule which specifically binds to ganglioside GD3 and has an N-glycoside-binding complex sugar chain in its Fc domain, where the N-glycoside-binding complex sugar chain is a sugar chain having no fucose attached to N-acetylglucosamine at the reducing end of the sugar chain. Also described are: a transformant (II) capable of producing (I), obtained by introducing DNA that encodes the antibody molecule which specifically binds with ganglioside GD3, to a host cell; producing (I), involving cultivating (I) in a culture medium, such that Cl (sic) is produced and accumulated in the culture, extracting and purifying Cl from the culture medium; a pharmaceutical (III) containing Cl as an active ingredient; and a therapeutic agent (A1) for ganglioside GD3 associated disease, comprising Cl as an active ingredient. (I) is useful for treating GD3 associated disease, which involves administering (I), where the GD3 associated disease is cancer. (A1) is also useful for treating GD3 associated disease. (II) is useful for producing (I). (I) is useful for manufacturing a therapeutic agent for GD3 associated disease. This sequence represents a ganglioside GD3 binding antibody associated protein.

XX Sequence 108 AA;

Query Match 100.0%; Score 574; DB 9; Length 108;  
Best Local Similarity 100.0%; Pred. No. 1.5e-34;  
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY      1 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQKPGKAPKLLIFYSSNLHSGVPS 60
      |||
Db      1 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQKPGKAPKLLIFYSSNLHSGVPS 60
      |||
QY      61 RFSGGSGTDYTLTISSLPQDFATYYCHQYSKLPWTFGQGTKEIKR 108
      |||
Db      61 RFSGGSGTDYTLTISSLPQDFATYYCHQYSKLPWTFGQGTKEIKR 108
      |||

```

## RESULT 3

AAB81996  
ID AAB81996 standard; protein; 128 AA.

XX AAB81996;

DT 03-JUL-2001 (first entry)

DE Ganglioside GD3 specific antibody related protein #5.

XX Ganglioside; GD3; complementarity determining region; CDR; antibody;

KW cancer.

XX Synthetic.

XX WO200123432-A1.

XX 05-APR-2001.

XX 29-SEP-2000; 2000WO-JP006774.

XX 30-SEP-1999; 99JP-00278291.

XX 06-APR-2000; 2000JP-00105088.

XX (KYOW ) KYOWA HAKKO KOGYO KK.

XX Hanai N, Shitara K, Nakamura K, Niwa R;

DR WPI; 2001-266143/27.

DR N-PSDB; AAF86904.

XX New human type complementation-determining region-transplanted antibody and derivatives against ganglioside GD3, useful in diagnosis and therapy of e.g. tumors, with low antigenicity, little side effects but potent activity in cancer.

PS Example 1; Page 159-160; 183pp; Japanese.

XX The present invention describes a monoclonal antibody which can react specifically with ganglioside GD3. The antibody and its derivatives are useful in the diagnosis and therapy of tumors, particularly cancer diagnosis. The present sequence is a protein used in the exemplification of the invention

XX Sequence 128 AA;

Query Match 99.5%; Score 571; DB 4; Length 128;

Best Local Similarity 99.1%; Pred. No. 2.9e-34;

Matches 107; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

QY      1 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQKPGKAPKLLIFYSSNLHSGVPS 60
      |||
Db      21 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQKPGKAPKLLIFYSSNLHSGVPS 80
      |||
QY      61 RFSGGSGTDYTLTISSLPQDFATYYCHQYSKLPWTFGQGTKEIKR 108
      |||
Db      81 RFSGGSGTDYTLTISSLPQDFATYYCHQYSKLPWTFGQGTKEIKR 128
      |||

```

## RESULT 4

AAB81993  
ID AAB81993 standard; protein; 128 AA.

XX

AC	AAB81993;	XX	08-OCT-2004; 2004WO-JP015314.	XX
DT	03-JUL-2001 (first entry)	XX		XX
DE	Ganglioside GD3 specific antibody related protein #2.	PR	08-OCT-2003; 2003JP-00350161.	XX
DE		XX	(KYOW ) KYOWA HAKKO KOGYO KK.	XX
KW	Ganglioside; GD3; complementarity determining region; CDR; antibody;	PA		XX
KW	cancer.	PI	Iida S, Satoh M, Urakubo M, Wakitani M, Uchida K, Niwa R;	XX
OS	Synthetic.	PI	Shitara K;	XX
XX		XX		XX
XX	WO200123432-A1.	DR	WPI; 2005-346195/35.	XX
XX		XX		XX
XX	05-APR-2001.	XX		XX
XX		XX		XX
XX	29-SEP-2000; 2000WO-JP006774.	XX		XX
PR	30-SEP-1999; 99JP-00278291.	XX		XX
PR	06-APR-2000; 2000JP-00105088.	XX		XX
XX		XX		XX
XX	(KYOW ) KYOWA HAKKO KOGYO KK.	XX		XX
XX		XX		XX
PI	Hanai N, Shitara K, Nakamura K, Niwa R;	XX		XX
XX		XX		XX
DR	WPI; 2001-266143/27.	XX		XX
DR	N-PSDB; AAF86895.	XX		XX
XX		XX		XX
XX	New human type complementation-determining region-transplanted antibody	CC	The invention describes an antibody composition (I), comprising a	CC
PT	and derivatives against ganglioside GD3, useful in diagnosis and therapy	CC	genetically modified antibody molecule which specifically binds to	CC
PT	of e.g. tumors, with low antigenicity, little side effects but potent	CC	ganglioside GD3 and has an N-glycoside-binding complex sugar chain in its	CC
PT	activity in cancer.	CC	Fc domain, where the N-glycoside-binding complex sugar chain is a sugar	CC
XX		CC	chain having no fucose attached to N-acetylglucosamine at the reducing	CC
XX		CC	end of the sugar chain. Also described are: a transformant (II) capable	CC
XX		CC	of producing (I), obtained by introducing DNA that encodes the antibody	CC
XX		CC	molecule which specifically binds with ganglioside GD3, to a host cell;	CC
XX		CC	producing (I), involving cultivating (I) in a culture medium, such that	CC
XX		CC	C1 (sic) is produced and accumulated in the culture, extracting and	CC
XX		CC	purifying C1 from the culture medium; a pharmaceutical (III) containing	CC
XX		CC	C1 as an active ingredient; and a therapeutic agent (A1) for ganglioside	CC
XX		CC	GD3 associated disease, comprising C1 as an active ingredient. (I) is	CC
XX		CC	useful for treating GD3 associated diseases, which involves administering	CC
XX		CC	(I), where the GD3 associated diseases is cancer. (A1) is also useful for	CC
XX		CC	treating GD3 associated disease. (II) is useful for producing (I). (I) is	CC
XX		CC	useful for manufacturing a therapeutic agent for GD3 associated disease.	CC
XX		CC	This sequence represents a ganglioside GD3 binding antibody associated	CC
XX		XX	protein.	XX
SQ	Sequence 128 AA;	SQ	Sequence 108 AA;	
	Query Match 99.3%; Score 570; DB 4; Length 128;		Query Match 98.3%; Score 564; DB 9; Length 108;	
	Best Local Similarity 99.1%; Pred. No. 3.4e-34;		Best Local Similarity 98.1%; Pred. No. 8e-34;	
	Matches 107; Conservative 1; Mismatches 0; Indels 0; Gaps 0;		Matches 106; Conservative 1; Mismatches 1; Indels 0; Gaps 0;	
OY	1 DIQMTQSPSSLSASVGRVTITCSAQDISNYLNWYQKPGKAPKLLIFYSNLSHGVPVS 60	OY	1 DIQMTQSPSSLSASVGRVTITCSAQDISNYLNWYQKPGKAPKLLIFYSNLSHGVPVS 60	
DB	21 DIQMTQSPSSLSASVGRVTITCSAQDISNYLNWYQKPGKAPKLLIFYSNLSHGVPVS 80	DB	1 DIQMTQSPSSLSASVGRVTITCSAQDISNYLNWYQKPGKAPKLLIFYSNLSHGVPVS 60	
OY	61 RFSGGSGTDYTLTISSLPEDFATYFCHQYSKLPWTFGGTKVEIKR 108	OY	61 RFSGGSGTDYTLTISSLPEDFATYFCHQYSKLPWTFGGTKVEIKR 108	
DB	81 RFSGGSGTDYTLTISSLPEDFATYFCHQYSKLPWTFGGTKVEIKR 128	DB	61 RFSGGSGTDYTLTISSLPEDFATYFCHQYSKLPWTFGGTKVEIKR 108	
RESULT 5		RESULT 6		
ADZ57822		AAB81997		
ID	ADZ57822 standard; protein; 108 AA.	ID	AAB81997 standard; protein; 128 AA.	
XX		XX		
AC	ADZ57822;	AC	AAB81997;	
XX		XX		
DT	30-JUN-2005 (first entry)	DT	03-JUL-2001 (first entry)	
DE	Ganglioside GD3 binding antibody associated protein SEQ ID NO 26.	DE	Ganglioside GD3 specific antibody related protein #6.	
XX		XX	Ganglioside; GD3; complementarity determining region; CDR; antibody;	
KW	cytostatic; antibody engineering; cancer; neoplasm; ganglioside; GD3;	XX	cancer.	
KW	pharmaceutical.	XX	Synthetic.	
OS	Synthetic.	OS		
XX		XX		
PN	WO2005035577-A1.	PN	WO200123432-A1.	
XX		XX		
XX	21-APR-2005.	XX	05-APR-2001.	

PF 29-SEP-2000; 2000WO-JP006774.  
 XX  
 PR 30-SEP-1999; 99JP-00278291.  
 PR 06-APR-2000; 2000JP-00105088.  
 XX  
 PA (KYOW ) KYOWA HAKKO KOGYO KK.  
 XX  
 PI Hanai N, Shitara K, Nakamura K, Niwa R;  
 XX  
 DR WPI; 2001-266143/27.  
 DR N-PSDB; AAF86907.  
 XX  
 PT New human type complementation-determining region-transplanted antibody  
 PT and derivatives against ganglioside GD3, useful in diagnosis and therapy  
 PT of e.g. tumors, with low antigenicity, little side effects but potent  
 PT activity in cancer.  
 XX  
 PS Example 1; Page 161-162; 183pp; Japanese.  
 XX  
 CC The present invention describes a monoclonal antibody which can react  
 CC specifically with ganglioside GD3. The antibody and its derivatives are  
 CC useful in the diagnosis and therapy of tumors, particularly cancer  
 CC diagnosis. The present sequence is a protein used in the exemplification  
 CC of the invention  
 XX  
 SQ Sequence 128 AA;  
 Query Match 98.3%; Score 564; DB 4; Length 128;  
 Best Local Similarity 98.1%; Pred. No. 9.4e-34;  
 Matches 106; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNWYQKPGKAPKLLIFYSNLSHGVP 60  
 DB 21 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNWYQKPGKAPKLLIFYSNLSHGVP 80  
 QY 61 RFSGGSGTDYTLTISSLPEDFATYCHQYKLPWTFGGTKVEIKR 108  
 DB 81 RFSGGSGTDYTLTISSLPEDFATYCHQYKLPWTFGGTKVEIKR 128  
 RESULT 7  
 ADZ57819  
 ID ADZ57819 standard; protein; 108 AA.  
 XX  
 AC ADZ57819;  
 XX  
 DT 30-JUN-2005 (first entry)  
 XX  
 DE Ganglioside GD3 binding antibody associated protein SEQ ID NO 23.  
 XX  
 KW cytostatic; antibody engineering; cancer; neoplasm; ganglioside; GD3;  
 KW pharmaceutical.  
 XX  
 OS Synthetic.  
 XX  
 PN WO2005035577-A1.  
 XX  
 PD 21-APR-2005.  
 XX  
 PF 08-OCT-2004; 2004WO-JP015314.  
 XX  
 PR 08-OCT-2003; 2003JP-00350161.  
 XX  
 PA (KYOW ) KYOWA HAKKO KOGYO KK.  
 XX  
 PI Iida S, Satoh M, Urakubo M, Wakitani M, Uchida K, Niwa R;  
 PI Shitara K;  
 XX  
 DR WPI; 2005-346195/35.  
 XX  
 PT Antibody composition for treating ganglioside GD3 associated disease e.g.  
 PT cancer, comprises genetically modified antibody molecule, which  
 PT specifically binds to ganglioside GD3 and has N-glycoside-binding sugar

PT chain in its Fc domain.  
 XX  
 PS Claim 20; SEQ ID NO 23; 124pp; Japanese.  
 XX  
 CC The invention describes an antibody composition (I), comprising a  
 CC genetically modified antibody molecule which specifically binds to  
 CC ganglioside GD3 and has an N-glycoside-binding complex sugar chain in its  
 CC Fc domain, where the N-glycoside-binding complex sugar chain is a sugar  
 CC chain having no fucose attached to N-acetylglucosamine at the reducing  
 CC end of the sugar chain. Also described are: a transformant (II) capable  
 CC of producing (I), obtained by introducing DNA that encodes the antibody  
 CC molecule which specifically binds with ganglioside GD3, to a host cell;  
 CC producing (I), involving cultivating (I) in a culture medium, such that  
 CC C1 (sic) is produced and accumulated in the culture, extracting and  
 CC purifying C1 from the culture medium; a pharmaceutical (III) containing  
 CC C1 as an active ingredient; and a therapeutic agent (A1) for ganglioside  
 CC GD3 associated disease, comprising C1 as an active ingredient. (I) is  
 CC useful for treating GD3 associated disease, which involves administering  
 CC (I), where the GD3 associated disease is cancer. (A1) is also useful for  
 CC treating GD3 associated disease. (II) is useful for producing (I). (I) is  
 CC useful for manufacturing a therapeutic agent for GD3 associated disease.  
 CC This sequence represents a ganglioside GD3 binding antibody associated  
 CC protein.  
 XX  
 SQ Sequence 108 AA;  
 Query Match 97.7%; Score 561; DB 9; Length 108;  
 Best Local Similarity 97.2%; Pred. No. 1.3e-33;  
 Matches 105; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNWYQKPGKAPKLLIFYSNLSHGVP 60  
 DB 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNWYQKPGKAPKLLIFYSNLSHGVP 60  
 QY 61 RFSGGSGTDYTLTISSLPEDFATYCHQYKLPWTFGGTKVEIKR 108  
 DB 61 RFSGGSGTDYTLTISSLPEDFATYCHQYKLPWTFGGTKVEIKR 108  
 RESULT 8  
 AAB81995  
 ID AAB81995 standard; protein; 128 AA.  
 XX  
 AC AAB81995;  
 XX  
 DT 03-JUL-2001 (first entry)  
 XX  
 DE Ganglioside GD3 specific antibody related protein #4.  
 XX  
 KW Ganglioside; GD3; complementarity determining region; CDR; antibody;  
 KW cancer.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200123432-A1.  
 XX  
 PD 05-APR-2001.  
 XX  
 PF 29-SEP-2000; 2000WO-JP006774.  
 XX  
 PR 30-SEP-1999; 99JP-00278291.  
 PR 06-APR-2000; 2000JP-00105088.  
 XX  
 PA (KYOW ) KYOWA HAKKO KOGYO KK.  
 XX  
 PI Hanai N, Shitara K, Nakamura K, Niwa R;  
 XX  
 DR WPI; 2001-266143/27.  
 DR N-PSDB; AAF86901.  
 XX  
 PT New human type complementation-determining region-transplanted antibody  
 PT and derivatives against ganglioside GD3, useful in diagnosis and therapy  
 PT of e.g. tumors, with low antigenicity, little side effects but potent





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XX AC ABU11011;
XX DT 04-FEB-2003 (first entry)
XX DE Modified ganglioside GD3 antibody associated protein #4.
XX KW Ganglioside GD3; anti-ganglioside GD3 antibody; tumour; melanoma.
XX OS Synthetic.
XX PN WO200278739-A1.
XX PD 10-OCT-2002.
XX PF 29-MAR-2002; 2002WO-JP003170.
XX PR 29-MAR-2001; 2001JP-00097483.
XX PA (KYOW ) KYOWA HAKKO KOGYO KK.
XX PI Shitara K, Niwa R, Kanazawa J, Asada M;
XX WPI; 2003-067410/06.
XX
XX Drugs containing genetically-modified antibody against ganglioside GD3,
XX its fragment, immunocompetent cell activators or/and antitumor agents in
XX combination, applicable in treating malignant tumor like melanoma.
XX PS Claim 8; Page 100; 121pp; Japanese.
XX
XX The invention describes drugs contain a genetically-modified antibody
XX against ganglioside GD3 or its fragment and at least 1 of a substance
XX capable of activating immunocompetent cells and a substance having an
XX antitumor activity in combination. The drugs can be used to treat tumour
XX like melanoma and can provide a treatment with enhanced therapeutic
XX effect and little side-reactions, particularly to relieve problems of
XX side-effects during the conventional single administration. This sequence
XX represents a protein associated with the anti- ganglioside GD3 antibody
XX
XX Sequence 108 AA;
XX
XX Query Match 97.0%; Score 557; DB 6; Length 108;
XX Best Local Similarity 97.2%; Pred. No. 2.6e-33;
XX Matches 105; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNWYQQKPKAPKLLIPYSSNLHSGVPS 60
XX Db 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNWYQQKPKAPKLLIPYSSNLHSGVPS 60
XX
XX QY 61 RFSGGSGTDYTLTISSLPQDPATYVCHQYSKLPWTFGGQTKVEIKR 108
XX Db 61 RFSGGSGTDYTLTISSLPQDPATYVCHQYSKLPWTFGGQTKVEIKR 108
XX
XX RESULT 12
XX AAB81988
XX ID AAB81988 standard; protein; 108 AA.
XX AC AAB81988;
XX DT 03-JUL-2001 (first entry)
XX DE Ganglioside GD3 specific antibody related protein SEQ ID NO: 54.
XX KW Ganglioside; GD3; complementarity determining region; CDR; antibody;
XX cancer.
XX OS Synthetic.
XX PN WO200123432-A1.
XX PD 05-APR-2001.

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XX PF 29-SEP-2000; 2000WO-JP006774.
XX PR 30-SEP-1999; 99JP-00278291.
XX PR 06-APR-2000; 2000JP-00105088.
XX PA (KYOW ) KYOWA HAKKO KOGYO KK.
XX PI Hanai N, Shitara K, Nakamura K, Niwa R;
XX WPI; 2001-266143/27.
XX
XX New human type complementation-determining region-transplanted antibody
XX and derivatives against ganglioside GD3, useful in diagnosis and therapy
XX of e.g. tumors, with low antigenicity, little side effects but potent
XX activity in cancer.
XX PS Claim 22; Page 172-173; 183pp; Japanese.
XX
XX The present invention describes a monoclonal antibody which can react
XX specifically with ganglioside GD3. The antibody and its derivatives are
XX useful in the diagnosis and therapy of tumours, particularly cancer
XX diagnosis. The present sequence is a protein used in the exemplification
XX of the invention
XX
XX Sequence 108 AA;
XX
XX Query Match 95.5%; Score 548; DB 4; Length 108;
XX Best Local Similarity 96.3%; Pred. No. 1.2e-32;
XX Matches 104; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
XX
XX QY 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNWYQQKPKAPKLLIFYSNLHSGVPS 60
XX Db 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNWYQQKPKAVKLLIFYSNLHSGVPS 60
XX
XX QY 61 RFSGGSGTDYTLTISSLPQDPATYVCHQYSKLPWTFGGQTKVEIKR 108
XX Db 61 RFSGGSGTDYTLTISSLPQDPATYVCHQYSKLPWTFGGQTKVEIKR 108
XX
XX RESULT 13
XX ADZ57823
XX ID ADZ57823 standard; protein; 108 AA.
XX AC ADZ57823;
XX DT 30-JUN-2005 (first entry)
XX DE Ganglioside GD3 binding antibody associated protein SEQ ID NO 27.
XX KW cytostatic; antibody engineering; cancer; neoplasm; ganglioside; GD3;
XX pharmaceutical.
XX OS Synthetic.
XX PN WO2005035577-A1.
XX PD 21-APR-2005.
XX PF 08-OCT-2004; 2004WO-JP015314.
XX PR 08-OCT-2003; 2003JP-00350161.
XX PA (KYOW ) KYOWA HAKKO KOGYO KK.
XX PI Iida S, Satoh M, Urakubo M, Wakitani M, Uchida K, Niwa R;
XX Shitara K;
XX WPI; 2005-346195/35.
XX
XX Antibody composition for treating ganglioside GD3 associated disease e.g.
XX cancer, comprises genetically modified antibody molecule, which
XX specifically binds to ganglioside GD3 and has N-glycoside-binding sugar

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Matches 104; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy	1	DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQOKPGKAPKLLIFYSNHLHSGVPS	60
Db	21	DIQMTQSASSLPASVGRVTITCSASQDISNYLNWYQOKPGKAVKLLIFYSNHLHSGVPS	80
Qy	61	RFSGGGSGTDYTLTISSLPQEDFATYVCHQYSKLPMTFGQGTKEIKR	108
Db	81	RFSGGGSGTDYTLTISSLPQEDFATVFCVCHQYSKLPMTFGQGTKEIKR	128

Search completed: April 6, 2006, 08:50:40  
Job time : 25.1439 secs

GenCore version 5.1.1.7  
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OM protein - protein search, using sw model

Run on: April 6, 2006, 08:49:11 ; Search time 5.53544 Seconds  
(without alignments)  
1877.250 Million cell updates/sec

Title: US-10-089-500-10  
Perfect score: 574  
Sequence: 1 DIQMTQSPSSLSASVGRVT.....HQYSKLPWTFGGTKVEIKR 108

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 80:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	496	86.4	108	1 KIHUHU	Ig kappa chain V-I
2	488	85.0	127	2 S40367	Ig kappa chain V-J
3	472	82.2	108	1 KIHURE	Ig kappa chain V-I
4	471	82.1	125	2 S40333	Ig kappa chain V-I
5	469	81.7	129	2 S52789	Ig kappa chain V r
6	468	81.5	123	2 S40331	Ig kappa chain - h
7	467	81.4	108	2 B49047	Ig kappa chain V r
8	466	81.2	110	2 S44118	Ig kappa chain V-J
9	466	81.2	111	2 A38740	Ig kappa chain V r
10	465	81.0	108	2 S44122	Ig kappa chain V r
11	464	80.8	111	2 E38740	Ig kappa chain V r
12	461	80.3	108	2 I39154	Ig kappa chain (BR
13	461	80.3	109	2 S31998	Ig kappa chain - h
14	460	80.1	107	2 S36264	Ig lambda chain V
15	459	80.0	108	1 KIHUWE	Ig kappa chain V-I
16	459	80.0	111	2 G38740	Ig kappa chain V r
17	459	80.0	139	2 S40365	Ig kappa chain - h
18	458	79.8	131	2 S40352	Ig kappa chain V-J
19	457	79.6	129	2 S40369	Ig kappa chain - h
20	456	79.4	111	2 G38740	Ig kappa chain V r
21	455	79.3	108	2 S19674	Ig kappa chain V r
22	455	79.3	141	2 A49134	Ig kappa chain V-I
23	454	79.1	108	1 KIHURY	Ig kappa chain V-I
24	453.5	79.0	107	2 S36275	Ig lambda chain V
25	453	78.9	107	2 B49026	Ig kappa chain V r
26	453	78.9	108	1 KIHUAG	Ig kappa chain V-I
27	453	78.9	109	2 S31981	Ig kappa chain - h
28	452.5	78.8	124	2 S40336	Ig kappa chain V-J
29	451	78.6	135	2 S24320	Ig kappa chain pre

30	450	78.4	108	1 KIHUHU	Ig kappa chain V-I
31	449.5	78.3	106	2 PC2397	anti-tetanus toxin
32	448	78.0	108	1 KVM873	Ig kappa chain V r
33	447	77.9	117	2 S46371	Ig kappa chain V-J
34	446	77.7	108	1 KIHURA	Ig kappa chain V-I
35	446	77.7	125	2 S40349	Ig kappa chain V-J
36	445.5	77.6	125	2 S40315	Ig kappa chain - h
37	445	77.5	108	1 KIHURN	Ig kappa chain V-I
38	445	77.5	108	1 KIHULY	Ig kappa chain V-I
39	445	77.5	122	2 S40370	Ig kappa chain - h
40	445	77.5	129	2 S52793	Ig kappa chain V r
41	445	77.5	132	2 S40334	Ig kappa chain - h
42	444	77.4	108	2 S47182	Ig kappa chain - h
43	444	77.4	117	2 S46376	Ig kappa chain V-J
44	444	77.4	122	2 S40314	Ig kappa chain - h
45	443	77.2	108	1 KIHUBI	Ig kappa chain V-I

ALIGNMENTS

RESULT 1

KIHUHU  
Ig kappa chain V-I region (Au) - human  
C:Species: Homo sapiens (man)  
C>Date: 24-Apr-1984 #sequence revision 02-Jul-1998 #text\_change 09-Jul-2004  
C:Accession: A91653; A01862; S02573  
R:Schiechl, H.; Hilschmann, N.  
Hoppe-Sejler's Z. Physiol. Chem. 353, 345-370, 1972  
A>Title: Die Primaerstruktur einer monoklonalen Immunglobulin-L-Kette vom kappa-Typ, Sub  
A:Reference number: A91653; MUID:72189444; PMID:5028201  
A:Accession: A91653  
A:Molecule type: protein  
A:Residues: 1-108 <SCH>  
A:Cross-references: UNIPROT:P01594; UNIPARC:UPI000012E13E  
A>Note: the C region of this chain has the Inv (3) marker  
B:Feilhammer, H.; Schiffer, M.; Epp, O.; Colman, P.M.; Lattman, E.E.; Schwager, P.; Stei  
Biophys. Struct. Mech. 1, 139-146, 1975  
A>Title: The structure determination of the variable portion of the Bence-Jones protein  
A:Reference number: A90729; MUID:77022433; PMID:1234024  
A:Contents: annotation; X-ray crystallography  
A>Note: the structure of the V region was determined by molecular replacement methods us  
R:Steiner, V.; Chang, J.Y.  
FEBS Lett. 222, 6-10, 1987

A>Title: Chemical modification of the carboxyl groups of protein substrates enhances the  
A:Reference number: S02572; MUID:88005152; PMID:3115831  
C:Contents: annotation  
C:Comment: This is a Bence Jones protein.  
C:Genetics:  
A:Gene: GDB:IGKV1  
A:Cross-references: GDB:136264  
A:Map position: 2p12-2p12  
C:Complex: an immunoglobulin heterotetramer subunit consists of two identical light (kap  
hain disulfide bond; in some cases, such as IGA and IGM, the subunits associate into la  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:16-90/Domain: immunoglobulin homology <IMM>  
F:23-88/Disulfide bonds: #status predicted

Query Match 86.4%; Score 496; DB 1; Length 108;  
Best Local Similarity 87.0%; Pred. No. 4.1e-37;  
Matches 94; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCSAQDISNLYNMYQQKPGKAPKLLIFYSNLSHGVPSS 60  
|||||

Db 1 DIQMTQSPSSLSASVGRVTITCSAQDISNLYNMYQQKPGKAPKLLIYDASNLSESGVPS 60  
|||||

QY 61 RFSGGSGSDTYLTITSSLPQDFATYYCHQYKSLPFWTFGGTKVEIKR 108  
|||||

Db 61 RFSGGSGGAHFTTITSSLPQEDIATYYCQYDYLPWTFGGTKVEIKR 108  
|||||

RESULT 2



A;Residues: 1-110 <HAW>  
A;Cross-references: UNIPARC:UPI0000116635; EMBL:Z31395; NID:G472972; PIDN:CAA83270.1; PI  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 81.2%; Score 466; DB 2; Length 110;  
Best Local Similarity 82.7%; Pred. NO. 1.9e-34;  
Matches 91; Conservative 5; Mismatches 12; Indels 2; Gaps 1;

Qy 1 DIQWTQSPSSLSASVGDRVTITCSASQDISNLYNWYQOKPGKAPKLLIFYSSNLHSGVPS 60  
Db 1 DIQWTQSPSSLSASVGDRVTITCSASQDISNLYNWYQOKPGKAPKLLIFYSSNLHSGVPS 60

Qy 61 RFSGGSGTDYTLTISSLOPEDFATYCHQYSKLP-WTFGGQTKVEIKR 108  
Db 61 RFSGGSGTDYTLTISSLOPEDFATYCHQYSKLP-WTFGGQTKVEIKR 110

RESULT 9  
A38740  
Ig kappa chain V region (Py20) - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 18-Oct-1991 #sequence\_revision 18-Oct-1991 #text\_change 09-Jul-2004  
C;Accession: A38740  
R;Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.  
J. Biol. Chem. 266, 6607-6613, 1991  
A;Title: Heavy and light chain variable region sequences and antibody properties of anti  
A;Reference number: A38740; MUID:91177923; PMID:1706720  
A;Accession: A38740  
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra  
A;Molecule type: mRNA  
A;Residues: 1-111 <RUF>  
A;Cross-references: UNIPROT:Q91WS9; UNIPARC:UPI0000176CD9  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;19-93/Domain: immunoglobulin homology <IMM>

Query Match 81.2%; Score 466; DB 2; Length 111;  
Best Local Similarity 79.6%; Pred. NO. 1.9e-34;  
Matches 86; Conservative 12; Mismatches 10; Indels 0; Gaps 0;

Qy 1 DIQWTQSPSSLSASVGDRVTITCSASQDISNLYNWYQOKPGKAPKLLIFYSSNLHSGVPS 60  
Db 4 DVQNTQTSSLSASLGRVITSCSASQGISNLYNWYQOKPGDGTVKLLIYTSLSLHSGVPS 63

Qy 61 RFSGGSGTDYTLTISSLOPEDFATYCHQYSKLP-WTFGGQTKVEIKR 108  
Db 64 RFSGGSGTDYTLTISSLOPEDFATYCHQYSKLP-WTFGGQTKVEIKR 111

RESULT 10  
S44122  
Ig kappa chain V region - human  
C;Species: Homo sapiens (man)  
C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 24-May-2001  
C;Accession: S44122  
R;Hawkins, R.E.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.  
submitted to the EMBL Data Library, March 1994  
A;Description: Idiotypic vaccination against human B-cell lymphoma: rescue of variable r  
A;Reference number: S44105  
A;Accession: S44122  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-108 <HAW>  
A;Cross-references: UNIPARC:UPI0000116630; EMBL:Z31390; NID:G472976; PIDN:CAA83265.1; PI  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 81.0%; Score 465; DB 2; Length 108;  
Best Local Similarity 83.3%; Pred. NO. 2.3e-34;  
Matches 90; Conservative 5; Mismatches 13; Indels 0; Gaps 0;

```
Qy 1 DIQMTQSPSSLSASVSGDRVTITCSAQDISNYLNWYQKPGKAPKLLIFYSSNLHSGVPS 60
Db 1 DIQMTQSPSSLSASVSGDRVTITCRASQSISSYLNWYQKGLKAPKLLIYSASSLSQSGVPS 60

Qy 61 RFSGGSGTDYTLTISSLPQDFATYCHQYSKLPWTFGQGTKEIKR 108
Db 61 TFSGGSGTDFTLTISSLPQDFATYCHQYSKLPWTFGQGTKEIKR 108

RESULT 11
E38740
Ig kappa chain V region (Py54) - mouse
C:Species: Mus musculus (house mouse)
C>Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 09-Jul-2004
C:Accession: E38740
J:Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.
A:Title: Heavy and light chain variable region sequences and antibody properties of anti-
A:Reference number: A38740; MUID:91177923; PMID:1706720
A:Accession: E38740
A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A:Molecule type: mRNA
A:Residues: 1-111 <RUF>
A:Cross-references: UNIPROT:Q91WS9; UNIPARC:UPI0000176CD8
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:19-93/Domain: immunoglobulin homology <IMM>

Query Match 80.8%; Score 464; DB 2; Length 111;
Best Local Similarity 79.6%; Pred. No. 2.9e-34;
Matches 86; Conservative 10; Mismatches 12; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVSGDRVTITCSAQDISNYLNWYQKPGKAPKLLIFYSSNLHSGVPS 60
Db 4 DVMTQTTSLSASIGDRVTITCSAQGISNYLNWYQKPGDVTVKLLIYTSLSHSGVPS 63

Qy 61 RFSGGSGTDYTLTISSLPQDFATYCHQYSKLPWTFGQGTKEIKR 108
Db 64 RFSGGSGTDYSLTISDLEPIATYCCQYSKLPWTFGGTKEIKR 111

RESULT 12
I39154
Ig kappa chain (BRE) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 21-Jan-2000
C:Accession: I39154
R:Schormann, N.; Murrell, J.R.; Liepieks, J.J.; Benson, M.D.
Proc. Natl. Acad. Sci. U.S.A. 92, 9490-9494, 1995
A:Title: Tertiary structure of an amyloid immunoglobulin light chain protein: A proposed
A:Reference number: I39154; MUID:96003804; PMID:7568160
A:Accession: I39154
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-108 <RES>
A:Cross-references: UNIPARC:UPI0000110713; EMBL:U31344; NID:G94925; PIDN:AAA79238.1; PI
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 80.3%; Score 461; DB 2; Length 108;
Best Local Similarity 82.4%; Pred. No. 5.1e-34;
Matches 89; Conservative 6; Mismatches 13; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVSGDRVTITCSAQDISNYLNWYQKPGKAPKLLIFYSSNLHSGVPS 60
Db 1 DIQMTQSPSSLSASVSGDRVTITCRASQDISYLNWYQKGLKAPKLLIYDASTLTETGVP 60

Qy 61 RFSGGSGTDYTLTISSLPQDFATYCHQYSKLPWTFGQGTKEIKR 108
Db 61 RFSGGSGTGYFTTISLPQDFATYCCQYDLPVTFGGTKEIKR 108
```

```
RESULT 13
S31998
Ig kappa chain - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
C:Accession: S31998
R:Portolano, S.; Chazenbalk, G.D.; Hutchison, S.J.; McLachlan, S.M.; Rapoport, B.
submitted to the EMBL Data Library, June 1992
A:Description: Lack of promiscuity in autoantigen-specific H and L chain combinations as
A:Reference number: S31977
A:Accession: S31998
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-109 <POR>
A:Cross-references: UNIPARC:UPI0000116497; EMBL:Z15081; NID:G38501; PIDN:CAA78790.1; PID
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 80.3%; Score 461; DB 2; Length 109;
Best Local Similarity 81.5%; Pred. No. 5.2e-34;
Matches 88; Conservative 7; Mismatches 13; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVSGDRVTITCSAQDISNYLNWYQKPGKAPKLLIFYSSNLHSGVPS 60
Db 1 ELVMTQSPSSLSASVSGDRVTITCRASQISAYLNWYQKPGKAPKLLIYSASSLSQSGVPS 60

Qy 61 RFSGGSGTDYTLTISSLPQDFATYCHQYSKLPWTFGQGTKEIKR 108
Db 61 RFSGGSGTDFTLTISSLPQDFATYCCQSYDTPMTFGHTKVEIKR 108

RESULT 14
S36284
Ig lambda chain V region (clone alpha-CEA4-8A) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jan-2000
C:Accession: S36284
R:Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.
EMBO J. 12, 725-734, 1993
A:Title: Human anti-self antibodies with high specificity from phage display libraries.
A:Reference number: S36256; MUID:93178448; PMID:7679990
A:Accession: S36284
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-107 <GRI>
A:Cross-references: UNIPARC:UPI0000118DF4; EMBL:Z18845; NID:G33426; PIDN:CAA79297.1; PID
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 80.1%; Score 460; DB 2; Length 107;
Best Local Similarity 82.2%; Pred. No. 6.2e-34;
Matches 88; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVSGDRVTITCSAQDISNYLNWYQKPGKAPKLLIFYSSNLHSGVPS 60
Db 1 EIVLTQSPSSLSASVSGDRVTITCRASQISYLNWYQKPGKAPKLLIYAASSLSQSGVPS 60

Qy 61 RFSGGSGTDYTLTISSLPQDFATYCHQYSKLPWTFGQGTKEIK 107
Db 61 RFSGGSGTDFTLTISSLPQDFATYCCQYSNYPLTFGGTKVDIK 107

RESULT 15
K1HUWE
Ig kappa chain V-I region (WEA) - human
C:Species: Homo sapiens (man)
C>Date: 03-Aug-1984 #sequence_revision 03-Aug-1984 #text_change 09-Jul-2004
C:Accession: A01876
R:Goni, F.; Frangione, B.
Proc. Natl. Acad. Sci. U.S.A. 80, 4837-4841, 1983
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GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: April 6, 2006, 08:48:06 ; Search time 33.4482 Seconds  
(without alignments)  
2278.061 Million cell updates/sec

Title: US-10-089-500-10

Perfect score: 574

Sequence: 1 DIQMTQSPSSLSASVGRVT.....HQYSLKLPWTFGQTKVEIKR 108

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot\_05.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	496	86.4	108	1 KV1B_HUMAN	P01594 homo sapien
2	472	82.2	108	1 KV1O_HUMAN	P01607 homo sapien
3	471	82.1	108	2 Q9UL77_HUMAN	Q9UL77 homo sapien
4	465	81.0	236	2 Q6GMW1_HUMAN	Q6GMW1 homo sapien
5	459.5	80.1	107	2 Q96SA9_HUMAN	Q96SA9 homo sapien
6	459	80.0	108	1 KV1R_HUMAN	P01610 homo sapien
7	456	79.4	236	2 Q723V4_HUMAN	Q723V4 homo sapien
8	455	79.3	236	2 Q502W4_HUMAN	Q502W4 homo sapien
9	454	79.1	108	1 KV1P_HUMAN	P01608 homo sapien
10	453	78.9	108	1 KV1A_HUMAN	P01593 homo sapien
11	453	78.9	236	2 Q6GMX8_HUMAN	Q6GMX8 homo sapien
12	452	78.7	108	1 KV1Y_HUMAN	P80362 homo sapien
13	450	78.4	108	1 KV1H_HUMAN	P01600 homo sapien
14	450	78.4	108	2 Q9UL70_HUMAN	Q9UL70 homo sapien
15	449	78.2	236	2 Q6GMX0_HUMAN	Q6GMX0 homo sapien
16	448	78.0	108	1 KV5J_MOUSE	P01643 mus musculus
17	448	78.0	236	2 Q6GMX9_HUMAN	Q6GMX9 homo sapien
18	446	77.7	108	1 KV1K_HUMAN	P01603 homo sapien
19	445	77.5	108	1 KV1M_HUMAN	P01605 homo sapien
20	445	77.5	108	1 KV1V_HUMAN	P04430 homo sapien
21	443	77.2	108	1 KV1C_HUMAN	P01595 homo sapien
22	442.5	77.1	107	2 Q9UL81_HUMAN	Q9UL81 homo sapien
23	442	77.0	108	1 KV1N_HUMAN	P01606 homo sapien
24	442	77.0	116	2 Q96PF6_HUMAN	Q96PF6 homo sapien
25	442	77.0	129	1 KV1W_HUMAN	P04431 homo sapien
26	440	76.7	236	2 Q6PIH7_HUMAN	Q6PIH7 homo sapien
27	439	76.5	244	2 Q65ZC8_HUMAN	Q65ZC8 homo sapien
28	438	76.3	108	1 KV1G_HUMAN	P01599 homo sapien
29	437	76.1	108	1 KV1E_HUMAN	P01597 homo sapien
30	437	76.1	234	2 Q72473_HUMAN	Q72473 homo sapien
31	436	76.0	108	1 KV1Q_HUMAN	P01609 homo sapien

## RESULT 1

KV1B\_HUMAN

ID	KV1B_HUMAN	STANDARD;	PRT;	108 AA.
AC	P01594;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	10-MAY-2005 (Rel. 47, Last annotation update)			
DE	Ig kappa chain V-I region AU.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	PROTEIN SEQUENCE.			
RX	MEDLINE=72189444; PubMed=5028201;			
RA	Schiechl H., Hilschmann N.;			
RT	"Rule of antibody structure. The primary structure of a monoclonal immunoglobulin L-chain of the kappa-type, subgroup I (Bence-Jones protein Au).";			
RT	Hoppe-Seyler's Z. Physiol. Chem. 353:345-370 (1972).			
RL	[2]			
RP	X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).			
RX	MEDLINE=7702433; PubMed=1234024;			
RA	Fehlhammer H., Schiffer M., Epp O., Colman P.M., Lattman E.E.,			
RA	Schwager P., Steigemann W., Schramm H.J.;			
RT	"The structure determination of the variable portion of the Bence-Jones protein Au.";			
RL	Biophys. Struct. Mech. 1:139-146 (1975).			
CC	-!- MISCELLANEOUS: The structure of the V region was determined by molecular replacement methods using the known structure of the V region of the kappa chain RE1.			
CC	-!- MISCELLANEOUS: The C region of this chain has the INV (3) marker.			
CC	-!- MISCELLANEOUS: This is a Bence-Jones protein.			
CC	-----			
CC	This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.			
CC	-----			
DR	PIR; A91653; K1HUNA.			
DR	PDB; 1UV5; X-ray; A=1-107.			
DR	Ensembl; ENSG00000173782; Homo sapiens.			
DR	GO; GO:0005576; C:extracellular region; NAS.			
DR	GO; GO:0003823; F:antigen binding; NAS.			
DR	GO; GO:0006955; P:immune response; NAS.			
DR	InterPro; IPR007110; IG-like.			
DR	InterPro; IPR003596; IG_V.			
DR	SMART; SM00406; IGV; 1.			
DR	PROSITE; PS50835; IG_LIKE; 1.			
KW	3D-structure; Bence-Jones protein; Direct protein sequencing;			
KW	Immunoglobulin domain; Immunoglobulin V region.			
FT	REGION	1	23	Framework-1.

P01596 homo sapien  
Q65ZC9 homo sapien  
P01604 homo sapien  
P01611 homo sapien  
Q569I7 homo sapien  
P01612 homo sapien  
Q9UL79 homo sapien  
Q9UL79 homo sapien  
P01644 mus musculus  
P01645 mus musculus  
P01646 mus musculus  
P01598 homo sapien  
P01648 mus musculus  
Q56FE6 homo sapien  
P01647 mus musculus

## ALIGNMENTS

```

FT REGION 24 34 Complementarity-determining-1.
FT REGION 35 49 Framework-2.
FT REGION 50 56 Complementarity-determining-2.
FT REGION 57 88 Framework-3.
FT REGION 89 97 Complementarity-determining-3.
FT REGION 98 107 Framework-4.
FT DISULFID 23 88 By similarity.
FT NON_TER 108 108
FT STRAND 4 5
FT STRAND 10 13
FT TURN 15 16
FT STRAND 19 25
FT TURN 30 31
FT STRAND 33 38
FT TURN 40 41
FT STRAND 44 49
FT TURN 50 52
FT STRAND 53 54
FT TURN 56 57
FT TURN 60 61
FT STRAND 62 67
FT TURN 68 69
FT STRAND 70 75
FT STRAND 80 82
FT STRAND 85 90
FT STRAND 97 98
FT STRAND 102 106
SQ SEQUENCE 108 AA; 11939 MW; E8011187EB6F6FB9 CRC64;

Query Match 86.4%; Score 496; DB 1; Length 108;
Best Local Similarity 87.0%; Pred. No. 1.1e-43;
Matches 94; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNVLNYYQKPGKAPKLLIFYSNLSHGVP 60
Db 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNVLNYYQKPGKAPKLLIFYSNLSHGVP 60

QY 61 RFSGGSGTDYTLTISSLPEDFATYYCHQYKLPWTFGGTKVEIKR 108
Db 61 RFSGGSGAHTFTISSLQPEDIAITYYCOQDYLPWTFGGTKVEIKR 108

RESULT 2
KV10 HUMAN STANDARD; PRT; 108 AA.
ID KV10_HUMAN STANDARD; PRT; 108 AA.
AC P01607;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-I region Rei.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP PROTEIN SEQUENCE.
RX MEDLINE=76023758; PubMed=809329;
RA Palm W., Hilschmann N.;
RT "The primary structure of a crystalline monoclonal immunoglobulin
RT kappa-type L-chain, subgroup I (Bence-Jones protein Rei); isolation
RT and characterization of the tryptic peptides; the complete amino acid
RT sequence of the protein; a contribution to the elucidation of the
RT three-dimensional structure of antibodies, in particular their
RT combining site."
RL Hoppe-Seyler's Z. Physiol. Chem. 356:167-191(1975).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX MEDLINE=76039968; PubMed=1182131;
RA Epp O., Lattman E.E., Schiffer M., Huber R., Palm W.;
RT "The molecular structure of a dimer composed of the variable portions
RT of the Bence-Jones protein Rei refined at 2.0-A resolution."
RL Biochemistry 14:4943-4952(1975).

```

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CC -|- MISCELLANEOUS: The C region of this chain has the INV (1,2)
CC marker.
CC -|- MISCELLANEOUS: This is a Bence-Jones protein.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR PIR; A91663; K1HURE.
DR PDB; IAR2; X-ray; @=1-107.
DR PDB; 1BWW; X-ray; A/B=1-107.
DR PDB; IREI; X-ray; A/B=1-107.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW 3D-structure; Bence-Jones protein; Direct protein sequencing;
KW Immunoglobulin domain; Immunoglobulin V region.
FT REGION 1 23 Framework-1.
FT REGION 24 34 Complementarity-determining-1.
FT REGION 35 49 Framework-2.
FT REGION 50 56 Complementarity-determining-2.
FT REGION 57 88 Framework-3.
FT REGION 89 97 Complementarity-determining-3.
FT REGION 98 107 Framework-4.
FT DISULFID 23 88
FT NON_TER 108 108
FT STRAND 4 7
FT STRAND 10 13
FT TURN 15 16
FT STRAND 19 25
FT TURN 30 31
FT STRAND 33 38
FT TURN 40 41
FT STRAND 45 49
FT TURN 50 52
FT STRAND 53 54
FT TURN 56 57
FT TURN 60 61
FT STRAND 62 67
FT TURN 68 69
FT STRAND 70 75
FT STRAND 80 82
FT STRAND 84 90
FT STRAND 97 98
FT STRAND 102 106
SQ SEQUENCE 108 AA; 11902 MW; 958143E1188BCE2A CRC64;

Query Match 82.2%; Score 472; DB 1; Length 108;
Best Local Similarity 82.4%; Pred. No. 3.4e-41;
Matches 89; Conservative 6; Mismatches 13; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNVLNYYQKPGKAPKLLIFYSNLSHGVP 60
Db 1 DIQMTQSPSSLSASVGDRTVITCSASQDI I K Y L N Y Q T P G K A P K L L I Y E A S N L Q G V P S 60

QY 61 RFSGGSGTDYTLTISSLPEDFATYYCHQYKLPWTFGGTKVEIKR 108
Db 61 RFSGGSGTDYTLTISSLPEDIAITYYCOQYQSLPYTFGGTKLQITR 108

RESULT 3
Q9UL77 HUMAN
ID Q9UL77_HUMAN PRELIMINARY; PRT; 108 AA.
AC Q9UL77;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)

```

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DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192 (1998).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=1516616;
RA Victor K.D., Pascual V., Williams C.L., Lennon V.A., Capra J.D.;
RT "Human monoclonal striational autoantibodies isolated from thymic B
RT lymphocytes of patients with myasthenia gravis use VH and VL gene
RT segments associated with the autoimmune repertoire.";
RL Eur. J. Immunol. 22:2231-2236 (1992).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=8436174;
Wagner S.D., Luzzatto L.;
RT "v kappa gene segments rearranged in chronic lymphocytic leukemia are
RT distributed over a large portion of the v kappa locus and do not show
RT somatic mutation.";
RL Eur. J. Immunol. 23:391-397 (1993).
DR EMBL; AF035037; AAD56273.1; -; mRNA.
DR PIR; B49047; B49047.
DR PIR; S34083; S34083.
DR HSP; P01607; IBMW.
DR SMR; Q9UL77; 1-108.
DR Ensembl; ENSG00000163245; Homo sapiens.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11738 MW; C06681716C4D16F3 CRC64;

Query Match 82.1%; Score 471; DB 2; Length 108;
Best Local Similarity 83.3%; Pred. No. 4.3e-41;
Matches 90; Conservative 6; Mismatches 12; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITCSASODISNVLNYYQKPGKAPKLLIFVSSNLHSGVPS 60
DB 1 DIQMTQSPSSLSASVGDRTVITCSASQSISSVLNYYQKPGKAPNLLIYAASSLSQGVPS 60

QY 61 RFSGSGSGTDYTLTISSLPEDFATYYCHQSKLPWTFGQTKVEIKR 108
DB 61 RFSGSGSGTDFTLTITSSLPEDFATYYCQQSISTSWTFEGTKVEIKR 108

RESULT 4
O6GMW1 HUMAN
ID O6GMW1_HUMAN PRELIMINARY; PRT; 236 AA.
AC O6GMW1;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE IGKC protein.
GN Name=IGKC;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]

Myosin-reactive immunoglobulin light chain variable region
TISSUE=Spleen;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.D., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.L., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Statchenko M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Maman A., Rodriguez S., Sanchez A.,
RA Whiting M., Maman A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skaleks U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RG NIH MGC Project;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073791; AAH73791.1; -; mRNA.
DR SMR; Q6GMW1; 24-236.
DR Ensembl; ENSG00000163245; Homo sapiens.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS0290; IG_MHC; UNKNOWN 1.
SQ SEQUENCE 236 AA; 25751 MW; 5BFE6A087AFAC437 CRC64;

Query Match 81.0%; Score 465; DB 2; Length 236;
Best Local Similarity 85.0%; Pred. No. 4.5e-40;
Matches 91; Conservative 4; Mismatches 12; Indels 0; Gaps 0;

QY 2 IQMTQSPSSLSASVGDRTVITCSASODISNVLNYYQKPGKAPKLLIFVSSNLHSGVPSR 61
DB 24 IQMTQSPSSLSASVGDRTVITCRASQGISNDLWYQKPGKAPKLLIYAASSLSQGVPSR 83

QY 62 FSGSGSGTDYTLTISSLPEDFATYYCHQSKLPWTFGQTKVEIKR 108
DB 84 FSGSGSGTDFTLTITSSLPEDFATYYCQDYNYPWTFGQTKVEIKR 130

RESULT 5
O96SA9 HUMAN
ID O96SA9_HUMAN PRELIMINARY; PRT; 107 AA.
AC O96SA9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Anti-streptococcal/anti-myoisin immunoglobulin kappa light chain
DE variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
```



```

OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Skeletal Muscle;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahay J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Glandular pool- thyroid;
RG NIH MGC Project;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC095489; AAH95489.1; -; mRNA.
DR SMR; Q502W4; 23-236.
DR Ensembl; ENSG00000163245; Homo sapiens.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG.cl.
DR InterPro; IPR003006; IG.MHC.
DR InterPro; IPR003596; IG.V.
DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 2.
DR PROSITE; PS00290; IG.MHC; UNKNOWN 1.
KW Hypothetical protein; Immunoglobulin domain.
SQ SEQUENCE 236 AA; 25702 MW; 7FBFE4ED23084BC6 CRC64;

Query Match 79.4%; Score 456; DB 2; Length 236;
Best Local Similarity 81.5%; Pred. No. 3.9e-39;
Matches 88; Conservative 7; Mismatches 13; Indels 0; Gaps 0;

QY 1 DIQQTSPSSLSASVGDRTTTCASQDISNLYNWYQKPGKAPKLLIFYSNLSHGVS 60
DB 23 DIQQTSPSSLSASVGDRTTTCASQDISNLYNWYQKPGKAPKLLIFYSNLSHGVS 82

QY 61 RFSGSGSGTDYTLTISSLPEDPATYCHQYKLPWTFQGGTKVEIKR 108
DB 83 RFSGSGSGTDYTLTISSLPEDPATYCHQYKLPWTFQGGTKVEIKR 130

RESULT 8
Q502W4 HUMAN
ID Q502W4 HUMAN PRELIMINARY; PRT; 236 AA.
AC Q502W4;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE IGKC protein.
GN Name=IGKC;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Skeletal Muscle;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahay J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Skeletal Muscle;
RG NIH MGC Project;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC005332; AAH05332.1; -; mRNA.
DR HSSP; P01834; 1HEZ.
DR Ensembl; ENSG00000163245; Homo sapiens.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG.cl.
DR InterPro; IPR003006; IG.MHC.
DR InterPro; IPR003596; IG.V.
DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 2.
DR PROSITE; PS00290; IG.MHC; UNKNOWN 1.
KW Hypothetical protein; Immunoglobulin domain.
SQ SEQUENCE 236 AA; 25702 MW; 7FBFE4ED23084BC6 CRC64;

Query Match 79.4%; Score 456; DB 2; Length 236;
Best Local Similarity 81.5%; Pred. No. 3.9e-39;
Matches 88; Conservative 7; Mismatches 13; Indels 0; Gaps 0;

QY 1 DIQQTSPSSLSASVGDRTTTCASQDISNLYNWYQKPGKAPKLLIFYSNLSHGVS 60
DB 23 DIQQTSPSSLSASVGDRTTTCASQDISNLYNWYQKPGKAPKLLIFYSNLSHGVS 82

QY 61 RFSGSGSGTDYTLTISSLPEDPATYCHQYKLPWTFQGGTKVEIKR 108
DB 83 RFSGSGSGTDYTLTISSLPEDPATYCHQYKLPWTFQGGTKVEIKR 130

RESULT 9
KV1P HUMAN
ID KV1P HUMAN STANDARD; PRT; 108 AA.
AC P01508;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE IG kappa chain V-I region Roy.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=68362076; PubMed=5595110;
RA Hilschmann N.;

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RT "Chemical structure of 2 kappa-type Bence Jones proteins (Roy and  
RT Cum.).";  
RL Hillebrand N., Barnikol H.U., Hess M., Langer B., Ponstingl H.,  
RN [2]  
RN SEQUENCE REVISION TO 39 AND 41.  
RA Hillebrand N., Barnikol H.U., Hess M., Langer B., Ponstingl H.,  
RA Steinmetz-Kayne M., Suter L., Watanabe S.;  
RL (In) Franek F., Shugar D. (eds.);  
RL Gamma globulins: structure and function, pp.57-74, Academic Press, New  
RL York (1969).  
CC -!- MISCELLANEOUS: The C region of this chain has the INV (1,2)  
CC marker.  
CC  
CC -!- MISCELLANEOUS: This is a Bence-Jones protein.  
CC  
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.  
CC  
CC PIR; A91638; KIHURY.  
CC HSP; P01607; LBW.  
CC SMR; P01608; 1-108.  
CC Ensembl; ENSG00000173782; Homo sapiens.  
CC GO; GO:0005576; C:extracellular region; NAS.  
CC GO; GO:0003823; P:antigen binding; NAS.  
CC GO; GO:0006955; P:immune response; NAS.  
CC InterPro; IPR007110; IG-like.  
CC InterPro; IPR003596; IG\_v.  
CC SMART; SM00406; IGV; 1.  
CC PROSITE; PS50835; IG LIKE; 1.  
CC Bence-Jones protein; Direct protein sequencing; Immunoglobulin domain;  
KW Immunoglobulin V region.  
FT REGION 1 23  
FT REGION 24 34  
FT REGION 35 49  
FT REGION 50 56  
FT REGION 57 88  
FT REGION 89 97  
FT REGION 98 107  
FT REGION 98 107  
FT DISULFID 23 88  
FT NON\_TER 108 108  
SQ SEQUENCE 108 AA; 11782 MW; F5ACEDE5A313DF3A CRC64;  
  
Query Match 79.1%; Score 454; DB 1; Length 108;  
Best Local Similarity 80.6%; Pred. No. 2.5e-39;  
Matches 87; Conservative 7; Mismatches 14; Indels 0; Gaps 0;  
  
QY 1 DIQMTQSPSSLSASVGRVTITCSASQDISINLVNWKYQKPKAPKLLIFYSNLSHGVP 60  
Db 1 DIQMTQSPSSLSASVGRVTITCSASQDISIFLNWKYQKPKAPKLLIYDASKLEAGVP 60  
  
QY 61 RFSGGSGTDYTLTSSLOPEDFATYCHQYKLPWTFQGTKEIKR 108  
Db 61 RFSGGSGTDYTLTSSLOPEDFATYCHQYKLPWTFQGTKEIKR 108  
  
RESULT 10  
KVIA HUMAN STANDARD; PRT; 108 AA.  
ID KVIA HUMAN  
AC P01593;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 10-MAY-2005 (Rel. 47, Last annotation update)  
DE Ig kappa chain V-I region AG.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP PROTEIN SEQUENCE.  
RX MEDLINE=69234734; PubMed=4893682;  
  
RT "Chemical structure of 2 kappa-type Bence Jones proteins (Roy and  
RT Cum.).";  
RL Hillebrand N., Barnikol H.U., Hess M., Langer B., Ponstingl H.,  
RN [2]  
RN SEQUENCE REVISION TO 39 AND 41.  
RA Hillebrand N., Barnikol H.U., Hess M., Langer B., Ponstingl H.,  
RA Steinmetz-Kayne M., Suter L., Watanabe S.;  
RL (In) Franek F., Shugar D. (eds.);  
RL Gamma globulins: structure and function, pp.57-74, Academic Press, New  
RL York (1969).  
CC -!- MISCELLANEOUS: The C region of this chain has the INV (1,2)  
CC marker.  
CC  
CC -!- MISCELLANEOUS: This is a Bence-Jones protein.  
CC  
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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CC use as long as its content is in no way modified and this statement is not  
CC removed.  
CC  
CC PIR; A01861; KIHUAG.  
CC HSP; P01607; LBW.  
CC SMR; P01593; 1-108.  
CC Ensembl; ENSG00000173782; Homo sapiens.  
CC GO; GO:0005576; C:extracellular region; NAS.  
CC GO; GO:0003823; P:antigen binding; NAS.  
CC GO; GO:0006955; P:immune response; NAS.  
CC InterPro; IPR007110; IG-like.  
CC InterPro; IPR003596; IG\_v.  
CC SMART; SM00406; IGV; 1.  
CC PROSITE; PS50835; IG LIKE; 1.  
CC Bence-Jones protein; Direct protein sequencing; Immunoglobulin domain;  
KW Immunoglobulin V region.  
FT REGION 1 23  
FT REGION 24 34  
FT REGION 35 49  
FT REGION 50 56  
FT REGION 57 88  
FT REGION 89 97  
FT REGION 98 107  
FT REGION 98 107  
FT DISULFID 23 88  
FT NON\_TER 108 108  
SQ SEQUENCE 108 AA; 11992 MW; E3B3B246C18F0C4F CRC64;  
  
Query Match 78.9%; Score 453; DB 1; Length 108;  
Best Local Similarity 79.6%; Pred. No. 3.2e-39;  
Matches 86; Conservative 8; Mismatches 14; Indels 0; Gaps 0;  
  
QY 1 DIQMTQSPSSLSASVGRVTITCSASQDISINLVNWKYQKPKAPKLLIFYSNLSHGVP 60  
Db 1 DIQMTQSPSSLSASVGRVTITCSASQDINHLNWKYQKPKAPKLLIYDASLETGVP 60  
  
QY 61 RFSGGSGTDYTLTSSLOPEDFATYCHQYKLPWTFQGTKEIKR 108  
Db 61 RFSGGSGTDYTLTSSLOPEDFATYCHQYKLPWTFQGTKEIKR 108  
  
RESULT 11  
Q6GMX8 HUMAN PRELIMINARY; PRT; 236 AA.  
ID Q6GMX8 HUMAN  
AC Q6GMX8;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE IGKC protein.  
GN Name=IGKC;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=23388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner B.D., Fellings F.S., Wagner L., Sherman C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Heng L.,



RA Stapleton M., Soares M.B., Bonaldo M.F., Cavaant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
 RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton B., Kettaman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Richmond J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Glimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RN NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Primary B-Cells;  
 RG NIH MGC Project;  
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC073764; AAH73764.1; -; mRNA.  
 DR SMR; Q6GMX8; 24-235.  
 DR Ensembl; ENSG00000163245; Homo sapiens.  
 DR InterPro; IPR003599; IG.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003597; IG-cl.  
 DR InterPro; IPR003006; IG-MHC.  
 DR InterPro; IPR003596; IG\_v.  
 DR Pfam; PF07654; Cl-set; 1.  
 DR SMART; SM00409; IG; 2.  
 DR SMART; SM00407; IGcl; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG LIKE; 2.  
 DR PROSITE; PS0290; IG MHC; UNKNOWN 1.  
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 Best Local Similarity 80.6%; Pred. No. 8e-39;  
 Matches 87; Conservative 9; Mismatches 12; Indels 0; Gaps 0;  
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 DB 23 DIQMTQSPSSLSASVGRVITTCASQDISNLYNMQKPKGKAPKLLIFYSNLSHGVS 82  
 QY 61 RFSGSGSGTDYTLTISSLPEDFATYYCHQSKLPWTFGQGKVEIKR 108  
 DB 83 RFSGSGSGTDYTLTISSLPEDFATYYCHQSKLPWTFGQGKVEIKR 130  
 RESULT 12  
 ID\_KVIY\_HUMAN STANDARD; PRT; 108 AA.  
 AC P80362;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 10-MAY-2005 (Rel. 47, Last annotation update)  
 DE Homo sapiens (Human).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RN PROTEIN SEQUENCE, AND X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).  
 RP MEDLINE=9506080; PubMed=7993911;  
 RA Huang D.-B., Chang C.-H., Ainsworth C., Bruenger A.T., Eulitz M.,  
 RA Solomon A., Stevens F.J., Schiffer M.;  
 RT "Comparison of crystal structures of two homologous proteins:  
 RT structural origin of altered domain interactions in immunoglobulin  
 RT light-chain dimers.";  
 RL Biochemistry 33:14848-14857(1994).  
 RN [2]  
 RP PROTEIN SEQUENCE OF 1-35.

RX MEDLINE=81267384; PubMed=6167731;  
 RA Stevens F.J., Weetholm F.A., Panagiotopoulos N., Schiffer M.,  
 RA Popp R.A., Solomon A.;  
 RT "Characterization and preliminary crystallographic data on the VL-  
 RT related fragment of the human kappa Bence Jones protein Wat.";  
 RL J. Mol. Biol. 147:185-193(1981).  
 CC 1- MISCELLANEOUS: This is a Bence-Jones protein.  
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC PDB; 1WTL; X-ray; A/B=1-108.  
 DR GO; GO:0005576; C:extracellular region; NAS.  
 DR GO; GO:0003823; F:antigen binding; NAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003596; IG\_v.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG LIKE; 1.  
 DR 3D-structure; Bence-Jones protein; Direct protein sequencing;  
 KW immunoglobulin domain; Immunoglobulin V region.  
 FT REGION 1 23  
 FT REGION 24 34  
 FT REGION 35 49  
 FT REGION 50 56  
 FT REGION 57 88  
 FT REGION 89 97  
 FT REGION 98 107  
 FT DISULFID 23 88  
 FT NON TER 30 31  
 FT STRAND 4 7  
 FT STRAND 10 13  
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 FT STRAND 19 25  
 FT TURN 30 31  
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 FT TURN 50 52  
 FT STRAND 53 54  
 FT TURN 56 57  
 FT TURN 60 61  
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 FT TURN 68 69  
 FT STRAND 70 75  
 FT HELIX 80 82  
 FT STRAND 84 90  
 FT STRAND 98 98  
 FT STRAND 102 106  
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 Query Match 78.7%; Score 452; DB 1; Length 108;  
 Best Local Similarity 78.7%; Pred. No. 4.1e-39;  
 Matches 85; Conservative 11; Mismatches 12; Indels 0; Gaps 0;  
 QY 1 DIQMTQSPSSLSASVGRVITTCASQDISNLYNMQKPKGKAPKLLIFYSNLSHGVS 60  
 DB 1 DIQMTQSPSSLSASVGRVITTCASQDISNLYNMQKPKGKAPKLLIFYSNLSHGVS 60  
 QY 61 RFSGSGSGTDYTLTISSLPEDFATYYCHQSKLPWTFGQGKVEIKR 108  
 DB 61 RFSGSGSGTDYTLTISSLPEDFATYYCHQSKLPWTFGQGKVEIKR 108  
 RESULT 13  
 ID\_KVIH\_HUMAN STANDARD; PRT; 108 AA.  
 AC P01600;  
 DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 10-MAY-2005 (Rel. 47, Last annotation update)  
DE Ig kappa chain V-I region Hau.  
OS Homo sapiens (human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP PROTEIN SEQUENCE.  
RX MEDLINE=71032830; PubMed=4097974;  
RA Watanabe S., Hilschmann N.;  
RT "The primary structure of a monoclonal kappa-type immunoglobulin L-chain of subgroup I (Bence-Jones Protein Hau): subdivision within subgroups";  
RL Hoppe-Seyler's Z. Physiol. Chem. 351:1291-1295(1970).  
CC -!- MISCELLANEOUS: The C region of this chain has the INV (3) marker.  
CC -!- MISCELLANEOUS: This is a Bence-Jones protein.  
CC -----  
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CC -----  
DR PIR; A01868; K1HUHU.  
DR PDB; 1F6L; X-ray; L=1-108.  
DR GO; GO:0005576; C:extracellular region; NAS.  
DR GO; GO:0003823; F:antigen binding; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
DR 3D-structure; Bence-Jones protein; Direct protein sequencing;  
KW Immunoglobulin domain; Immunoglobulin V region.  
FT REGION 1 23 Framework-1.  
FT REGION 24 34 Complementarity-determining-1.  
FT REGION 35 49 Framework-2.  
FT REGION 50 56 Complementarity-determining-2.  
FT REGION 57 88 Framework-3.  
FT REGION 89 97 Complementarity-determining-3.  
FT REGION 98 107 Framework-4.  
FT DISULFID 23 88 By similarity.  
FT NON\_TER 108 108  
SQ SEQUENCE 108 AA; 11671 MW; 08D3A616D8D0618 CRC64;  
  
Query Match 78.4%; Score 450; DB 1; Length 108;  
Best Local Similarity 80.6%; Pred. No. 6.6e-39;  
Matches 87; Conservative 10; Mismatches 11; Indels 0; Gaps 0;  
  
QY 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNWYQKPGKAPKLLIFYSNLSHGVP 60  
Db 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNWYQKPGKAPKLLIFYSNLSHGVP 60  
  
QY 61 RFSGGSGDTYLTITSSLPQEDFATYVCHQYKLPWTFCQGTQKVEIKR 108  
Db 61 RFSGGSGDTYLTITSSLPQEDFATYVCHQYKLPWTFCQGTQKVEIKR 108  
  
RESULT 14  
Q9UL70 HUMAN  
ID Q9UL70 HUMAN PRELIMINARY; PRT; 108 AA.  
AC Q9UL70;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Myosin-reactive immunoglobulin light chain variable region (fragment).  
OS Homo sapiens (human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.

OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;  
RA Wu X., Liu B., Van der Werwe F.L., Kallis N.N., Berney S.W.,  
RA Young D.C.;  
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus";  
RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RX PubMed=1660528;  
RA Manheimer-Lory A., Katz J.B., Pillinger M., Ghossein C., Smith A.,  
RA Diamond B.;  
RT "Molecular characteristics of antibodies bearing an anti-DNA-associated idiotype";  
RL J. Exp. Med. 174:1639-1652(1991).  
DR EMBL; AF035044; AAD56280.1; -; mRNA.  
DR PIR; PH0863; PH0863.  
DR HSSP; P01607; 1BMW.  
DR SMR; Q9UL70; 1-108.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
FT NON\_TER 1 1  
FT NON\_TER 108 108  
SQ SEQUENCE 108 AA; 11633 MW; B7BEDC3E41FCCA37 CRC64;  
  
Query Match 78.4%; Score 450; DB 2; Length 108;  
Best Local Similarity 80.6%; Pred. No. 6.6e-39;  
Matches 87; Conservative 6; Mismatches 15; Indels 0; Gaps 0;  
  
QY 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNWYQKPGKAPKLLIFYSNLSHGVP 60  
Db 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNWYQKPGKAPKLLIFYSNLSHGVP 60  
  
QY 61 RFSGGSGDTYLTITSSLPQEDFATYVCHQYKLPWTFCQGTQKVEIKR 108  
Db 61 RFSGGSGDTYLTITSSLPQEDFATYVCHQYKLPWTFCQGTQKVEIKR 108  
  
RESULT 15  
Q6GMX0 HUMAN  
ID Q6GMX0 HUMAN PRELIMINARY; PRT; 236 AA.  
AC Q6GMX0;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=23288257; PubMed=12477932; DOI=10.1073/pnas.2426038999;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altachul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whitting R.M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,	
	Butterfield Y.S.N., Krywinski M.I., Skalska U., Smalusz D.E.,	
	Schmerer A., Schein J.E., Jones S.J.M., Marra M.A.;	
	"Generation and initial analysis of more than 15,000 full-length human	
	and mouse cDNA sequences.";	
	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).	
	[2]	
RA	NUCLEOTIDE SEQUENCE.	
RP	TISSUE=Spleen;	
RC	Straussberg R.;	
RA	Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.	
RL	EWBL; BC073775; AAH73775.1; -, mRNA.	
DR	SWR; Q6GXKX0; 23-236.	
DR	GO; GO:0016021; C:integral to membrane; IEA.	
DR	InterPro; IPR003599; IG.	
DR	InterPro; IPR007110; Ig-like.	
DR	InterPro; IPR003597; IG cl.	
DR	InterPro; IPR003006; IG_MHC.	
DR	InterPro; IPR003596; IG_v.	
DR	Pfam; PF07654; Cl-set; 1.	
DR	SMART; SM00409; IG; 2.	
DR	SMART; SM00407; IGcl; 1.	
DR	SMART; SM00406; IGv; 1.	
DR	PROSITE; PS50835; IG_LIKE; 2.	
DR	PROSITE; PS00290; IG_MHC; UNKNOWN 1.	
KW	Hypothetical protein.	
SQ	SEQUENCE 236 AA; 864EA08C7E92BF8F CRC64;	
	Query Match                78.2%; Score 449; DB 2; Length 236;	
	Best Local Similarity      79.6%; Pred. No. 2.le-3g;	
	Matches     86; Conservative    9; Mismatches   13; Indels     0; Gaps     0;	
Qy	1 DIQMTPSPSLSASVGRDVITTCASODISNLNWYQQKPCKAPKLIFYSNNLHGVP 60       :       :	
Dd	23 DIQMTPSPSLSASVGRDVITTCASQNINYNLNWYLKPKCAPNLLIYAASSIQSGVP 82       :       :	
Qy	61 RFSCGGGSDTYTLTIISSLQPEDFYATYYCHQVSCLKLPWTFGQGTVKEIKR 108       :       :	
Dd	83 RFSCGGGTFTLTIISSLRDDFYATYYCOOSNYPLTFGGGTNVIEIKR 130       :       :	

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GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: April 6, 2006, 08:50:25 ; Search time 6.7132 Seconds  
(without alignments)  
1330.063 Million cell updates/sec

Title: US-10-089-500-10  
Perfect score: 574  
Sequence: 1 DIQMTQSPSSLSASVGRVT.....HOVSKLPWTFGGTKVEIKR 108

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/prodata/1/iaa/5 COMB.pep.\*  
2: /cgn2\_6/prodata/1/iaa/6 COMB.pep.\*  
3: /cgn2\_6/prodata/1/iaa/H COMB.pep.\*  
4: /cgn2\_6/prodata/1/iaa/PCUS COMB.pep.\*  
5: /cgn2\_6/prodata/1/iaa/RE COMB.pep.\*  
6: /cgn2\_6/prodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	533	92.9	110	2	US-08-908-469-103
2	533	92.9	237	2	US-08-908-469-100
3	533	92.9	491	2	US-10-011-125A-2
4	531	92.5	107	2	US-08-908-469-15
5	530	92.3	110	2	US-08-908-469-105
6	529	92.2	108	2	US-08-908-469-8
7	529	92.2	110	2	US-09-440-781-94
8	527	91.8	107	2	US-08-908-469-13
9	526	91.6	110	2	US-08-908-469-107
10	526	91.6	110	2	US-08-908-469-117
11	523	91.1	108	2	US-08-908-469-126
12	510	88.9	108	2	US-09-905-243-73
13	507	88.3	110	2	US-09-440-781-95
14	507	88.3	110	2	US-08-908-469-109
15	507	88.3	110	2	US-08-908-469-111
16	507	88.3	110	2	US-08-908-469-113
17	507	88.3	110	2	US-08-908-469-115
18	506	88.2	107	1	US-07-934-373C-17
19	506	88.2	107	1	US-08-437-642B-17
20	506	88.2	107	2	US-08-146-206C-17
21	506	88.2	107	2	US-09-705-686-17
22	506	88.2	107	2	US-09-705-392A-17
23	506	88.2	107	2	US-09-705-398-17
24	506	88.2	107	4	PCT-US93-07832-17
25	506	88.2	109	1	US-07-934-373C-47
26	506	88.2	109	2	US-08-437-642B-47
27	506	88.2	127	2	US-08-649-100-33

28	506	88.2	214	1	US-07-934-373C-40	Sequence 40, Appl
29	506	88.2	214	1	US-08-788-800-11	Sequence 11, Appl
30	506	88.2	214	2	US-08-437-642B-40	Sequence 40, Appl
31	506	88.2	214	2	US-09-097-309-2	Sequence 2, Appl
32	506	88.2	214	2	US-09-097-171A-2	Sequence 2, Appl
33	506	88.2	214	2	US-09-460-587-2	Sequence 2, Appl
34	506	88.2	214	2	US-09-940-166A-2	Sequence 2, Appl
35	506	88.2	214	4	PCT-US93-07832-40	Sequence 40, Appl
36	506	88.2	233	1	US-07-934-373C-25	Sequence 25, Appl
37	506	88.2	233	2	US-08-437-642B-25	Sequence 25, Appl
38	506	88.2	233	2	US-08-146-206C-25	Sequence 25, Appl
39	506	88.2	233	2	US-09-705-686-25	Sequence 25, Appl
40	506	88.2	233	2	US-09-705-392A-25	Sequence 25, Appl
41	506	88.2	233	2	US-09-705-398-25	Sequence 25, Appl
42	506	88.2	233	4	PCT-US93-07832-25	Sequence 25, Appl
43	506	88.2	237	2	US-09-097-309-6	Sequence 6, Appl
44	506	88.2	237	2	US-09-097-171A-10	Sequence 10, Appl
45	506	88.2	237	2	US-09-422-712B-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1  
US-08-908-469-103  
; Sequence 103, Application US/08908469  
; Patent No. 6884879  
; GENERAL INFORMATION:  
; APPLICANT: Baca, Manuel  
; Wells, James A.  
; Presta, Leonard G.  
; Lowman, Henry B.  
; Chen, Yvonne M.  
; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES  
; NUMBER OF SEQUENCES: 131  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/908,469  
; FILING DATE: 21-May-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/833,504  
; FILING DATE: 07-APR-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Cui, Steven X.  
; REGISTRATION NUMBER: 44,637  
; REFERENCE/DOCKET NUMBER: P1093P1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-8674  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 103:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 110 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
; SEQUENCE DESCRIPTION: SEQ ID NO: 103:  
US-08-908-469-103

Query Match 92.9%; Score 533; DB 2; Length 110;  
Best Local Similarity 91.7%; Pred. No. 8,8e-44;  
Matches 99; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNLYNWYQKPGKAPKLLIFYSSNLHSGVPS 60  
 ; TITLE OF INVENTION: BACTERIAL HOST STRAINS  
 ; FILE REFERENCE: P1804R1  
 ; CURRENT APPLICATION NUMBER: US/10/011.125A  
 ; CURRENT FILING DATE: 2001-12-07  
 ; PRIOR APPLICATION NUMBER: US 60/256,162  
 ; PRIOR FILING DATE: 2000-12-14  
 ; NUMBER OF SEQ ID NOS: 12  
 ; SEQ ID NO 2  
 ; LENGTH: 491  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Sequence is synthesized.  
 ; Patent No. 6828121  
 ; Patent No. 6828121  
 ; US-10-011-125A-2

## RESULT 2

US-08-908-469-100  
 ; Sequence 100, Application US/08908469  
 ; Patent No. 6884879  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Baca, Manuel  
 ; Wells, James A.  
 ; Presta, Leonard G.  
 ; Lowman, Henry B.  
 ; Chen, Yvonne M.

## TITLE OF INVENTION: ANTI-VEGF ANTIBODIES

NUMBER OF SEQUENCES: 131

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

## COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA: US/08/908,469

FILING DATE: 21-May-2001

CLASSIFICATION: <Unknown>

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/833,504

FILING DATE: 07-APR-1997

ATTORNEY/AGENT INFORMATION:

NAME: Cui, Steven X.

REGISTRATION NUMBER: 44,637

REFERENCE/DOCKET NUMBER: P1093P1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-8674

TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 100:

SEQUENCE CHARACTERISTICS:

LENGTH: 237 amino acids

TYPE: Amino Acid

TOPOLOGY: Linear

SEQUENCE DESCRIPTION: SEQ ID NO: 100:

US-08-908-469-100

Query Match 92.9%; Score 533; DB 2; Length 237;  
 Best Local Similarity 91.7%; Pred. No. 2.1e-43;  
 Matches 99; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNLYNWYQKPGKAPKLLIFYSSNLHSGVPS 60  
 ; TITLE OF INVENTION: BACTERIAL HOST STRAINS  
 ; FILE REFERENCE: P1804R1  
 ; CURRENT APPLICATION NUMBER: US/10/011.125A  
 ; CURRENT FILING DATE: 2001-12-07  
 ; PRIOR APPLICATION NUMBER: US 60/256,162  
 ; PRIOR FILING DATE: 2000-12-14  
 ; NUMBER OF SEQ ID NOS: 12  
 ; SEQ ID NO 2  
 ; LENGTH: 491  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Sequence is synthesized.  
 ; Patent No. 6828121  
 ; Patent No. 6828121  
 ; US-10-011-125A-2

Db 24 DIQMTQSPSSLSASVGDRTVITCSASQDISNLYNWYQKPGKAPKLLIFYSSNLHSGVPS 83  
 ; TITLE OF INVENTION: BACTERIAL HOST STRAINS  
 ; FILE REFERENCE: P1804R1  
 ; CURRENT APPLICATION NUMBER: US/10/011.125A  
 ; CURRENT FILING DATE: 2001-12-07  
 ; PRIOR APPLICATION NUMBER: US 60/256,162  
 ; PRIOR FILING DATE: 2000-12-14  
 ; NUMBER OF SEQ ID NOS: 12  
 ; SEQ ID NO 2  
 ; LENGTH: 491  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Sequence is synthesized.  
 ; Patent No. 6828121  
 ; Patent No. 6828121  
 ; US-10-011-125A-2

## RESULT 3

US-10-011-125A-2  
 ; Sequence 2, Application US/10011125A  
 ; Patent No. 6828121  
 ; Patent No. 6828121  
 ; GENERAL INFORMATION:

; APPLICANT: Chen, Christina Yu-Ching  
 ; TITLE OF INVENTION: BACTERIAL HOST STRAINS  
 ; FILE REFERENCE: P1804R1  
 ; CURRENT APPLICATION NUMBER: US/10/011.125A  
 ; CURRENT FILING DATE: 2001-12-07  
 ; PRIOR APPLICATION NUMBER: US 60/256,162  
 ; PRIOR FILING DATE: 2000-12-14  
 ; NUMBER OF SEQ ID NOS: 12  
 ; SEQ ID NO 2  
 ; LENGTH: 491  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Sequence is synthesized.  
 ; Patent No. 6828121  
 ; Patent No. 6828121  
 ; US-10-011-125A-2

Query Match 92.9%; Score 533; DB 2; Length 491;  
 Best Local Similarity 91.7%; Pred. No. 4.7e-43;  
 Matches 99; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNLYNWYQKPGKAPKLLIFYSSNLHSGVPS 60  
 ; TITLE OF INVENTION: BACTERIAL HOST STRAINS  
 ; FILE REFERENCE: P1804R1  
 ; CURRENT APPLICATION NUMBER: US/10/011.125A  
 ; CURRENT FILING DATE: 2001-12-07  
 ; PRIOR APPLICATION NUMBER: US 60/256,162  
 ; PRIOR FILING DATE: 2000-12-14  
 ; NUMBER OF SEQ ID NOS: 12  
 ; SEQ ID NO 2  
 ; LENGTH: 491  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Sequence is synthesized.  
 ; Patent No. 6828121  
 ; Patent No. 6828121  
 ; US-10-011-125A-2

Db 24 DIQMTQSPSSLSASVGDRTVITCSASQDISNLYNWYQKPGKAPKLLIFYSSNLHSGVPS 83  
 ; TITLE OF INVENTION: BACTERIAL HOST STRAINS  
 ; FILE REFERENCE: P1804R1  
 ; CURRENT APPLICATION NUMBER: US/10/011.125A  
 ; CURRENT FILING DATE: 2001-12-07  
 ; PRIOR APPLICATION NUMBER: US 60/256,162  
 ; PRIOR FILING DATE: 2000-12-14  
 ; NUMBER OF SEQ ID NOS: 12  
 ; SEQ ID NO 2  
 ; LENGTH: 491  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Sequence is synthesized.  
 ; Patent No. 6828121  
 ; Patent No. 6828121  
 ; US-10-011-125A-2

## RESULT 4

US-08-908-469-15  
 ; Sequence 15, Application US/08908469  
 ; Patent No. 6884879  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Baca, Manuel  
 ; Wells, James A.  
 ; Presta, Leonard G.  
 ; Lowman, Henry B.  
 ; Chen, Yvonne M.

## TITLE OF INVENTION: ANTI-VEGF ANTIBODIES

NUMBER OF SEQUENCES: 131

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

## COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/908,469

FILING DATE: 21-May-2001

CLASSIFICATION: <Unknown>

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/833,504

FILING DATE: 07-APR-1997

ATTORNEY/AGENT INFORMATION:

NAME: Cui, Steven X.

REGISTRATION NUMBER: 44,637

REFERENCE/DOCKET NUMBER: P1093P1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-8674

TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 15:

SEQUENCE CHARACTERISTICS:

LENGTH: 107 amino acids

TYPE: Amino Acid

TOPOLOGY: Linear

SEQUENCE DESCRIPTION: SEQ ID NO: 15:

US-08-908-469-15

Query Match 92.5%; Score 531; DB 2; Length 107;  
Best Local Similarity 92.5%; Pred. No. 1.3e-43;  
Matches 99; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCSASQDINLWYQKPKAPKLLIFYSNLSHGVP 60  
Db 1 DIQMTQSPSSLSASVGRVTITCSASQDINLWYQKPKAPKLLIFYSNLSHGVP 60  
Qy 61 RFGSGSGTDYTLTISSLPEDFATYYCHQYSKLPWTFGQGTKEIKR 107  
Db 61 RFGSGSGTDYTLTISSLPEDFATYYCHQYSKLPWTFGQGTKEIKR 107

RESULT 5

US-08-908-469-105  
; Sequence 105, Application US/08908469  
; Patent No. 6884879

GENERAL INFORMATION:

APPLICANT: Baca, Manuel  
Wells, James A.  
Presta, Leonard G.  
Lowman, Henry B.  
Chen, Yvonne M.

TITLE OF INVENTION: ANTI-VEGF ANTIBODIES

NUMBER OF SEQUENCES: 131

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/908,469

FILING DATE: 21-May-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/833,504

FILING DATE: 07-APR-1997

ATTORNEY/AGENT INFORMATION:

NAME: Cui, Steven X.

REGISTRATION NUMBER: 44,637

REFERENCE/DOCKET NUMBER: P1093P1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-8674

TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 105:

SEQUENCE CHARACTERISTICS:

LENGTH: 110 amino acids

TYPE: Amino Acid

TOPOLOGY: Linear

SEQUENCE DESCRIPTION: SEQ ID NO: 105:

US-08-908-469-105

Query Match 92.3%; Score 530; DB 2; Length 110;  
Best Local Similarity 90.7%; Pred. No. 1.7e-43;  
Matches 98; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCSASQDINLWYQKPKAPKLLIFYSNLSHGVP 60  
Db 1 DIQMTQSPSSLSASVGRVTITCSASQDINLWYQKPKAPKLLIFYSNLSHGVP 60  
Qy 61 RFGSGSGTDYTLTISSLPEDFATYYCHQYSKLPWTFGQGTKEIKR 108  
Db 61 RFGSGSGTDYTLTISSLPEDFATYYCHQYSKLPWTFGQGTKEIKR 108

RESULT 6

US-08-908-469-8  
; Sequence 8, Application US/08908469  
; Patent No. 6884879

GENERAL INFORMATION:

APPLICANT: Baca, Manuel  
Wells, James A.  
Presta, Leonard G.  
Lowman, Henry B.  
Chen, Yvonne M.

TITLE OF INVENTION: ANTI-VEGF ANTIBODIES

NUMBER OF SEQUENCES: 131

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/908,469

FILING DATE: 21-May-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/833,504

FILING DATE: 07-APR-1997

ATTORNEY/AGENT INFORMATION:

NAME: Cui, Steven X.

REGISTRATION NUMBER: 44,637

REFERENCE/DOCKET NUMBER: P1093P1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-8674

TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 108 amino acids

TYPE: Amino Acid

TOPOLOGY: Linear

SEQUENCE DESCRIPTION: SEQ ID NO: 8:

US-08-908-469-8

Query Match 92.2%; Score 529; DB 2; Length 108;  
Best Local Similarity 90.7%; Pred. No. 2.1e-43;  
Matches 98; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCSASQDINLWYQKPKAPKLLIFYSNLSHGVP 60  
Db 1 DIQMTQSPSSLSASVGRVTITCSASQDINLWYQKPKAPKLLIFYSNLSHGVP 60  
Qy 61 RFGSGSGTDYTLTISSLPEDFATYYCHQYSKLPWTFGQGTKEIKR 108  
Db 61 RFGSGSGTDYTLTISSLPEDFATYYCHQYSKLPWTFGQGTKEIKR 108

RESULT 7

US-09-440-781-94  
; Sequence 94, Application US/09440781  
; Patent No. 6632926

GENERAL INFORMATION:

APPLICANT: Yvonne Man-ye Chen et al.

TITLE OF INVENTION: ANTIBODY VARIANTS

FILE REFERENCE: P1469R1

CURRENT APPLICATION NUMBER: US/09/440,781

CURRENT FILING DATE: 1999-11-16

NUMBER OF SEQ ID NOS: 99

SEQ ID NO 94

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; LENGTH: 110
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: artificial
; LOCATION: 1-110
; OTHER INFORMATION: humanized antibody light chain variable domain
US-09-440-781-94

Query Match          92.2%; Score 529; DB 2; Length 110;
Best Local Similarity 90.7%; Pred. No. 2.1e-43;
Matches 98; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQKPGKAPKLLIYFTSSLSHGVP 60
Db 1 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQKPGKAPKLLIYFTSSLSHGVP 60

Qy 61 RFGSGSGTDYTLTISSLPEDFATYYCHQYSKLPWTFGQGTKVEIK 108
Db 61 RFGSGSGTDFTLTITSLQLPEDFATYYCQYSTVPTVTFGQGTKVEIKR 108

RESULT 8
US-08-908-469-13
; Sequence 13, Application US/08908469
; Patent No. 6884879
; GENERAL INFORMATION:
; APPLICANT: Baca, Manuel
; Wells, James A.
; Presta, Leonard G.
; Lowman, Henry B.
; Chen, Yvonne M.
; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
; NUMBER OF SEQUENCES: 131
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/908,469
; FILING DATE: 21-May-2001
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/833,504
; FILING DATE: 07-APR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Cui, Steven X.
; REGISTRATION NUMBER: 44,637
; REFERENCE/DOCKET NUMBER: P1093P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-8674
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-08-908-469-13

Query Match          91.8%; Score 527; DB 2; Length 107;
Best Local Similarity 91.6%; Pred. No. 3.2e-43;
Matches 98; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQKPGKAPKLLIYFTSSLSHGVP 60

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Db 1 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQKPGKAPKLLIYFTSSLSHGVP 60

Qy 61 RFGSGSGTDYTLTISSLPEDFATYYCHQYSKLPWTFGQGTKVEIK 107
Db 61 RFGSGSGTDFTLTITSLQLPEDFATYYCQYSTVPTVTFGQGTKVEIK 107

RESULT 9
US-08-908-469-107
; Sequence 107, Application US/08908469
; Patent No. 6884879
; GENERAL INFORMATION:
; APPLICANT: Baca, Manuel
; Wells, James A.
; Presta, Leonard G.
; Lowman, Henry B.
; Chen, Yvonne M.
; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
; NUMBER OF SEQUENCES: 131
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/908,469
; FILING DATE: 21-May-2001
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/833,504
; FILING DATE: 07-APR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Cui, Steven X.
; REGISTRATION NUMBER: 44,637
; REFERENCE/DOCKET NUMBER: P1093P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-8674
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 107:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 110 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 107:
US-08-908-469-107

Query Match          91.6%; Score 526; DB 2; Length 110;
Best Local Similarity 89.8%; Pred. No. 4.1e-43;
Matches 97; Conservative 8; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQKPGKAPKLLIYFTSSLSHGVP 60
Db 1 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQKPGKAPKLLIYFTSSLSHGVP 60

Qy 61 RFGSGSGTDYTLTISSLPEDFATYYCHQYSKLPWTFGQGTKVEIKR 108
Db 61 RFGSGSGTDFTLTITSLQLPEDFATYYCQYSTVPTVTFGQGTKVEIKR 108

RESULT 10
US-08-908-469-117
; Sequence 117, Application US/08908469
; Patent No. 6884879
; GENERAL INFORMATION:
; APPLICANT: Baca, Manuel

```





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RESULT 13
US-09-440-781-95
; Sequence 95, Application US/09440781
; Patent No. 6632926
; GENERAL INFORMATION:
; APPLICANT: Yvonne Man-Yee Chen et al.
; TITLE OF INVENTION: ANTIBODY VARIANTS
; FILE REFERENCE: P1469R1
; CURRENT APPLICATION NUMBER: US/09/440,781
; CURRENT FILING DATE: 1999-11-16
; NUMBER OF SEQ ID NOS: 99
; SEQ ID NO 95
; LENGTH: 110
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: artificial
; LOCATION: 1-110
; OTHER INFORMATION: humanized antibody light chain variable domain
US-09-440-781-95

Query Match      88.3%; Score 507; DB 2; Length 110;
Best Local Similarity 85.2%; Pred. No. 2.7e-41;
Matches 92; Conservative 11; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNLYNWYQQKPGKAPKLLIFYSNLSHGVPVS 60
DB 1 DIQLTQSPSSLSASVGDRTVITCRANEQLSNLYNWYQQKPGKAPKVLIIYFTSSLHSGVPVS 60

QY 61 RFSGGSGTDYTLTSSLOPEDFATYYCHQYSKLPWTFGQGTKEIKR 108
DB 61 RFSGGSGTDFTLTSSLPEDFATYYCQYSTVPWTFGQGTKEIKR 108

RESULT 14
US-08-908-469-109
; Sequence 109, Application US/08908469
; Patent No. 6884879
; GENERAL INFORMATION:
; APPLICANT: Baca, Manuel
; Wells, James A.
; Presta, Leonard G.
; Lowman, Henry B.
; Chen, Yvonne M.
; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
; NUMBER OF SEQUENCES: 131
; CORRESPONDENCE ADDRESS:
; ADDRESS: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/908,469
; FILING DATE: 21-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/833,504
; FILING DATE: 07-APR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Cui, Steven X.
; REGISTRATION NUMBER: 44,637
; REFERENCE/DOCKET NUMBER: P1093P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-8674
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/908,469
; FILING DATE: 21-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/833,504
; FILING DATE: 07-APR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Cui, Steven X.
; REGISTRATION NUMBER: 44,637
; REFERENCE/DOCKET NUMBER: P1093P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-8674

Query Match      88.3%; Score 507; DB 2; Length 110;
Best Local Similarity 85.2%; Pred. No. 2.7e-41;
Matches 92; Conservative 11; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNLYNWYQQKPGKAPKLLIFYSNLSHGVPVS 60
DB 1 DIQLTQSPSSLSASVGDRTVITCRANEQLSNLYNWYQQKPGKAPKVLIIYFTSSLHSGVPVS 60

QY 61 RFSGGSGTDYTLTSSLOPEDFATYYCHQYSKLPWTFGQGTKEIKR 108
DB 61 RFSGGSGTDFTLTSSLPEDFATYYCQYSTVPWTFGQGTKEIKR 108

RESULT 15
US-08-908-469-111
; Sequence 111, Application US/08908469
; Patent No. 6884879
; GENERAL INFORMATION:
; APPLICANT: Baca, Manuel
; Wells, James A.
; Presta, Leonard G.
; Lowman, Henry B.
; Chen, Yvonne M.
; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
; NUMBER OF SEQUENCES: 131
; CORRESPONDENCE ADDRESS:
; ADDRESS: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/908,469
; FILING DATE: 21-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/833,504
; FILING DATE: 07-APR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Cui, Steven X.
; REGISTRATION NUMBER: 44,637
; REFERENCE/DOCKET NUMBER: P1093P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-8674
; INFORMATION FOR SEQ ID NO: 111:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 110 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 111:
US-08-908-469-111

Query Match      88.3%; Score 507; DB 2; Length 110;
Best Local Similarity 85.2%; Pred. No. 2.7e-41;
Matches 92; Conservative 11; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNLYNWYQQKPGKAPKLLIFYSNLSHGVPVS 60
DB 1 DIQLTQSPSSLSASVGDRTVITCRANEQLSNLYNWYQQKPGKAPKVLIIYFTSSLHSGVPVS 60

QY 61 RFSGGSGTDYTLTSSLOPEDFATYYCHQYSKLPWTFGQGTKEIKR 108
DB 61 RFSGGSGTDFTLTSSLPEDFATYYCQYSTVPWTFGQGTKEIKR 108
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Db 1 DIQLTQSPSSLASVGDRTITCRANEQLSNVLNMYQKPKAPKVLIVFTSSLHSGVPS 60  
Qy 61 RESGSGGTDTLTITSSLOPEDPATYCHQYSKLPWTFQGTKEIKR 108  
Db 61 RESGSGGTDTLTITSSLOPEDPATYCHQYSKLPWTFQGTKEIKR 108

Search completed: April 6, 2006, 08:51:30  
Job time : 6.7132 secs

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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model  
Run on: April 6, 2006, 08:53:30 ; Search time 19.3152 Seconds  
(without alignments)  
2336.277 Million cell updates/sec

Title: US-10-089-500-10  
Perfect score: 574  
Sequence: 1 DIQMTQSPSSLSASVGRVT.....HQYSKLPWTFGGTKVEIKR 108

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA Main:  
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2: /cgn2\_6/ptodata/1/pubpaa/us08\_PUBCOMB.pep.\*  
3: /cgn2\_6/ptodata/1/pubpaa/us09\_PUBCOMB.pep.\*  
4: /cgn2\_6/ptodata/1/pubpaa/us10A\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/1/pubpaa/us10B\_PUBCOMB.pep.\*  
6: /cgn2\_6/ptodata/1/pubpaa/us11\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	533	92.9	110	3	US-09-056-160B-103
2	533	92.9	110	4	US-10-234-671-101
3	533	92.9	110	5	US-10-974-591-101
4	533	92.9	237	3	US-09-056-160B-100
5	533	92.9	237	4	US-10-234-671-100
6	533	92.9	237	5	US-10-974-591-100
7	533	92.9	491	4	US-10-011-125-2
8	531	92.5	107	3	US-09-056-160B-15
9	531	92.5	107	4	US-10-234-671-15
10	531	92.5	107	5	US-10-974-591-15
11	530	92.3	110	3	US-09-056-160B-105
12	530	92.3	110	4	US-10-234-671-103
13	530	92.3	110	5	US-10-974-591-103
14	529	92.2	108	3	US-09-056-160B-8
15	529	92.2	108	4	US-10-153-159-2
16	529	92.2	108	4	US-10-153-159-16
17	529	92.2	108	4	US-10-153-176-2
18	529	92.2	108	4	US-10-153-176-16
19	529	92.2	108	4	US-10-443-134A-2
20	529	92.2	108	4	US-10-443-134A-16
21	529	92.2	108	4	US-10-443-134A-127
22	529	92.2	108	5	US-10-877-532-7
23	529	92.2	110	4	US-10-234-671-8
24	529	92.2	110	4	US-10-624-153-94
25	529	92.2	110	5	US-10-683-043-1
26	529	92.2	110	5	US-10-974-591-8
27	529	92.2	667	5	US-10-764-428-25

28	527	91.8	107	3	US-09-056-160B-13	Sequence 13, Appl
29	527	91.8	107	4	US-10-234-671-13	Sequence 13, Appl
30	527	91.8	107	5	US-10-974-591-13	Sequence 13, Appl
31	526	91.6	108	4	US-10-153-159-4	Sequence 4, Appl
32	526	91.6	108	4	US-10-153-176-4	Sequence 4, Appl
33	526	91.6	110	3	US-09-056-160B-107	Sequence 107, App
34	526	91.6	110	3	US-09-056-160B-117	Sequence 117, App
35	526	91.6	110	4	US-10-234-671-105	Sequence 105, App
36	526	91.6	110	4	US-10-234-671-115	Sequence 115, App
37	526	91.6	110	5	US-10-683-043-5	Sequence 5, Appl
38	526	91.6	110	5	US-10-974-591-105	Sequence 105, App
39	526	91.6	110	5	US-10-974-591-115	Sequence 115, App
40	526	91.6	213	4	US-10-379-392-135	Sequence 135, App
41	526	91.6	213	4	US-10-379-392-137	Sequence 137, App
42	526	91.6	213	4	US-10-379-392-139	Sequence 139, App
43	526	91.6	214	4	US-10-364-953-1	Sequence 1, Appl
44	526	91.6	237	4	US-10-020-786-10	Sequence 10, Appl
45	526	91.6				

## ALIGNMENTS

RESULT 1

US-09-056-160B-103  
; Sequence 103, Application US/09056160B  
; Patent No. US2002003315A1  
; GENERAL INFORMATION:  
; APPLICANT: Baca, Manuel  
; APPLICANT: Wells, James A.  
; APPLICANT: Presta, Leonard G.  
; APPLICANT: Lowman, Henry B.  
; APPLICANT: Chen, Yvonne M.  
; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES  
; NUMBER OF SEQUENCES: 131  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/056.160B  
; FILING DATE: 06-Apr-1998  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/054,856  
; FILING DATE: 06-AUG-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hasak, Janet E.  
; REGISTRATION NUMBER: 28,616  
; REFERENCE/DOCKET NUMBER: P1093R2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-1896  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 103:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 110 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
US-09-056-160B-103

Query Match 92.9%; Score 533; DB 3; Length 110;  
Best Local Similarity 91.7%; Pred. No. 5.6e-37;  
Matches 99; Conservative 6; Mismatches 3; Indels 0; Gaps 0;  
QY 1 DIQMTQSPSSLSASVGRVTITCSASQDISNLYNQKPGKAPKLLIFYSNLSHGVP 60





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;
; REGISTRATION NUMBER: 44,637
; REFERENCE/DOCKET NUMBER: P1093PID1C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-8674
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 100:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 237 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 100:
US-10-974-591-100

Query Match          92.9%; Score 533; DB 5; Length 237;
Best Local Similarity 91.7%; Pred. No. 1.2e-36;
Matches 99; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNLYNWYQKPGKAPKLLIFYSSNLHSGVPS 60
Db 24 DIQLTQSPSSLSASVGDRTVITCSASQDISNLYNWYQKPGKAPKLLIFYTSSLHSGVPS 83

Qy 61 RFGSGSGTDYTLTISSLPEDFATYYCHQYSKLPWTFGQGTKEIKR 108
Db 84 RFGSGSGTDYTLTISSLPEDFATYYCQYSTVPWTFGQGTKEIKR 131

RESULT 7
US-10-011-125-2
; Sequence 2, Application US/10011125
; Publication No. US20020142388A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Christina Yu-Ching
; TITLE OF INVENTION: BACTERIAL HOST STRAINS
; FILE REFERENCE: P1804R1
; CURRENT APPLICATION NUMBER: US/10/011,125
; CURRENT FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: US 60/256,162
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 10
; SEQ ID NO 2
; LENGTH: 491
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized.
US-10-011-125-2

Query Match          92.9%; Score 533; DB 4; Length 491;
Best Local Similarity 91.7%; Pred. No. 2.3e-36;
Matches 99; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNLYNWYQKPGKAPKLLIFYSSNLHSGVPS 60
Db 24 DIQLTQSPSSLSASVGDRTVITCSASQDISNLYNWYQKPGKAPKLLIFYTSSLHSGVPS 83

Qy 61 RFGSGSGTDYTLTISSLPEDFATYYCHQYSKLPWTFGQGTKEIKR 108
Db 84 RFGSGSGTDYTLTISSLPEDFATYYCQYSTVPWTFGQGTKEIKR 131

RESULT 8
US-09-056-160B-15
; Sequence 15, Application US/09056160B
; Patent No. US20020032315A1
; GENERAL INFORMATION:
; APPLICANT: Baca, Manuel
; APPLICANT: Welle, James A.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Lowman, Henry B.
; APPLICANT: Chen, Yvonne M.
; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
; NUMBER OF SEQUENCES: 131
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; City: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/234,671
; FILING DATE: 03-Sep-2002
; CLASSIFICATION: <Unknown>
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;
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/056,160B
; FILING DATE: 06-Apr-1998
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/054,856
; FILING DATE: 06-AUG-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hasak, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: P1093R2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1896
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-09-056-160B-15

Query Match          92.5%; Score 531; DB 3; Length 107;
Best Local Similarity 92.5%; Pred. No. 8.1e-37;
Matches 99; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNLYNWYQKPGKAPKLLIFYSSNLHSGVPS 60
Db 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNLYNWYQKPGKAPKLLIFYTSSLHSGVPS 60

Qy 61 RFGSGSGTDYTLTISSLPEDFATYYCHQYSKLPWTFGQGTKEIK 107
Db 61 RFGSGSGTDYTLTISSLPEDFATYYCQYSTVPWTFGQGTKEIK 107

RESULT 9
US-10-234-671-15
; Sequence 15, Application US/10234671
; Publication No. US20030190317A1
; GENERAL INFORMATION:
; APPLICANT: Baca, Manuel
; APPLICANT: Welle, James A.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Lowman, Henry B.
; APPLICANT: Chen, Yvonne M.
; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
; NUMBER OF SEQUENCES: 131
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; City: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/234,671
; FILING DATE: 03-Sep-2002
; CLASSIFICATION: <Unknown>
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/056160
; FILING DATE: 06-APR-1998
; APPLICATION NUMBER: 60/126446
; FILING DATE: 07-APR-1997
; APPLICATION NUMBER: 60/054856
; FILING DATE: 06-AUG-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Cui, Steven X.
; REGISTRATION NUMBER: 44,637
; REFERENCE/DOCKET NUMBER: P1093R2C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-8674
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-10-234-671-15

Query Match          92.5%; Score 531; DB 4; Length 107;
Best Local Similarity 92.5%; Pred. No. 8.1e-37;
Matches 99; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNLYNMYQQKPGKAPKLLIFYSNLSHGVP 60
DB 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNLYNMYQQKPGKAPKLLIFYSNLSHGVP 60
QY 61 RFGSGSGTDYTLTISSLPEDPATYVCHQYKSLPWTFGQGTKEIK 107
DB 61 RFGSGSGTDYTLTISSLPEDPATYVCHQYKSLPWTFGQGTKEIK 107

RESULT 10
US-10-974-591-15
; Sequence 15, Application US/10974591
; Publication No. US20050112126A1
; GENERAL INFORMATION:
; APPLICANT: Baca, Manuel
; APPLICANT: Wells, James A.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Lowman, Henry B.
; APPLICANT: Chen, Yvonne M.
; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
; NUMBER OF SEQUENCES: 131
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/974,591
; FILING DATE: 26-Oct-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/723752
; FILING DATE: 27-NOV-2000
; APPLICATION NUMBER: 08/908469
; FILING DATE: 06-AUG-1997
; APPLICATION NUMBER: 08/833504
; FILING DATE: 07-APR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Cui, Steven X.
; REGISTRATION NUMBER: 44,637

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; REFERENCE/DOCKET NUMBER: P1093PID1C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-8674
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-10-974-591-15

Query Match          92.5%; Score 531; DB 5; Length 107;
Best Local Similarity 92.5%; Pred. No. 8.1e-37;
Matches 99; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNLYNMYQQKPGKAPKLLIFYSNLSHGVP 60
DB 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNLYNMYQQKPGKAPKLLIFYSNLSHGVP 60
QY 61 RFGSGSGTDYTLTISSLPEDPATYVCHQYKSLPWTFGQGTKEIK 107
DB 61 RFGSGSGTDYTLTISSLPEDPATYVCHQYKSLPWTFGQGTKEIK 107

RESULT 11
US-09-056-160B-105
; Sequence 105, Application US/09056160B
; Patent No. US20020032315A1
; GENERAL INFORMATION:
; APPLICANT: Baca, Manuel
; APPLICANT: Wells, James A.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Lowman, Henry B.
; APPLICANT: Chen, Yvonne M.
; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
; NUMBER OF SEQUENCES: 131
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/056,160B
; FILING DATE: 06-Apr-1998
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/054,856
; FILING DATE: 06-AUG-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hsiao, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: P1093R2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1896
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 105:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 110 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 105:
US-09-056-160B-105

Query Match          92.3%; Score 530; DB 3; Length 110;
Best Local Similarity 90.7%; Pred. No. 1e-36;
Matches 98; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

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; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
; NUMBER OF SEQUENCES: 131
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/056,160B
; FILING DATE: 06-Apr-1998
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/054,856
; FILING DATE: 06-AUG-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hasak, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: P1093R2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1896
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
;
US-09-056-160B-8

Query Match 92.2%; Score 529; DB 3; Length 108;
Best Local Similarity 90.7%; Pred. No. 1.2e-36;
Matches 98; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNWYQOKPGKAPKLLIFYSSNLHSGVPS 60
Db 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNWYQOKPGKAPKLLIFYSSNLHSGVPS 60

QY 61 RFGSGSGTDYTLTISSLPEDFATYYCHQYSKLPWTFGQGTKVEIKR 108
Db 61 RFGSGSGTDFTLTITSSLPEDFATYYCQYSTVPWFQGTQKVEIKR 108

Search completed: April 6, 2006, 08:56:21
Job time : 19.3152 secs

; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
; NUMBER OF SEQUENCES: 131
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/056,160B
; FILING DATE: 06-Apr-1998
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/054,856
; FILING DATE: 06-AUG-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hasak, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: P1093R2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1896
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
;
US-09-056-160B-8

Query Match 92.2%; Score 529; DB 3; Length 108;
Best Local Similarity 90.7%; Pred. No. 1.2e-36;
Matches 98; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNWYQOKPGKAPKLLIFYSSNLHSGVPS 60
Db 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNWYQOKPGKAPKLLIFYSSNLHSGVPS 60

QY 61 RFGSGSGTDYTLTISSLPEDFATYYCHQYSKLPWTFGQGTKVEIKR 108
Db 61 RFGSGSGTDFTLTITSSLPEDFATYYCQYSTVPWFQGTQKVEIKR 108

RESULT 15
US-10-153-159-2
; Sequence 2, Application US/10153159
; Publication No. US20020177170A1
; GENERAL INFORMATION:
; APPLICANT: Luo, Peter
; APPLICANT: Hsieh, Mark
; APPLICANT: Zhong, Pingyu
; APPLICANT: Wang, Caili
; TITLE OF INVENTION: STRUCTURE-BASED SELECTION AND AFFINITY MATURATION OF ANTIBODY LIBRARY
; TITLE OF INVENTION: SILICO
; FILE REFERENCE: 26050-704
; CURRENT APPLICATION NUMBER: US/10/153,159
; CURRENT FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: US 10/125,687
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: US 60/284,407
; PRIOR FILING DATE: 2001-04-17
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 2
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

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(without alignments)  
893.845 Million cell updates/sec

Title: US-10-089-500-10  
Perfect score: 574  
Sequence: 1 DIQMTQSPSSLSASVGRVT.....HOYSKLPWTFGGTKVEIKR 108

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 184161 seqs, 31191982 residues

Total number of hits satisfying chosen parameters: 184161

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

- Database : Published Applications AA New:\*
- 1: /SIDSS/ptodaca/2/pubpaa/US08\_NEW\_PUB pep.\*
  - 2: /SIDSS/ptodaca/2/pubpaa/US06\_NEW\_PUB pep.\*
  - 3: /SIDSS/ptodaca/2/pubpaa/US07\_NEW\_PUB pep.\*
  - 4: /SIDSS/ptodaca/2/pubpaa/PCT\_NEW\_PUB pep.\*
  - 5: /SIDSS/ptodaca/2/pubpaa/US05\_NEW\_PUB pep.\*
  - 6: /SIDSS/ptodaca/2/pubpaa/US10\_NEW\_PUB pep.\*
  - 7: /SIDSS/ptodaca/2/pubpaa/US11\_NEW\_PUB pep.\*
  - 8: /SIDSS/ptodaca/2/pubpaa/US60\_NEW\_PUB pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	557	97.0	108	US-10-473-037-10	Sequence 10, Appl
2	529	92.2	108	US-11-208-422-9	Sequence 9, Appl
3	529	92.2	110	US-10-648-816-1	Sequence 1, Appl
4	526	91.6	108	US-11-208-422-11	Sequence 11, Appl
5	526	91.6	110	US-10-648-816-5	Sequence 5, Appl
6	507	88.3	110	US-10-648-816-2	Sequence 2, Appl
7	507	88.3	110	US-10-648-816-3	Sequence 3, Appl
8	507	88.3	110	US-10-648-816-4	Sequence 4, Appl
9	507	88.3	110	US-10-648-816-6	Sequence 6, Appl
10	507	88.3	110	US-10-648-816-7	Sequence 7, Appl
11	507	88.3	110	US-10-648-816-8	Sequence 8, Appl
12	506	88.2	214	US-11-025-712-11	Sequence 11, Appl
13	503	87.6	214	US-11-183-205-55	Sequence 55, Appl
14	501	87.3	108	US-10-665-658-3	Sequence 3, Appl
15	501	87.3	108	US-11-120-338-3	Sequence 3, Appl
16	501	87.3	108	US-11-143-077-3	Sequence 3, Appl
17	501	87.3	108	US-11-190-364-3	Sequence 3, Appl
18	501	87.3	108	US-11-147-780-3	Sequence 3, Appl
19	501	87.3	108	US-11-143-386-3	Sequence 3, Appl
20	501	87.3	108	US-11-187-364-3	Sequence 3, Appl
21	501	87.3	109	US-10-981-356A-5	Sequence 5, Appl
22	501	87.3	109	US-11-096-046-5	Sequence 5, Appl
23	498	86.8	107	US-11-183-205-51	Sequence 51, Appl
24	496	86.4	107	US-11-154-337-5	Sequence 5, Appl
25	496	86.4	107	US-11-182-908-5	Sequence 5, Appl

26	496	86.4	107	7	US-11-102-120-5	Sequence 5, Appl
27	496	86.4	107	7	US-11-223-361-5	Sequence 5, Appl
28	496	86.4	108	7	US-11-106-820-3	Sequence 3, Appl
29	494	86.1	108	6	US-10-473-037-50	Sequence 50, Appl
30	494	86.1	128	6	US-10-473-037-2	Sequence 2, Appl
31	494	86.1	128	7	US-11-228-293-10	Sequence 10, Appl
32	494	86.1	128	7	US-11-228-293-19	Sequence 19, Appl
33	494	86.1	128	7	US-11-228-319-10	Sequence 10, Appl
34	494	86.1	128	7	US-11-228-319-19	Sequence 19, Appl
35	487	84.8	108	7	US-11-049-536-184	Sequence 184, App
36	487	84.8	109	7	US-11-199-739-184	Sequence 184, App
37	482	84.0	109	7	US-11-127-932-14	Sequence 14, Appl
38	482	84.0	109	7	US-11-127-932-18	Sequence 18, Appl
39	482	84.0	109	7	US-11-127-903-14	Sequence 14, Appl
40	482	84.0	109	7	US-11-127-903-18	Sequence 18, Appl
41	481	83.8	108	6	US-10-834-397-14	Sequence 14, Appl
42	479	83.4	112	7	US-11-127-932-15	Sequence 15, Appl
43	479	83.4	112	7	US-11-127-903-15	Sequence 15, Appl
44	478	83.3	109	7	US-11-102-201-2	Sequence 2, Appl
45	478	83.3	127	7	US-11-193-512-71	Sequence 71, Appl

ALIGNMENTS

RESULT 1

US-10-473-037-10  
; Sequence 10, Application US/10473037  
; Publication No. US20050260206A1  
; GENERAL INFORMATION:  
; APPLICANT: KYOWA HAKKO KOGYO CO., LTD.  
; TITLE OF INVENTION: Agents for treatment of cancer using recombinant anti-GD3 antitumor antibody  
; FILE REFERENCE: 11374WO1  
; CURRENT APPLICATION NUMBER: US/10/473,037  
; CURRENT FILING DATE: 2003-09-26  
; PRIOR APPLICATION NUMBER: JP2001-097483  
; PRIOR FILING DATE: 2001-03-29  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 10  
; LENGTH: 108  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:synthetic protein  
US-10-473-037-10

Query Match	97.0%	Score 557;	DB 6;	Length 108;
Best Local Similarity	97.2%	Pred. No. 2e+41;		
Matches 105;	Conservative 1;	Mismatches 2;	Indels 0;	Gaps 0;
Qy	1	DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQOKPGKAPKLLIFYSNLSHGVP	60	
Db	1	DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQOKPGKAPKLLIFYSNLSHGVP	60	
Qy	61	RFSGGSGGTDYTLTSSLPQEDFATYCHQYSKLPWTFGGTKVEIKR	108	
Db	61	RFSGGSGGTDYTLTSSLPQEDFATYCHQYSKLPWTFGGTKVEIKR	108	

RESULT 2

US-11-208-422-9  
; Sequence 9, Application US/11208422  
; Publication No. US20060067930A1  
; GENERAL INFORMATION:  
; APPLICANT: Adams, Camellia W.  
; APPLICANT: Lien, Samantha  
; APPLICANT: Lowman, Henry B.  
; APPLICANT: Marvin, Jonathan S.  
; APPLICANT: Meng, Yu-Ju G.  
; TITLE OF INVENTION: POLYPEPTIDE VARIANTS WITH ALTERED EFFECTOR FUNCTION  
; FILE REFERENCE: P2158R1

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; CURRENT APPLICATION NUMBER: US/11/208,422
; CURRENT FILING DATE: 2005-08-19
; PRIOR APPLICATION NUMBER: US 60/603,057
; PRIOR FILING DATE: 2004-08-19
; NUMBER OF SEQ ID NOS: 54
; SEQ ID NO 9
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized
US-11-208-422-9

```

```

Query Match          92.2%; Score 529; DB 7; Length 108;
Best Local Similarity 90.7%; Pred. No. 5e-39;
Matches 98; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNWYQKPGKAPKLLIFYSNLSHGVP 60
Db 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNWYQKPGKAPKLLIFYSNLSHGVP 60

QY 61 RFGSGSGTDYTLTISSLPEDFATYYCHOYSKLPWTFGQGTKEIKR 108
Db 61 RFGSGSGTDYTLTISSLPEDFATYYCQYSTVPWTFGQGTKEIKR 108

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RESULT 3
US-10-648-816-1
; Sequence 1, Application US/10648816
; Publication No. US2005024405A1
; GENERAL INFORMATION:
; APPLICANT: Van Bruggen, Nicholas
; APPLICANT: Ferrara, Napoleone
; TITLE OF INVENTION: Vascular Endothelial Cell Growth Factor Antagonists
; TITLE OF INVENTION: and Uses Thereof
; FILE REFERENCE: P1717D1
; CURRENT APPLICATION NUMBER: US/10/648,816
; CURRENT FILING DATE: 2003-08-26
; PRIOR APPLICATION NUMBER: US/09/718,694
; PRIOR FILING DATE: 2000-11-21
; PRIOR APPLICATION NUMBER: US 09/218,481
; PRIOR FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 16
; SEQ ID NO 1
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-648-816-1

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Query Match          92.2%; Score 529; DB 6; Length 110;
Best Local Similarity 90.7%; Pred. No. 5.1e-39;
Matches 98; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNWYQKPGKAPKLLIFYSNLSHGVP 60
Db 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNWYQKPGKAPKLLIFYSNLSHGVP 60

QY 61 RFGSGSGTDYTLTISSLPEDFATYYCHOYSKLPWTFGQGTKEIKR 108
Db 61 RFGSGSGTDYTLTISSLPEDFATYYCQYSTVPWTFGQGTKEIKR 108

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RESULT 4
US-11-208-422-11
; Sequence 11, Application US/11208422
; Publication No. US20060067930A1
; GENERAL INFORMATION:
; APPLICANT: Adams, Camellia W.
; APPLICANT: Lien, Samantha
; APPLICANT: Lowman, Henry B.
; APPLICANT: Marvin, Jonathan S.
; APPLICANT: Meng, Yu-Ju G.
; TITLE OF INVENTION: POLYPEPTIDE VARIANTS WITH ALTERED EFFECTOR FUNCTION

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; FILE REFERENCE: P2158R1
; CURRENT APPLICATION NUMBER: US/11/208,422
; CURRENT FILING DATE: 2005-08-19
; PRIOR APPLICATION NUMBER: US 60/603,057
; PRIOR FILING DATE: 2004-08-19
; NUMBER OF SEQ ID NOS: 54
; SEQ ID NO 11
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized
US-11-208-422-11

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Query Match          91.6%; Score 526; DB 7; Length 108;
Best Local Similarity 89.8%; Pred. No. 9.1e-39;
Matches 97; Conservative 8; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNWYQKPGKAPKLLIFYSNLSHGVP 60
Db 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNWYQKPGKAPKLLIFYSNLSHGVP 60

QY 61 RFGSGSGTDYTLTISSLPEDFATYYCHOYSKLPWTFGQGTKEIKR 108
Db 61 RFGSGSGTDYTLTISSLPEDFATYYCQYSTVPWTFGQGTKEIKR 108

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RESULT 5
US-10-648-816-5
; Sequence 5, Application US/10648816
; Publication No. US2005024405A1
; GENERAL INFORMATION:
; APPLICANT: Van Bruggen, Nicholas
; APPLICANT: Ferrara, Napoleone
; TITLE OF INVENTION: Vascular Endothelial Cell Growth Factor Antagonists
; TITLE OF INVENTION: and Uses Thereof
; FILE REFERENCE: P1717D1
; CURRENT APPLICATION NUMBER: US/10/648,816
; CURRENT FILING DATE: 2003-08-26
; PRIOR APPLICATION NUMBER: US/09/718,694
; PRIOR FILING DATE: 2000-11-21
; PRIOR APPLICATION NUMBER: US 09/218,481
; PRIOR FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 16
; SEQ ID NO 5
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-648-816-5

```

```

Query Match          91.6%; Score 526; DB 6; Length 110;
Best Local Similarity 89.8%; Pred. No. 9.2e-39;
Matches 97; Conservative 8; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNWYQKPGKAPKLLIFYSNLSHGVP 60
Db 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNWYQKPGKAPKLLIFYSNLSHGVP 60

QY 61 RFGSGSGTDYTLTISSLPEDFATYYCHOYSKLPWTFGQGTKEIKR 108
Db 61 RFGSGSGTDYTLTISSLPEDFATYYCQYSTVPWTFGQGTKEIKR 108

```

```

RESULT 6
US-10-648-816-2
; Sequence 2, Application US/10648816
; Publication No. US2005024405A1
; GENERAL INFORMATION:
; APPLICANT: Van Bruggen, Nicholas
; APPLICANT: Ferrara, Napoleone
; TITLE OF INVENTION: Vascular Endothelial Cell Growth Factor Antagonists
; TITLE OF INVENTION: and Uses Thereof
; FILE REFERENCE: P1717D1

```

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; CURRENT APPLICATION NUMBER: US/10/648,816
; CURRENT FILING DATE: 2003-08-26
; PRIOR APPLICATION NUMBER: US/09/718,694
; PRIOR FILING DATE: 2000-11-21
; PRIOR APPLICATION NUMBER: US 09/218,481
; PRIOR FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 16
; SEQ ID NO 2
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-648-816-2

Query Match      88.3%; Score 507; DB 6; Length 110;
Best Local Similarity 85.2%; Pred. No. 3.9e-37;
Matches 92; Conservative 11; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNWYQKPGKAPKLLIFYSSNLHSGVPS 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 DIQLTQSPSSLSASVGDRTVITCRANEQLSNYLNWYQKPGKAPKLLIFYTSSLHSGVPS 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 RFSGGSGTDYTLTISSLOPEDFATYCHQYSKLPWTFGQGTKEIKR 108
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 RFSGGSGTDFTLTISLQPEDFATYCCQYSTVPWTFGQGTKEIKR 108
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 7
US-10-648-816-3
; Sequence 3, Application US/10648816
; Publication No. US2005024405A1
; GENERAL INFORMATION:
; APPLICANT: Van Bruggen, Nicholas
; APPLICANT: Ferrara, Napoleone
; TITLE OF INVENTION: Vascular Endothelial Cell Growth Factor Antagonists
; FILE OF INVENTION: and Uses Thereof
; FILE REFERENCE: P1717D1
; CURRENT APPLICATION NUMBER: US/10/648,816
; CURRENT FILING DATE: 2003-08-26
; PRIOR APPLICATION NUMBER: US/09/718,694
; PRIOR FILING DATE: 2000-11-21
; PRIOR APPLICATION NUMBER: US 09/218,481
; PRIOR FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 16
; SEQ ID NO 3
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-648-816-3

Query Match      88.3%; Score 507; DB 6; Length 110;
Best Local Similarity 85.2%; Pred. No. 3.9e-37;
Matches 92; Conservative 11; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNWYQKPGKAPKLLIFYSSNLHSGVPS 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 DIQLTQSPSSLSASVGDRTVITCRANEQLSNYLNWYQKPGKAPKLLIFYTSSLHSGVPS 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 RFSGGSGTDYTLTISSLOPEDFATYCHQYSKLPWTFGQGTKEIKR 108
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 RFSGGSGTDFTLTISLQPEDFATYCCQYSTVPWTFGQGTKEIKR 108
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 8
US-10-648-816-4
; Sequence 4, Application US/10648816
; Publication No. US2005024405A1
; GENERAL INFORMATION:
; APPLICANT: Van Bruggen, Nicholas
; APPLICANT: Ferrara, Napoleone
; TITLE OF INVENTION: Vascular Endothelial Cell Growth Factor Antagonists
; FILE OF INVENTION: and Uses Thereof
; FILE REFERENCE: P1717D1
; CURRENT APPLICATION NUMBER: US/10/648,816
; CURRENT FILING DATE: 2003-08-26
; PRIOR APPLICATION NUMBER: US/09/718,694
; PRIOR FILING DATE: 2000-11-21
; PRIOR APPLICATION NUMBER: US 09/218,481
; PRIOR FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 16
; SEQ ID NO 4
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-648-816-4

Query Match      88.3%; Score 507; DB 6; Length 110;
Best Local Similarity 85.2%; Pred. No. 3.9e-37;
Matches 92; Conservative 11; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNWYQKPGKAPKLLIFYSSNLHSGVPS 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 DIQLTQSPSSLSASVGDRTVITCRANEQLSNYLNWYQKPGKAPKLLIFYTSSLHSGVPS 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 RFSGGSGTDYTLTISSLOPEDFATYCHQYSKLPWTFGQGTKEIKR 108
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 RFSGGSGTDFTLTISLQPEDFATYCCQYSTVPWTFGQGTKEIKR 108
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 9
US-10-648-816-6
; Sequence 6, Application US/10648816
; Publication No. US2005024405A1
; GENERAL INFORMATION:
; APPLICANT: Van Bruggen, Nicholas
; APPLICANT: Ferrara, Napoleone
; TITLE OF INVENTION: Vascular Endothelial Cell Growth Factor Antagonists
; FILE OF INVENTION: and Uses Thereof
; FILE REFERENCE: P1717D1
; CURRENT APPLICATION NUMBER: US/10/648,816
; CURRENT FILING DATE: 2003-08-26
; PRIOR APPLICATION NUMBER: US/09/718,694
; PRIOR FILING DATE: 2000-11-21
; PRIOR APPLICATION NUMBER: US 09/218,481
; PRIOR FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 16
; SEQ ID NO 6
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-648-816-6

Query Match      88.3%; Score 507; DB 6; Length 110;
Best Local Similarity 85.2%; Pred. No. 3.9e-37;
Matches 92; Conservative 11; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNWYQKPGKAPKLLIFYSSNLHSGVPS 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 DIQLTQSPSSLSASVGDRTVITCRANEQLSNYLNWYQKPGKAPKLLIFYTSSLHSGVPS 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 RFSGGSGTDYTLTISSLOPEDFATYCHQYSKLPWTFGQGTKEIKR 108
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 RFSGGSGTDFTLTISLQPEDFATYCCQYSTVPWTFGQGTKEIKR 108
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 10
US-10-648-816-7
; Sequence 7, Application US/10648816
; Publication No. US2005024405A1
; GENERAL INFORMATION:
; APPLICANT: Van Bruggen, Nicholas
; APPLICANT: Ferrara, Napoleone
; TITLE OF INVENTION: Vascular Endothelial Cell Growth Factor Antagonists
; FILE OF INVENTION: and Uses Thereof
; FILE REFERENCE: P1717D1
; CURRENT APPLICATION NUMBER: US/10/648,816
; CURRENT FILING DATE: 2003-08-26
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; PRIOR APPLICATION NUMBER: US/09/718,694
; PRIOR FILING DATE: 2000-11-21
; PRIOR APPLICATION NUMBER: US 09/218,481
; PRIOR FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 16
; SEQ ID NO 7
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-648-816-7

Query Match      88.3%; Score 507; DB 6; Length 110;
Best Local Similarity 85.2%; Pred. No. 3.9e-37;
Matches 92; Conservative 11; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRVTITCSASQDISNLYNQKPGKAPKLLIFYSNLSHGVP 60
DB 1 DIQLTQSPSSLSASVGDRVTITCRANEQLSNLYNQKPGKAPKLLIFTSSLHSGVP 60

QY 61 RFGSGSGTDYTLTISSLPEDFATYYCHQYKLPWTFGQTKVEIKR 108
DB 61 RFGSGSGTDYTLTISSLPEDFATYYCQYSTVPTWTFGQTKVEIKR 108

RESULT 11
US-10-648-816-8
; Sequence 8, Application US/10648816
; Publication No. US2005024405A1
; GENERAL INFORMATION:
; APPLICANT: Van Bruggen, Nicholas
; APPLICANT: Ferrara, Napoleone
; TITLE OF INVENTION: Vascular Endothelial Cell Growth Factor Antagonists
; TITLE OF INVENTION: and Uses Thereof
; FILE REFERENCE: P1717D1
; CURRENT APPLICATION NUMBER: US/10/648,816
; CURRENT FILING DATE: 2003-08-26
; PRIOR APPLICATION NUMBER: US/09/718,694
; PRIOR FILING DATE: 2000-11-21
; PRIOR APPLICATION NUMBER: US 09/218,481
; PRIOR FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 16
; SEQ ID NO 8
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-648-816-8

Query Match      88.3%; Score 507; DB 6; Length 110;
Best Local Similarity 85.2%; Pred. No. 3.9e-37;
Matches 92; Conservative 11; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRVTITCSASQDISNLYNQKPGKAPKLLIFYSNLSHGVP 60
DB 1 DIQLTQSPSSLSASVGDRVTITCRANEQLSNLYNQKPGKAPKLLIFTSSLHSGVP 60

QY 61 RFGSGSGTDYTLTISSLPEDFATYYCHQYKLPWTFGQTKVEIKR 108
DB 61 RFGSGSGTDYTLTISSLPEDFATYYCQYSTVPTWTFGQTKVEIKR 108

RESULT 12
US-11-025-712-11
; Sequence 11, Application US/11025712
; Publication No. US20050255108A1
; GENERAL INFORMATION:
; APPLICANT: Bednar, Martin M.
; APPLICANT: Thomas, G. Roger
; APPLICANT: Gross, Cordell E.
; TITLE OF INVENTION: ANTI-CD18 ANTIBODIES IN STROKE
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way

```

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; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/025,712
; FILING DATE: 28-Dec-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/10/404,286
; FILING DATE: 31-Mar-2003
; APPLICATION NUMBER: 09/811384
; FILING DATE: 20-DEC-2000
; APPLICATION NUMBER: 09/251652
; FILING DATE: 17-FEB-2000
; APPLICATION NUMBER: 08/788800
; FILING DATE: 22-JAN-1997
; APPLICATION NUMBER: 60/093038
; FILING DATE: 23-JAN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Evans, David W.
; REGISTRATION NUMBER: NONE
; REFERENCE/DOCKET NUMBER: P1729C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1739
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 214 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-11-025-712-11

Query Match      88.2%; Score 506; DB 7; Length 214;
Best Local Similarity 89.8%; Pred. No. 8.6e-37;
Matches 97; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRVTITCSASQDISNLYNQKPGKAPKLLIFYSNLSHGVP 60
DB 1 DIQMTQSPSSLSASVGDRVTITCRASQDINNLYNQKPGKAPKLLIYTTSLHSGVP 60

QY 61 RFGSGSGTDYTLTISSLPEDFATYYCHQYKLPWTFGQTKVEIKR 108
DB 61 RFGSGSGTDYTLTISSLPEDFATYYCQGNLTLPPTFGQTKVEIKR 108

RESULT 13
US-11-183-205-55
; Sequence 55, Application US/11183205
; Publication No. US20060030521A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: Defrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Bove, Caryn
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; TITLE OF INVENTION: REMODELING AND GLYCOCONJUGATION OF PEPTIDES
; FILE REFERENCE: 040853-01-5052-US01
; CURRENT APPLICATION NUMBER: US/11/183,205
; CURRENT FILING DATE: 2005-07-15
; PRIOR APPLICATION NUMBER: US 11/183,205
; PRIOR FILING DATE: 2005-07-15
; PRIOR APPLICATION NUMBER: US 60/334,233
; PRIOR FILING DATE: 2001-11-28
; PRIOR APPLICATION NUMBER: US 60/334,301

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; PRIOR FILING DATE: 2001-11-28
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: PCT/US2002/032263
; PRIOR FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US 10/287,994
; PRIOR FILING DATE: 2002-11-05
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 55
; LENGTH: 214
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-183-205-55

Query Match      87.6%; Score 503; DB 7; Length 214;
Best Local Similarity 85.2%; Pred. No. 1.6e-36;
Matches 92; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQKPKAPKLLIFYSSNLHSGVPS 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQKPKAPKLLIYTTSTLHSGVPS 60

Qy 61 RFSGSGGTDTLTITSSLOPEDPATYCHQYKSLPWTFGQGTKEIKR 108
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 RFSGSGGTDTLTITSSLOPEDPATYCHQYKSLPWTFGQGTKEIKR 108

RESULT 14
US-10-665-658-3
; Sequence 3, Application US/10665658
; Publication NO. US20050276801A1
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
; NUMBER OF SEQUENCES: 71
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/665,658
; FILING DATE: 19-Sep-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/031971
; FILING DATE: 27-NOV-1996
; APPLICATION NUMBER: 08/974899
; FILING DATE: 20-NOV-1997
; APPLICATION NUMBER: 09/420745
; FILING DATE: 20-OCT-1999
; APPLICATION NUMBER: 09/975798
; FILING DATE: 28-FEB-2001
; ATTORNEY/AGENT INFORMATION:
; NAME: Tan, Lee K.
; REGISTRATION NUMBER: 39,447

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; REFERENCE/DOCKET NUMBER: P1014R1C1D1C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-4462
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-665-658-3

Query Match      87.3%; Score 501; DB 6; Length 108;
Best Local Similarity 88.0%; Pred. No. 1.3e-36;
Matches 95; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQKPKAPKLLIFYSSNLHSGVPS 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQKPKAPKLLIYAASLSGVS 60

Qy 61 RFSGSGGTDTLTITSSLOPEDPATYCHQYKSLPWTFGQGTKEIKR 108
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 RFSGSGGTDTLTITSSLOPEDPATYCHQYKSLPWTFGQGTKEIKR 108

RESULT 15
US-11-120-338-3
; Sequence 3, Application US/11120338
; Publication NO. US20050271658A1
; GENERAL INFORMATION:
; APPLICANT: BRUNETTA, PAUL G.
; APPLICANT: GREWAL, IQBAL S.
; APPLICANT: WALICKS, PATRICIA A.
; TITLE OF INVENTION: PREVENTING AUTOIMMUNE DISEASE
; FILE REFERENCE: P2079R2
; CURRENT APPLICATION NUMBER: US/11/120,338
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: US 60/568,460
; PRIOR FILING DATE: 2004-05-05
; NUMBER OF SEQ ID NOS: 25
; SEQ ID NO 3
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-11-120-338-3

Query Match      87.3%; Score 501; DB 7; Length 108;
Best Local Similarity 88.0%; Pred. No. 1.3e-36;
Matches 95; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQKPKAPKLLIFYSSNLHSGVPS 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQKPKAPKLLIYAASLSGVS 60

Qy 61 RFSGSGGTDTLTITSSLOPEDPATYCHQYKSLPWTFGQGTKEIKR 108
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 RFSGSGGTDTLTITSSLOPEDPATYCHQYKSLPWTFGQGTKEIKR 108

Search completed: April 6, 2006, 08:55:06
Job time : 3.76881 secs

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GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: April 6, 2006, 08:47:08 ; Search time 130.109 Seconds  
(without alignments)  
1965.416 Million cell updates/sec

Title: US-10-089-500-53

Perfect score: 3071

Sequence: 1 EVQLVESGGDFVPGGSLRV.....IVEFLNRWTFQCSIIITLT 582

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq 21:\*

- 1: Geneseqp1980s:\*
- 2: Geneseqp1990s:\*
- 3: Geneseqp2000s:\*
- 4: Geneseqp2001s:\*
- 5: Geneseqp2002s:\*
- 6: Geneseqp2003as:\*
- 7: Geneseqp2003bs:\*
- 8: Geneseqp2004s:\*
- 9: Geneseqp2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3071	100.0	582	4 AAB81987	Aab81987 Gangliosi
2	3026	98.5	582	4 AAB81991	Aab81991 Gangliosi
3	2780.5	90.5	583	4 AAB83156	Aab83156 Gangliosi
4	2760.5	89.9	581	4 AAB81972	Aab81972 Gangliosi
5	2750.5	89.6	579	6 AAE33444	Aae33444 KS antibo
6	2750.5	89.6	579	6 AAO30910	Aao30910 di-KS-ala
7	2719.5	88.6	575	8 ADP42961	Adp42961 Humanised
8	2621	85.3	580	6 AAO30915	Aao30915 di-NHS76
9	2589	84.3	580	6 AAO30913	Aao30913 di-NHS76
10	2247	73.2	449	8 ADR23346	Adr23346 Human CD7
11	2246.5	73.2	447	6 AAE33522	Aae33522 Human AQC
12	2240.5	73.0	447	6 AAE33523	Aae33523 Human AQC
13	2238.5	72.9	449	5 AAO18400	Aao18400 Mature hu
14	2238.5	72.9	449	9 AEA36337	Aea36337 Human CBE
15	2238.5	72.9	697	8 ADQ07403	Adq07403 hCBE11/hB
16	2238.5	72.9	697	8 ADQ12180	Adq12180 Heavy cha
17	2238.5	72.9	701	8 ADQ07409	Adq07409 hCBE11 mo
18	2238.5	72.9	701	8 ADQ12186	Adq12186 Heavy cha
19	2237.5	72.9	448	9 ADW90319	Adw90319 Phage scf
20	2237.5	72.9	448	9 ADO01871	Ado01871 SARS coro
21	2236.5	72.8	447	6 AAE33524	Aae33524 Human AQC
22	2236.5	72.8	448	9 AEB46960	Aeb46960 CD1a spec
23	2236.5	72.8	450	8 ADH34587	Adh34587 023 heavy
24	2236	72.8	464	9 AEA41072	Aea41072 Human ant

25	2234.5	72.8	445	6 AAO31101	Aao31101 Human A2-
26	2233	72.7	449	6 ABP58273	Abp58273 Humanised
27	2233	72.7	468	6 ABP58275	Abp58275 Humanised
28	2232	72.7	451	8 ADH34584	Adh34584 008 heavy
29	2231.5	72.7	444	6 AAE35327	Aae35327 Humanised
30	2231.5	72.7	444	6 AAE34876	Aae34876 BIWA4/8 a
31	2231.5	72.7	444	8 ADL15443	Adl15443 Humanised
32	2231.5	72.7	444	8 ADO00851	Ado00851 Humanised
33	2231.5	72.7	444	9 AEB29789	Aeb29789 Humanised
34	2231.5	72.7	444	9 AEB29780	Aeb29780 Humanised
35	2231	72.6	451	9 ADX01865	Adx01865 SARS coro
36	2229.5	72.6	475	7 ADMA47075	Adma47075 Mouse ant
37	2229	72.6	451	8 ADP88494	Adp88494 Humanised
38	2229	72.6	470	9 AEA41070	Aea41070 Human ant
39	2226	72.5	449	3 AAY68810	Aay68810 A rat hea
40	2224	72.4	447	9 AEB46964	Aeb46964 CD1a spec
41	2222.5	72.4	450	9 ADX02216	Adx02216 SARS coro
42	2222.5	72.4	477	4 AAU14288	Aau14288 Human nov
43	2221.5	72.3	446	7 ADF11425	Adf11425 2D8 anti-
44	2220.5	72.3	448	9 AEB46956	Aeb46956 CD1a spec
45	2220	72.3	451	8 ADR23344	Adr23344 Human CD7

## ALIGNMENTS

RESULT 1  
AAB81987  
ID AAB81987 standard; protein; 582 AA.  
XX  
AC AAB81987;  
XX  
DT 03-JUL-2001 (first entry)  
XX  
DE Ganglioside GD3 specific antibody related protein SEQ ID NO: 53.  
XX  
KW Ganglioside; GD3; complementarity determining region; CDR; antibody;  
KW cancer.  
XX  
OS Synthetic.  
XX  
PN WC200123432-A1.  
XX  
PD 05-APR-2001.  
XX  
PF 29-SEP-2000; 2000WO-JP006774.  
PR  
PR 30-SEP-1999; 99JP-00278291.  
PR  
PR 06-APR-2000; 2000JP-00105088.  
XX  
XX (KYOW ) KYOWA HAKKO KOGYO KK.  
XX  
XX Hanai N, Shitara K, Nakamura K, Niwa R;  
XX  
XX WPI; 2001-266143/27.

New human type complementation-determining region-transplanted antibody and derivatives against ganglioside GD3, useful in diagnosis and therapy of e.g. tumors, with low antigenicity, little side effects but potent activity in cancer.  
XX  
XX Claim 41; Page 168-172; 183pp; Japanese.  
XX  
XX The present invention describes a monoclonal antibody which can react specifically with ganglioside GD3. The antibody and its derivatives are useful in the diagnosis and therapy of tumours, particularly cancer diagnosis. The present sequence is a protein used in the exemplification of the invention  
XX  
SQ Sequence 582 AA;

Query Match 100.0%; Score 3071; DB 4; Length 582;  
Best Local Similarity 100.0%; Pred. No. 2.6e-153;

Matches 582; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	1	EVQLVESGGDFVQPGGSLRVSCAASGFAFASHYAMSWVRQAPGKGLEWVAYISSGSGTYY	60
Db	1	EVQLVESGGDFVQPGGSLRVSCAASGFAFASHYAMSWVRQAPGKGLEWVAYISSGSGTYY	60
Qy	61	SDSVKGRFTISRDNKNTLYLQMSRLRAEDSAVYFCTRVLKGTYYFDSWGQGTLLTVSSA	120
Db	61	SDSVKGRFTISRDNKNTLYLQMSRLRAEDSAVYFCTRVLKGTYYFDSWGQGTLLTVSSA	120
Qy	121	STKGPSVFPFLAPSSKTSGGTAALGCLVKDYFPEPTVSVNSGALTSGVHTFPAVLQSSG	180
Db	121	STKGPSVFPFLAPSSKTSGGTAALGCLVKDYFPEPTVSVNSGALTSGVHTFPAVLQSSG	180
Qy	181	LYSLSSVTVTPSSSLGTQYICNVNHKPSNTKVDKVEPKSCDKTHTCPPCAPPELLGGP	240
Db	181	LYSLSSVTVTPSSSLGTQYICNVNHKPSNTKVDKVEPKSCDKTHTCPPCAPPELLGGP	240
Qy	241	SVFLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN	300
Db	241	SVFLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN	300
Qy	301	TYRVSVLTVLHQDLNKGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDEL	360
Db	301	TYRVSVLTVLHQDLNKGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDEL	360
Qy	361	TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSLKLTVDKSRWQ	420
Db	361	TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSLKLTVDKSRWQ	420
Qy	421	QGNVFSCVMHEALHNHYTQKSLSLSPGKAPTSSSTKKTQLQLEHLLLDLQMLINGINNY	480
Db	421	QGNVFSCVMHEALHNHYTQKSLSLSPGKAPTSSSTKKTQLQLEHLLLDLQMLINGINNY	480
Qy	541	IVLELKGSETTFMCEYADETATIVFELNRWITFCQSIISTLT	582
Db	541	IVLELKGSETTFMCEYADETATIVFELNRWITFCQSIISTLT	582

RESULT 2			
AAB81991			
ID	AAB81991	standard; protein; 582 AA.	
XX			
AC			
XX			
DT	03-JUL-2001	(first entry)	
XX			
DE	Ganglioside GD3 specific antibody related protein SEQ ID NO: 57.		
XX			
KW	Ganglioside; GD3; complementarity determining region; CDR; antibody;		
KW	cancer.		
OS	Synthetic.		
XX			
FN	WO200123432-A1.		
XX			
PD	05-APR-2001.		
XX			
PF	29-SEP-2000; 2000WO-JP006774.		
XX			
PR	30-SEP-1999; 99JP-00278291.		
PR	06-APR-2000; 2000JP-00105088.		
XX			
PA	(KTOW ) KYOWA HAKKO KOGYO KK.		
XX			
PI	Hanai N, Shitara K, Nakamura K, Niwa R;		
XX			
DR	WPI; 2001-266143/27.		
XX			

PT	New human type complementation-determining region-transplanted antibody				
PT	and derivatives against ganglioside GD3, useful in diagnosis and therapy				
PT	of e.g. tumors, with low antigenicity, little side effects but potent				
PT	activity in cancer.				
XX					
PS	Claim 39; Page 175-179; 183pp; Japanese.				
XX					
CC	The present invention describes a monoclonal antibody which can react				
CC	specifically with ganglioside GD3. The antibody and its derivatives are				
CC	useful in the diagnosis and therapy of tumors, particularly cancer				
CC	diagnosis. The present sequence is a protein used in the exemplification				
CC	of the invention				
XX					
SQ	Sequence 582 AA;				
	Query Match	98.5%;	Score 3026;	DB 4; Length 582;	
	Best Local Similarity	98.3%;	Pred. No. 6e-151;		
	Matches 572; Conservative	5; Mismatches	5; Indels	0; Gaps	
QY	1	EVQLVESGGDFVQPGGSLRVSCAASGFAFASHYAMSWVRQAPGKGLEWVAYISSGSGTYY	60		
DB	1	EVTLVESGGDFVQPGGSLKVCASAGFAFASHYAMSWVRQTPAKRLEWVAYISSGSGTYY	60		
QY	61	SDSVKGRFTISRDNKNTLYLQMSRLRAEDSAVYFCTRVLKGTYYFDSWGQGTLLTVSSA	120		
DB	61	SDSVKGRFTISRDNKNTLYLQMSRLRSEDSAMYFCTRVLKGTYYFDSWGQGTLLTVSSA	120		
QY	121	STKGPSVFPFLAPSSKTSGGTAALGCLVKDYFPEPTVSVNSGALTSGVHTFPAVLQSSG	180		
DB	121	STKGPSVFPFLAPSSKTSGGTAALGCLVKDYFPEPTVSVNSGALTSGVHTFPAVLQSSG	180		
QY	181	LYSLSSVTVTPSSSLGTQYICNVNHKPSNTKVDKVEPKSCDKTHTCPPCAPPELLGGP	240		
DB	181	LYSLSSVTVTPSSSLGTQYICNVNHKPSNTKVDKVEPKSCDKTHTCPPCAPPELLGGP	240		
QY	241	SVFLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS	300		
DB	241	SVFLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS	300		
QY	301	TYRVSVLTVLHQDLNKGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDEL	360		
DB	301	TYRVSVLTVLHQDLNKGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDEL	360		
QY	361	TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQ	420		
DB	361	TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQ	420		
QY	421	QGNVFSCVMHEALHNHYTQKSLSLSPGKAPTSSSTKKTQLQLEHLLLDLQMLINGINNY	480		
DB	421	QGNVFSCVMHEALHNHYTQKSLSLSPGKAPTSSSTKKTQLQLEHLLLDLQMLINGINNY	480		
QY	481	KNPKLTRMLTFKFPMPKATLKHLCLEELKPLEEVNLAKSNKPHLRPRDLISINNV	540		
DB	481	KNPKLTRMLTFKFPMPKATLKHLCLEELKPLEEVNLAKSNKPHLRPRDLISINNV	540		
QY	541	IVLELKGSETTFMCEYADETATIVFELNRWITFCQSIISTLT	582		
DB	541	IVLELKGSETTFMCEYADETATIVFELNRWITFCQSIISTLT	582		
RESULT 3					
AAB83156					
ID	AAB83156 standard; protein; 583 AA.				
XX					
AC	AAB83156;				
XX					
DT	02-JUL-2001 (first entry)				
XX					
DE	Ganglioside GM2 antibody-related protein #1.				
XX					
KW	Ganglioside; GM2; antibody; cytostatic; cytotoxic; cancer.				
XX					
OS	Unidentified.				



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Db      360 TKQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFYLKSLVDRSRWQ 419
Qy      421 QGNVFCSCVMHEALHNHYTQKSLSLSPGKAPTSSSTKKTQLEHLLLDLQMLINGINNY 480
Db      420 QGNVFCSCVMHEALHNHYTQKSLSLSPGKAPTSSSTKKTQLEHLLLDLQMLINGINNY 479
Qy      481 KNPKLIRMLTFKFMYPKPKATELKHLOCLEBELKPLEEVNLAKSNFHLRPRDLISINIV 540
Db      480 KNPKLIRMLTFKFMYPKPKATELKHLOCLEBELKPLEEVNLAKSNFHLRPRDLISINIV 539
Qy      541 IVLELKGSETTFMCEYADETATIVFELNLRWITFCQSIISTLT 582
Db      540 IVLELKGSETTFMCEYADETATIVFELNLRWITFCQSIISTLT 581

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RESULT 5
AAE33444
ID AAE33444 standard; protein; 579 AA.
AC AAE33444;
XX
XX 02-APR-2003 (first entry)
XX
XX KS antibody heavy chain-interleukin 2 (IL-2) fusion protein.
XX
XX Immunoglobulin; diagnosis; epithelial cell adhesion molecule; EpCAM;
KW cancer; gene therapy; interleukin-2; IL2; fusion protein.
XX
XX Unidentified.
XX
XX WO200290566-A2.
XX
XX 14-NOV-2002.
XX
XX 03-MAY-2002; 2002WO-US013844.
XX
XX 03-MAY-2001; 2001US-0288564P.
XX
XX (LEXI-) LEXIGEN PHARM CORP.
XX
XX Gillies SD, Lo K, Qian X;
XX
XX WPI; 2003-111985/10.
XX
XX N-PSDB; AAD51139.
XX
XX New recombinant anti-EpCAM antibody having an amino acid sequence
XX defining an immunoglobulin light or heavy chain framework region, useful
XX for the diagnosis, prognosis and treatment of cancer.
XX
XX Disclosure; Page 80-82; 82pp; English.
XX
XX The present invention relates to novel recombinant anti-EpCAM (human
XX epithelial cell adhesion molecule) antibodies comprising an amino acid
XX sequence defining an immunoglobulin light or heavy chain framework
XX region. Sequences of the present invention are useful for the diagnosis,
XX prognosis and treatment of cancer. They are also used in gene therapy.
XX The present sequence is KS antibody heavy chain-interleukin 2 (IL-2)
XX fusion protein. This sequence is used to illustrate the method of the
XX invention
XX
XX Sequence 579 AA;

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Query Match      89.6%; Score 2750.5; DB 6; Length 579;
Best Local Similarity 88.5%; Pred. No. 1.8e-136;
Matches 516; Conservative 32; Mismatches 30; Indels 5; Gaps 2;

Qy      1 EVQLVESGGDFVQPGSLRVSCAAGFAPSHYAMSWVQAPQKGLIEWAYISSGSGSTYY 60
Db      1 QIQLVQSGAEVKKPQGTVKISKASGYTFNRYGMNVRKQTFGKGLKMWGWINTYTGPTY 60
Qy      61 SDSVKGRTIISRDNSKNTLYIQMRSRAEDSAVYFCTR-VKLGITYYFDSWGQGLTLTVSS 119

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Db      61 ADDFKGRPAFSLSTSTSTAFLQINLRSEDTATYFCVRFISKGDY----WGQTSVTVSS 116
Qy      120 ASTKGPSVPLAPSSKSTSGGTAALGCLVKDYFPEPTVYSWNSGALTSGVHTFPAVLQSS 179
Db      117 ASTKGPSVPLAPSSKSTSGGTAALGCLVKDYFPEPTVYSWNSGALTSGVHTFPAVLQSS 176
Qy      180 GLYSLSVVTVFPSSSLGTQTYICNVNHPKSNTKVDKKVBPCKSDKTHTCPPCPAPPELLGG 239
Db      177 GLYSLSVVTVFPSSSLGTQTYICNVNHPKSNTKVDKKVBPCKSDKTHTCPPCPAPPELLGG 236
Qy      240 PSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNNYVDSGVFNHAKTKPREQYN 299
Db      237 PSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNNYVDSGVFNHAKTKPREQYN 296
Qy      300 STYRVSVLTVLHODWLNKGEYKCVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDE 359
Db      297 STYRVSVLTVLHODWLNKGEYKCVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDE 356
Qy      360 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFYLKSLTVDKSRW 419
Db      357 MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFYLKSLTVDKSRW 416
Qy      420 QGNVFCSCVMHEALHNHYTQKSLSLSPGKAPTSSSTKKTQLEHLLLDLQMLINGINN 479
Db      417 QGNVFCSCVMHEALHNHYTQKSLSLSPGKAPTSSSTKKTQLEHLLLDLQMLINGINN 476
Qy      480 YKNPKLIRMLTFKFMYPKPKATELKHLOCLEBELKPLEEVNLAKSNFHLRPRDLISIN 539
Db      477 YKNPKLIRMLTFKFMYPKPKATELKHLOCLEBELKPLEEVNLAKSNFHLRPRDLISIN 536
Qy      540 VIVLELKGSETTFMCEYADETATIVFELNLRWITFCQSIISTLT 582
Db      537 VIVLELKGSETTFMCEYADETATIVFELNLRWITFCQSIISTLT 579

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RESULT 6
AAO30910
ID AAO30910 standard; protein; 579 AA.
XX
XX AAO30910;
XX
XX 22-SEP-2003 (first entry)
XX
XX dI-KS-ala-IL2 (D20T) variant protein.
XX
XX Cytokine; interleukin-2; IL-2; cancer; viral infection; immune disorder;
XX gene therapy; immunoglobulin; Ig; fusion protein; human.
XX
XX Homo sapiens.
XX Unidentified.
XX Chimeric.
XX
XX WO2003048334-A2.
XX
XX 12-JUN-2003.
XX
XX 04-DEC-2002; 2002WO-US038780.
XX
XX 04-DEC-2001; 2001US-0337113P.
XX
XX 12-APR-2002; 2002US-0371966P.
XX
XX (EMDL-) EMD LEXIGEN RES CENT CORP.
XX
XX Gillies SD;
XX
XX WPI; 2003-513757/48.
XX
XX New fusion protein comprising a non-IL-2 moiety fused to a mutant IL-2
XX moiety, useful for preparing a composition for treating cancer, viral
XX infections or immune disorders.
XX
XX Example 10; Page 60-63; 71pp; English.
XX

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Db	534	IVLELKGSETTFMCEYADETATIVFELNRWITFCQSIISTLT	575
RESULT 8			
AAO30915	ID	AAO30915 standard; protein; 580 AA.	
XX	AC	AAO30915;	
XX	AC	AAO30915;	
DT	22-SEP-2003	(first entry)	
DE	di-NHS76 (gamma4h) (FN>AQ)-ala-IL2 (D20T) variant protein.		
XX	Cytokine; interleukin-2; IL-2; cancer; viral infection; immune disorder;		
XX	gene therapy; immunoglobulin; Ig; fusion protein; human; variant.		
OS	Homo sapiens.		
OS	Unidentified.		
OS	Chimeric.		
XX	WO2003048334-A2.		
PN	12-JUN-2003.		
XX	04-DEC-2002; 2002WO-US038780.		
XX	04-DEC-2001; 2001US-0337113P.		
PR	12-APR-2002; 2002US-0371966P.		
XX	(EMDL-) EMD LEXIGEN RES CENT CORP.		
PA	Gillies SD;		
XX	WPI; 2003-513757/48.		
XX	New fusion protein comprising a non-IL-2 moiety fused to a mutant IL-2		
XX	moiety, useful for preparing a composition for treating cancer, viral		
PT	infections or immune disorders.		
XX	Example 10; Page 68-71; 71pp; English.		
XX	The invention relates to cytokine fusion proteins with increased		
CC	therapeutic index and methods for increasing the therapeutic index of		
CC	such fusion proteins. The fusion protein comprises a non-interleukin-2		
CC	(IL-2) moiety fused to a mutant IL-2 moiety. It is useful for preparing a		
CC	composition for treating cancer, viral infections or immune disorders.		
CC	The fusion protein is also used in gene therapy. The present sequence is		
CC	di-NHS76 (gamma4h) (FN>AQ)-ala-IL2 (D20T) variant protein comprising di-		
CC	KS heavy chain fused to human IL-2 (D20T) variant protein. This sequence		
CC	is used to illustrate the method of the invention		
XX	Sequence 580 AA;		
SQ	Query Match	85.3%; Score 2621; DB 6; Length 580;	
	Best Local Similarity	85.8%; Pred. No. 1.1e-129;	
	Matches 500; Conservative 29; Mismatches 50; Indels 4; Gaps 3;		
Qy	1	EVQLVESGGDFVQPGGSLRVCAASGFAFSH-YAMSWVRQAPGKLEWVAYISSGGSTY	59
Db	1	QVQLQESGPGLVKPSSETLSLTCAVSGYSISSGYGMIRPPGKLEWIGSIYHSGS-TY	59
Qy	60	YSDSVKGRFTISRDNKNTLYLQWRLRAEDSAVFTCRVKGITGYFDPSWGQGLLTVSS	119
Db	60	YNPSLKRVTISVDTSKNQFSLKLSVTAADTAVYICARGKWSK--FDYWGQGLTVTVSS	117
Qy	120	ASTKGPSVFPLAPSSKSTSGGTAAALGCLVADYFEPPVTWNSGALTSGVHTFPAVLQSS	179
Db	118	ASTKGPSVFPLAPCSRSTSESTAALGCLVADYFEPPVTWNSGALTSGVHTFPAVLQSS	177
Qy	180	GLYSLSVVTVTPSSSLGTTQYICNVNHPKSNITKVDKVEPKSCDKTHTCPCPAPELGG	239
Db	178	GLYSLSVVTVTPSSSLGTTKTYTCNVNHPKSNITKVDKVEPKSCDKTHTCPCPAPEFLGG	237



SQ	Sequence 580 AA;									
Query Match	84.3%; Score 2589; DB 6; Length 580;									
Best Local Similarity	85.1%; Pred. No. 5.3e-128;									
Matches 497; Conservative	29; Mismatches 52; Indels 6; Gaps 5;									
Qy	1	EVQLVESGGDFVQPGGSLRVSCAASGFAPFASH-YAMSMVVRQAPGKGLWVAIVISGGSGTY	59							
Db	1	QVQLQESGPGLVKPSETLSLTCAVSGYSISGYTWGIRQPPGKGLWIGSIYHSGS-TY	59							
Qy	60	YSDSVKGRFTISRDNKNTLYLQWRSRAEDSAVYFCTRVKLGYYFDSNGQGLTLTVSS	119							
Db	60	YNPSLKSRTVTSVDTSKNQFSLKSLSSVTAADTAVYYCARGKWSK--FDYWGQGLTLTVSS	117							
Qy	120	-ASTKGPSVFLAPSSKTSSTGTAALGCLVKDYPPEPVTVSWNSGALTSGVHTTTPAVLAQS	178							
Db	118	GASTKGPSVFLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTTTPAVLAQS	177							
Qy	179	SGLYSLSSVTVTPSSSLGTQTYICNVNHPKPSNTKVDKKVPSKCDKTKHTCCPPCAPPELLG	238							
Db	178	SGLYSLSSVTVTPSSNFGTQTYTCNVNHPKPSNTKVDKTVPSKCDKTKHTCCPPCAPPP-VA	236							
Qy	239	GPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVVHNAKTKPREEQY	298							
Db	237	GPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVVHNAKTKPREEQA	296							
Qy	299	NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRD	358							
Db	297	QSTFRVSVLTVLHQDWLNGKEYKCKVSNKGLPAPIEKTISKAKGQPREPOVYTLPPSRE	356							
Qy	359	ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSKLTVDKSR	418							
Db	357	EMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPMLDSDGSFFLYSKLTVDKSR	416							
Qy	419	WQGNVFCSCVMHEALNHYTKQSLSLSPGKAPTSSSTKTKTQLQLEHLHLLDQLMILNGIN	478							
Db	417	WQGNVFCSCVMHEALNHYTKQSATATPGAAPTSSSTKTKTQLQLEHLHLLDQLMILNGIN	476							
Qy	479	NYKNPKLTRLMTFKFYPNPKATELKHLCLEELKPLEEVNLQAQSNFHLRPRDLISNI	538							
Db	477	NYKNPKLTRLMTFKFYPNPKATELKHLCLEELKPLEEVNLQAQSNFHLRPRDLISNI	536							
Qy	539	NVTVLELKGSETFMCEYADETATIVFELNRWITFCOSIIISTLT	582							
Db	537	NVTVLELKGSETFMCEYADETATIVFELNRWITFCOSIIISTLT	580							
RESULT 10										
ADR23346										
ADR23346 standard; protein; 449 AA.										
XX	ADR23346;									
AC	ADR23346;									
XX	04-NOV-2004 (first entry)									
DT	Human CD72-targeted IgG1 heavy chain.									
XX										
DE										
DE										
KW	Human; CD72; B-lymphocyte; receptor; scFv; antibody; cytostatic;									
KW	immunosuppressive; cancer; autoimmune disease; gene therapy.									
XX										
OS	Homo sapiens.									
XX										
XX	Key Location/Qualifiers									
FT	Region 1..119									
FT	/label= V_region									
FT	Region 120..449									
FT	/label= C_region									
XX										
PN	WO2004067569-A1.									
XX										
PD	12-AUG-2004.									
XX										
PF	27-JAN-2003; 2003WO-EP050004.									

XX	27-JAN-2003; 2003WO-EP050004.
XX	
PA	(CRUC-) CRUCCELL HOLLAND BV.
XX	
PI	Bakker ABH, Marissen WE;
XX	
DR	WPI; 2004-580978/56.
DR	N-PSDB; ADR23345.
XX	
PT	New internalizing human binding molecules capable of specifically binding
PT	to CD72, useful for diagnosing and/or treating B-cell associated
PT	diseases, such as cancer or autoimmune disorders.
XX	
PS	Claim 69; SEQ ID NO 38; 174pp; English.
XX	
CC	The present sequence is the protein sequence of the heavy chain of human
CC	IgG1 antibody 004, which specifically recognises human B cell associated
CC	antigen CD72. An ecFv ADR23320 selected from an antibody phage display
CC	library was shown to specifically recognise the human CD72 receptor. The
CC	scFv was cloned in IgG expression vector C01 using primers designed to
CC	restore complete human frameworks, thereby generating antibody 004. Such
CC	anti-CD72 immunoglobulins or their antigen-binding fragments can be used
CC	as internalising human binding molecules of the invention. These
CC	internalising human binding molecules are capable of (specifically)
CC	binding to CD72 or its antigenic determinant, and preferably bind to CD72
CC	associated with cells. Upon binding to CD72 present on the surface of
CC	target cells, the binding molecules internalise. In addition to the
CC	internalising human binding molecules, the invention provides
CC	immunoconjugates comprising an internalising human binding molecule and a
CC	tag (toxic substance, radioactive substance, liposome and/or enzyme),
CC	nucleic acids encoding these, and compositions comprising them. The
CC	internalising human binding molecule, immunoconjugate, nucleic acid
CC	molecule or composition can be used in the diagnosis and/or treatment of
CC	a B cell associated disorder or disease, especially a B cell associated
CC	cancer and B cell associated autoimmune disorder (claimed). An
CC	internalising human binding molecule comprising the present heavy chain
CC	sequence is specifically claimed.
XX	
SQ	Sequence 449 AA;

Query Match 73.2%; Score 2247; DB 8; Length 449;	
Best Local Similarity 94.0%; Pred. No. 3.8e-110;	
Matches 422; Conservative 9; Mismatches 18; Indels 0; Gaps 0;	
Qy	1 EVQLVESGGDFVQPGGSLRVSCAASGFAPFASHYAMSMVVRQAPGKGLWVAIVISGGSGTY 60
Db	1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSGYLMVMVRQAPGKGLWVAIVYDGSNKYY 60
Qy	61 SDSVKGRFTISRDNKNTLYLQWRSRAEDSAVYFCTRVKLGTYFDSNGQGLTLTVSSA 120
Db	61 ADSVKGRFTISRDNKNTLYLQWDSRAEDTAVYYCARARRDTNLFYMGQGLTLTVSSA 120
Qy	121 STKGPSVFLPAPSSKTSSTGTAALGCLVKDYPPEPVTVSWNSGALTSGVHFPVAVLQSSG 180
Db	121 STKGPSVFLPAPSSKTSSTGTAALGCLVKDYPPEPVTVSWNSGALTSGVHFPVAVLQSSG 180
Qy	181 LYSLSWVTVTPSSSLGTQTYICNVNHPKPSNTKVDKKEVPKSCDKTKHTCCPPCAPPELLGGP 240
Db	181 LYSLSWVTVTPSSSLGTQTYICNVNHPKPSNTKVDKKEVPKSCDKTKHTCCPPCAPPELLGGP 240
Qy	241 SVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVVHNAKTKPREEQYNS 300
Db	241 SVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVVHNAKTKPREEQYNS 300
Qy	301 TYRVSVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL 360
Db	301 TYRVSVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEE 360
Qy	361 TKNQVSLTCLVKGFPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSKLTVDKSRWQ 420
Db	361 TKNQVSLTCLVKGFPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSKLTVDKSRWQ 420

QY	421	QGNVFCSCVMHEALHNHYTKSLSPGK 449	CC	human AQC2 heavy chain protein	73.2%; Score 2246.5; DB 6; Length 447;
DB	421	QGNVFCSCVMHEALHNHYTKSLSPGK 449	XX	Sequence 447 AA;	Best Local Similarity 95.1%; Pred. No. 4e-110;
			SQ		Matches 426; Conservative 4; Mismatches 17; Indels 1; Gaps 1;
RESULT 11					
AAE33522					
ID	AAE33522	standard; protein; 447 AA.			
AC	AAE33522;				
XX					
DT	02-APR-2003	(first entry)			
DE	Human AQC2 heavy chain protein.				
XX					
KW	Human; very late activation antigen; VLA-1; betal containing integrin;				
KW	immunological disorder; inflammatory disorder; skin related condition;				
KW	psoriasis; eczema; burn; dermatitis; respiratory distress syndrome;				
KW	fibrosis; allergic rhinitis; asthma; bronchitis; tendonitis; bursitis;				
KW	fever; migraine headache; inflammatory bowel disease; Crohn's disease;				
KW	irritable bowel syndrome; colitis; colorectal cancer; vascular disease;				
KW	atherosclerosis; thyroiditis; aplastic anaemia; periarthritis nodosa;				
KW	gastroenteritis; Hodgkin's disease; rheumatic fever; autoimmune disease;				
KW	osteoarthritis; type I diabetes; myasthenia gravis; rheumatoid arthritis;				
KW	systemic lupus erythematosus; multiple sclerosis; nephrotic syndrome;				
KW	renal failure; sarcoidosis; Behcet's syndrome; gingivitis; polymyositis;				
KW	hypersensitivity; graft rejection; transplant rejection; conjunctivitis;				
KW	graft versus host disease; myocardial ischaemia.				
OS	Homo sapiens.				
XX					
PN	WO200283854-A2.				
XX					
PD	24-OCT-2002.				
XX					
PF	12-APR-2002; 2002WO-US011521.				
XX					
PI	(BIOJ ) BIOGEN INC.				
XX					
PI	Lyne PD, Garber EA, Saldanha JW, Karpusas M;				
XX					
DR	WPI; 2003-093009/08.				
XX					
PT	New anti-VLA-1 antibodies are useful for preventing or treating VLA-1-				
PT	mediated immunological or inflammatory disorders, e.g. psoriasis, eczema,				
PT	burns, dermatitis, and abnormal proliferation of hair follicle cells or				
PT	fibrosis.				
XX					
PS	Claim 6; Page 75; 248pp; English.				
XX					
CC	The present invention relates to novel antibodies that specifically bind				
CC	to very late activation (VLA-1; betal containing integrin) antigens and				
CC	methods of using these antibodies to treat immunological disorders. The				
CC	anti-VLA-1 antibodies are useful for preventing or treating VLA-1-				
CC	mediated immunological or inflammatory disorders such as skin related				
CC	conditions (e.g. psoriasis, eczema, burns, dermatitis and abnormal				
CC	proliferation of hair follicle cells), fibrosis (e.g. kidney or lung				
CC	fibrosis), allergic rhinitis, respiratory distress syndrome, asthma,				
CC	bronchitis, tendonitis, bursitis, fever, migraine headaches, gastro-				
CC	intestinal conditions (e.g. inflammatory bowel disease, Crohn's disease,				
CC	gastroenteritis, irritable bowel syndrome, colitis and colorectal cancer),				
CC	vascular diseases (e.g. atherosclerosis), thyroiditis, aplastic anaemia,				
CC	periarthritis nodosa, Hodgkin's disease, rheumatic fever, osteoarthritis,				
CC	autoimmune diseases (e.g. type I diabetes, myasthenia gravis, rheumatoid				
CC	arthritis, systemic lupus erythematosus and multiple sclerosis), renal				
CC	failure, sarcoidosis, nephrotic syndrome, Behcet's syndrome, gingivitis,				
CC	polymyositis, hypersensitivity (e.g. delayed type hypersensitivity or				
CC	immediate hypersensitivity), graft and transplant rejections, graft				
CC	versus host disease, conjunctivitis, swelling occurring after injury,				
CC	myocardial ischaemia or endotoxin shock syndrome. The present sequence is				

CC	human AQC2 heavy chain protein				
XX					
SQ	Sequence 447 AA;				
	Query Match	73.2%; Score 2246.5; DB 6; Length 447;			
	Best Local Similarity	95.1%; Pred. No. 4e-110;			
	Matches 426; Conservative	4; Mismatches 17; Indels 1; Gaps 1;			
QY	1	EVOLVESGGDFVQPGSLRVSCAAGFAFASHVAMSVROAPGKGLWVAVYISGGSGTYY 60			
DB	1	EVOLVESGGGLVQPGSLRLSCAAGFTFSRTMTMSVROAPGKGLWVAVTISGGGH-TYY 59			
QY	61	SDSVKGRFTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLGTYYPFDSNGQGLLTVSSA 120			
DB	60	LDSVKGRFTISRDNKNTLYLQWNSLRAEDTAVYYCTRGFGDGGYFDVWGQGLTVTVSSA 119			
QY	121	STKGPSVFPFLAPSSKTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSSG 180			
DB	120	STKGPSVFPFLAPSSKTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSSG 179			
QY	181	LYSLSSVTVTPSSSLGTQYICNVNHPKNTKVDKKVEPKSCDKTHTCPPCPAPELLGSP 240			
DB	180	LYSLSSVTVTPSSSLGTQYICNVNHPKNTKVDKKVEPKSCDKTHTCPPCPAPELLGSP 239			
QY	241	SVFLFPFKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNAKTKPREQYNS 300			
DB	240	SVFLFPFKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNAKTKPREQYNS 299			
QY	301	TYRVSVLVTLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDEL 360			
DB	300	TYRVSVLVTLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDEL 359			
QY	361	TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFPLYSKLTVDKSRWQ 420			
DB	360	TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFPLYSKLTVDKSRWQ 419			
QY	421	QGNVFCSCVMHEALHNHYTKSLSPG 448			
DB	420	QGNVFCSCVMHEALHNHYTKSLSPG 447			
RESULT 12					
AAE33523					
ID	AAE33523	standard; protein; 447 AA.			
XX					
AC	AAE33523;				
XX					
DT	02-APR-2003	(first entry)			
XX					
DE	Human AQC2 heavy chain mutant protein, haaQC2.				
XX					
KW	Human; very late activation antigen; VLA-1; betal containing integrin;				
KW	immunological disorder; inflammatory disorder; skin related condition;				
KW	psoriasis; eczema; burn; dermatitis; respiratory distress syndrome;				
KW	fibrosis; allergic rhinitis; asthma; bronchitis; tendonitis; bursitis;				
KW	fever; migraine headache; inflammatory bowel disease; Crohn's disease;				
KW	irritable bowel syndrome; colitis; colorectal cancer; vascular disease;				
KW	atherosclerosis; thyroiditis; aplastic anaemia; periarthritis nodosa;				
KW	gastroenteritis; Hodgkin's disease; rheumatic fever; autoimmune disease;				
KW	osteoarthritis; type I diabetes; myasthenia gravis; rheumatoid arthritis;				
KW	systemic lupus erythematosus; multiple sclerosis; nephrotic syndrome;				
KW	renal failure; sarcoidosis; Behcet's syndrome; gingivitis; polymyositis;				
KW	hypersensitivity; graft rejection; transplant rejection; conjunctivitis;				
KW	graft versus host disease; myocardial ischaemia; mutant; mutein.				
OS	Homo sapiens.				
XX					
PN	WO200283854-A2.				
XX					
PD	24-OCT-2002.				
XX					
PF	12-APR-2002; 2002WO-US011521.				
XX					

PR 13-APR-2001; 2001US-0283794P.  
PR 06-JUL-2001; 2001US-0303689P.  
XX  
PA (BIOJ ) BIOGEN INC.  
XX  
XX Lyne PD, Garber EA, Saldanha JW, Karpusas M;  
DR WPI; 2003-093009/08.  
XX  
XX New anti-VLA-1 antibodies are useful for preventing or treating VLA-1-  
PT mediated immunological or inflammatory disorders, e.g. psoriasis, eczema,  
PT burns, dermatitis, and abnormal proliferation of hair follicle cells or  
PT fibrosis.  
XX  
XX Example 23; Page 91-92; 248pp; English.  
PS  
XX The present invention relates to novel antibodies that specifically bind  
CC to very late activation (VLA-1; beta1 containing integrins) antigens and  
CC methods of using these antibodies to treat immunological disorders. The  
CC anti-VLA-1 antibodies are useful for preventing or treating VLA-1-  
CC mediated immunological or inflammatory disorders such as skin related  
CC conditions (e.g. psoriasis, eczema, burns, dermatitis and abnormal  
CC proliferation of hair follicle cells), fibrosis (e.g. kidney or lung  
CC fibrosis), allergic rhinitis, respiratory distress syndrome, asthma,  
CC bronchitis, tendonitis, bursitis, fever, migraine headaches, gastro-  
CC intestinal conditions (e.g. inflammatory bowel disease, Crohn's disease,  
CC gastritis, irritable bowel syndrome, colitis and colorectal cancer),  
CC vascular diseases (e.g. atherosclerosis), thyroiditis, aplastic anaemia,  
CC periarteritis nodosa, Hodgkin's disease, rheumatic fever, osteoarthritis,  
CC autoimmune diseases (e.g. type I diabetes, myasthenia gravis, rheumatoid  
CC arthritis, systemic lupus erythematosus and multiple sclerosis), renal  
CC failure, sarcoidosis, nephrotic syndrome, Behcet's syndrome, gingivitis,  
CC polymyositis, hypersensitivity (e.g. delayed type hypersensitivity or  
CC immediate hypersensitivity), graft and transplant rejections, graft  
CC versus host disease, conjunctivitis, swelling occurring after injury,  
CC myocardial ischaemia or endotoxin shock syndrome. The present sequence is  
CC human AQC2 heavy chain mutant protein, haaQC2  
XX  
SQ Sequence 447 AA;

Query Match 73.0%; Score 2240.5; DB 6; Length 447;  
Best Local Similarity 94.9%; Pred. No. 8.2e-110;  
Matches 425; Conservative 4; Mismatches 18; Indels 1; Gaps 1;

Qy 1 EVLVESGGDFVQPGGSLRVSCAASGFAPSHYAMSWVRQAPGKLEWVAISSGSGSTYY 60  
Db 1 EVLVESGGGLVQPGGSLRLSCLAAAGFTFSRYTMSWVRQAPGKLEWVAISSGSH-TYY 59  
Qy 61 SDSVKGRTTISRDNKNTLYLQMSLRADSAVYFCTRVKLGTYTFDSWGQGTLLTVSSA 120  
Db 60 LDSVKGRTTISRDNKNTLYLQMSLRADSAVYFCTRVKLGTYTFDSWGQGTLLTVSSA 119  
Qy 121 STKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSNVNSGALTSGVHTFPAVLQSSG 180  
Db 120 STKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSNVNSGALTSGVHTFPAVLQSSG 179  
Qy 181 LYSLSVSVTVPPSSSLGTQTYICNVNHPKSNTKVDKVPKSCDKHTHCPCPAPPELLGGP 240  
Db 180 LYSLSVSVTVPPSSSLGTQTYICNVNHPKSNTKVDKVPKSCDKHTHCPCPAPPELLGGP 239  
Qy 241 SVFLFPKPKDPTLMISRTPEVTCVVVDVSHEDPEVKENWYVDGVEVHNATKPREEQYN 300  
Db 240 SVFLFPKPKDPTLMISRTPEVTCVVVDVSHEDPEVKENWYVDGVEVHNATKPREEQYN 299  
Qy 301 TYRVSVLTVLHODWLNKGEYCKVSNKALPAPIEKTISKAKGQPREPPQVYTLPPSRDEL 360  
Db 300 TYRVSVLTVLHODWLNKGEYCKVSNKALPAPIEKTISKAKGQPREPPQVYTLPPSRDEL 359  
Qy 361 TKQVSLTCLVKGPYPSDIAVEVESNGQPENNYKTPPVLDSDGSFPLYSKLTVDKSRWQ 420  
Db 360 TKQVSLTCLVKGPYPSDIAVEVESNGQPENNYKTPPVLDSDGSFPLYSKLTVDKSRWQ 419  
Qy 421 QGNVFCSCVMHEALHNHYTQKSLSLSPG 448

Db 420 QGNVFCSCVMHEALHNHYTQKSLSLSPG 447  
RESULT 13  
AAOI8400  
ID AAOI8400 standard; protein; 449 AA.  
XX  
XX AAOI8400;  
XX  
XX 11-OCT-2002 (first entry)  
XX  
XX Mature humanised murine CBE11 heavy chain variable domain.  
XX  
XX Mouse; humanised antibody; lymphotoxin beta receptor; antibody; cancer;  
XX neoplasia; LT-beta-R; light chain; heavy chain; variable region.  
XX  
XX Mus sp.  
XX  
XX Synthetic.  
XX  
XX WO200230986-A2.  
XX  
XX 18-APR-2002.  
XX  
XX 12-OCT-2001; 2001WO-US032140.  
XX  
XX 13-OCT-2000; 2000US-0240285P.  
XX  
XX 13-MAR-2001; 2001US-0275289P.  
XX  
XX 21-JUN-2001; 2001US-0299987P.  
XX  
XX (BIOJ ) BIOGEN INC.  
XX  
XX Garber E, Lyne P, Saldanha JW;  
XX  
XX WPI; 2002-583337/62.  
XX  
XX New humanized anti-lymphotoxin-beta receptor antibody, useful for  
XX treating or reducing the advancement, severity or effects of neoplasia,  
XX particularly solid tumors (i.e. carcinomas) including colorectal cancer  
XX and breast cancer.  
XX  
XX Example 5; Page 25-26; 41pp; English.  
XX  
XX The present invention relates to humanised anti-lymphotoxin beta receptor  
XX (LT-beta-R) antibodies. These are derived from the murine LT-beta-R  
XX binding antibody CBE11 and can be used to treat neoplasia in humans. The  
XX present sequence is a humanised murine CBE11 heavy chain variable region  
XX  
XX Sequence 449 AA;

Query Match 72.9%; Score 2238.5; DB 5; Length 449;  
Best Local Similarity 94.0%; Pred. No. 1.1e-109;  
Matches 422; Conservative 8; Mismatches 18; Indels 1; Gaps 1;

Qy 1 EVLVESGGDFVQPGGSLRVSCAASGFAPSHYAMSWVRQAPGKLEWVAISSGSGSTYY 60  
Db 1 EVLVESGGGLVQPGGSLRLSCLAAAGFTFSRYTMSWVRQAPGKLEWVAISSGSGSTYY 60  
Qy 61 SDSVKGRTTISRDNKNTLYLQMSLRADSAVYFCTRVKLGTYTFDSWGQGTLLTVSS 119  
Db 61 PDSVKGRTTISRDNKNTLYLQMSLRADSAVYFCTRVKLGTYTFDSWGQGTLLTVSS 120  
Qy 120 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSNVNSGALTSGVHTFPAVLQSS 179  
Db 121 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSNVNSGALTSGVHTFPAVLQSS 180  
Qy 180 GLYSLSVSVTVPPSSSLGTQTYICNVNHPKSNTKVDKVPKSCDKHTHCPCPAPPELLGG 239  
Db 181 GLYSLSVSVTVPPSSSLGTQTYICNVNHPKSNTKVDKVPKSCDKHTHCPCPAPPELLGG 240  
Qy 240 PSVFLFPKPKDPTLMISRTPEVTCVVVDVSHEDPEVKENWYVDGVEVHNATKPREEOYN 299  
Db 241 PSVFLFPKPKDPTLMISRTPEVTCVVVDVSHEDPEVKENWYVDGVEVHNATKPREEOYN 300

QY 300 STYRVSVLTVLHODWLNKGYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDE 359  
 DB 301 STYRVSVLTVLHODWLNKGYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDE 360  
 QY 360 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSFPLYSKLTVDKSRW 419  
 DB 361 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSFPLYSKLTVDKSRW 420  
 QY 420 QQGNVFCSCVMHEALHNHYTQKSLSLSPG 448  
 DB 421 QQGNVFCSCVMHEALHNHYTQKSLSLSPG 449  
 RESULT 14  
 AEA36337  
 ID AEA36337 standard; protein; 449 AA.  
 AC AEA36337;  
 DT 28-JUL-2005 (first entry)  
 DE Human CBE11 heavy chain amino acid sequence - SEQ ID 4.  
 KW cancer; cytostatic; carcinoma; sarcoma; leukemia; lymphoma; tumor;  
 KW immune disorder; inflammation; antiinflammatory;  
 KW neurodegenerative disease; neuroprotective; heavy chain; CBE11.  
 OS Homo sapiens.  
 XX WO2005047327-A2.  
 XX 26-MAY-2005.  
 XX 12-NOV-2004; 2004WO-US037929.  
 XX 12-NOV-2003; 2003US-0519733P.  
 PR 12-NOV-2003; 2003US-0519743P.  
 PR 12-NOV-2003; 2003US-0519744P.  
 XX (BIOJ ) BIOGEN IDEC MA INC.  
 XX Farrington GK, Lugovskoy AA, Eldredge JK, Garber B;  
 XX WPI; 2005-372348/38.  
 DR N-PSDB; AEA36336.  
 XX New neonatal Fc receptor-binding polypeptide variants, useful for  
 PT treating cancer, immune, inflammatory or neurodegenerative disorders.  
 XX Example 4; SEQ ID NO 4; 168pp; English.  
 PS The invention comprises a polypeptide which contains an Fc receptor  
 CC (FcRn) binding portion of an Fc region, where the polypeptide contains at  
 CC least one mutation. The polypeptide of the invention is useful for the  
 CC treatment of cancer (e.g. carcinomas, sarcomas, leukemias, lymphomas, or  
 CC tumors), immune disorders, inflammatory disorders, and neurodegenerative  
 CC disorders. The present amino acid sequence represents the human CBE11  
 CC heavy chain.  
 XX Sequence 449 AA;  
 SQ Query Match 72.9%; Score 2238.5; DB 9; Length 449;  
 Best Local Similarity 94.0%; Pred. NO. 1.1e-109;  
 Matches 422; Conservative 8; Mismatches 18; Indels 1; Gaps 1;  
 QY 1 EVQLVESGGDPVQPGGSLRVSCAASGFAFSHYAMSVRQAPGKLEWVAYISSGSGITYY 60  
 DB 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSYIMFRQAPGKLEWVATISDGSTYY 60  
 QY 61 SDSVKGRFTISRDNSKNTLYIQMRSRAEDSAVFTCRVKLGT-YYFDWSQGGTLTVSS 119  
 DB 61 PDSVKGRFTISRDNAKNSLYIQMSSLRAEDTAVYICAREENGNFYFDYWGQGTITVTVSS 120

QY 120 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVYSWMNGALTSGVHTFPAVLQSS 179  
 DB 121 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVYSWMNGALTSGVHTFPAVLQSS 180  
 QY 180 GLYSLSVSVTVSPSSSISGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHHTCPCPAPPELLGG 239  
 DB 181 GLYSLSVSVTVSPSSSISGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHHTCPCPAPPELLGG 240  
 QY 240 PSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKENWYVDGVVHNAKTKPREEQYN 299  
 DB 241 PSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVVHNAKTKPREEQYN 300  
 QY 300 STYRVSVLTVLHODWLNKGYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDE 359  
 DB 301 STYRVSVLTVLHODWLNKGYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDE 360  
 QY 360 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSFPLYSKLTVDKSRW 419  
 DB 361 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSFPLYSKLTVDKSRW 420  
 QY 420 QQGNVFCSCVMHEALHNHYTQKSLSLSPG 448  
 DB 421 QQGNVFCSCVMHEALHNHYTQKSLSLSPG 449  
 RESULT 15  
 ADQ07403  
 ID ADQ07403 standard; protein; 697 AA.  
 XX ADQ07403;  
 XX 07-OCT-2004 (first entry)  
 DE hCBEl1/hBHA10 bispecific-1 antibody construct mature heavy chain.  
 KW tumour volume; lymphotoxin-beta receptor; LT-beta-R; agonist; antibody;  
 KW chemotherapeutic; supra-additive; inhibition; cytostatic; gene therapy;  
 KW cancer; mature heavy chain; hCBEl1/hBHA10 bispecific-1.  
 XX Homo sapiens.  
 OS Synthetic.  
 XX WO2004058183-A2.  
 XX 15-JUL-2004.  
 XX 22-DEC-2003; 2003WO-US041243.  
 XX 20-DEC-2002; 2002US-0435185P.  
 XX (BIOG-) BIOGEN IDEC MA INC.  
 XX Lepage D, Gill A;  
 XX WPI; 2004-525785/50.  
 DR N-PSDB; ADQ07402.  
 XX Inhibiting tumor volume comprising administering an amount of a  
 PT lymphotoxin-beta receptor agonist or antibody and a chemotherapeutic  
 PT agent (e.g. gemcitabine or adriamycin).  
 XX Disclosure; SEQ ID NO 2; 161pp; English.  
 XX The invention relates to a novel method for inhibiting tumour volume. The  
 CC method comprises administering an amount of a lymphotoxin-beta receptor  
 CC (LT-beta-R) agonist or antibody and an amount of at least one  
 CC chemotherapeutic agent, where the administration of the LT-beta-R agonist  
 CC or antibody and the chemotherapeutic agent results in supra-additive  
 CC inhibition of the tumour. The invention further relates to: a  
 CC pharmaceutical composition comprising an amount of an LT-beta-R agonist  
 CC and at least one chemotherapeutic agent, and a pharmaceutical carrier,  
 CC which upon administration to a subject results in supra-additive



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OM protein - protein search, using sw model

Run on: April 6, 2006, 08:49:11 ; Search time 29.8299 Seconds  
(without alignments)  
1877.250 Million cell updates/sec

Title: US-10-089-500-53  
Perfect score: 3071  
Sequence: 1 EVQLVESGGDFVQPGGSLRV.....IVEFLNRWITCQSIISTLT 582

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 80:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1767	57.5	330	1 GHU	Ig gamma-1 chain C
2	1630.5	53.1	377	2 A23511	Ig gamma-3 chain C
3	1628.5	53.0	377	2 A60764	Ig gamma-3 chain C
4	1604	52.2	326	1 G2HU	Ig gamma-2 chain C
5	1590.5	51.8	327	1 G4HU	Ig gamma-4 chain C
6	1508.5	49.1	444	2 PC4436	monoclonal antibody
7	1487	48.4	470	2 S22080	Ig heavy chain pre
8	1440.5	46.9	469	2 S37483	Ig gamma-2a chain
9	1437	46.8	446	2 S40295	Ig gamma-2a chain
10	1434	46.7	472	2 S31459	Ig gamma-1 chain -
11	1429	46.5	374	2 S69339	Ig heavy chain v r
12	1390	45.3	474	1 G2MS11	Ig gamma-2b chain
13	1367.5	44.5	475	2 S01321	Ig gamma-2b chain
14	1263	41.1	328	2 I47159	Ig gamma-2a chain
15	1260	41.0	255	4 S31866	Ig gamma-1 chain C
16	1257	40.9	328	2 I47160	Ig gamma 2b chain
17	1254	40.8	324	2 P70207	Ig gamma chain C r
18	1231	40.1	328	2 I47158	Ig gamma 1 chain c
19	1230.5	40.1	323	1 GHRB	Ig gamma chain C r
20	1227	40.0	328	2 I47161	Ig gamma 3 chain c
21	1216.5	39.6	329	1 G2GP	Ig gamma-2 chain C
22	1161.5	37.8	308	2 C30554	Ig heavy chain C r
23	1152	37.5	326	2 PS0017	Ig gamma-1 chain C
24	1151	37.5	289	1 G3HUW1	Ig gamma-3 heavy c
25	1146.5	37.3	333	2 PS0018	Ig gamma-2b chain
26	1142	37.2	324	1 G1MS	Ig gamma-1 chain C
27	1141	37.2	329	1 G3MSC	Ig gamma-3 chain C
28	1139	37.1	393	1 G1MSM	Ig gamma-1 chain C
29	1130	36.8	398	1 G3MSM	Ig gamma-3 chain C

30	1126	36.7	330	1 G2MSA	Ig gamma-2a chain
31	1123.5	36.6	335	1 G2MSAB	Ig gamma-2a chain
32	1121	36.5	399	1 G2MSAB	Ig gamma-2a chain
33	1118.5	36.4	329	2 S00847	Ig gamma-2c chain
34	1112	36.2	322	2 PS0019	Ig gamma-2a chain
35	1102	35.9	548	2 S38864	Ig epsilon chain C
36	1092.5	35.6	327	2 S06611	Ig gamma-2 chain C
37	1082	35.2	405	1 G2MSBM	Ig gamma-2b chain
38	1066	34.7	277	2 I47162	Ig gamma 4 chain c
39	866.5	28.2	549	2 S04845	Ig heavy chain pre
40	856.5	27.9	249	2 S69340	Ig heavy chain VHI
41	820.5	26.7	241	2 S69131	Ig heavy chain (DO
42	817.5	26.6	572	2 B46529	Ig y heavy chain (
43	810	26.4	218	2 A36040	Ig heavy chain V-I
44	792	25.8	220	2 A49444	Ig gamma-1 heavy c
45	750	24.4	246	2 S38950	Ig gamma chain - m

ALIGNMENTS

RESULT 1

GHU

Ig gamma-1 chain C region - human

C:Species: Homo sapiens (man)

C:Date: 31-Jan-1981 #sequence revision 18-Aug-1982 #text change 09-Jul-2004  
C:Accession: A93433; S33887; B90563; A90564; B91668; A91723; A02146

R:Ellison, J.W.; Berson, B.J.; Hood, L.E.  
Nucleic Acids Res. 10, 4071-4079, 1982

A:Title: The nucleotide sequence of a human immunoglobulin C-gamma1 gene.

A:Reference number: A93433; MUID:82274238; PMID:6287432

A:Accession: A93433

A:Molecule type: DNA

A:Residues: 1-330 <ELL>

A:Cross-references: UNIPROT:P01857; UNIPARC:UPI0000034C0E; EMBL:Z17370

A:Note: this sequence has the G1m(17) allotypic marker, 97-Lys, and the G1m(1) markers,  
A:Note: Lys-330 is removed after translation

R:Harris, L.J.  
submitted to the EMBL Data Library, October 1992

A:Reference number: S33904

A:Accession: S36861

A:Molecule type: DNA

A:Residues: 2-330 <HAR>

A:Cross-references: UNIPARC:UPI0000013C6FE; EMBL:Z17370

R:Takahashi, N.; Ueda, S.; Obata, M.; Nikaido, T.; Nakai, S.; Honjo, T.  
Cell 29, 671-679, 1982

A:Title: Structure of human immunoglobulin gamma genes: implications for evolution of a  
A:Reference number: S33887; MUID:83001943; PMID:6811139

A:Accession: S33887

A:Molecule type: DNA

A:Residues: 88-113;235-330 <TAK>

A:Cross-references: UNIPARC:UPI0000017378B; UNIPARC:UPI0000017378C; EMBL:Z17370

R:Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman, G.M.  
Biochemistry 9, 3161-3170, 1970

A:Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid sequen

A:Reference number: A90563; MUID:71064024; PMID:5489771

A:Contents: myeloma protein Eu

A:Accession: B90563

A:Molecule type: protein

A:Residues: 1-96, R', 98-135 <CUN>

A:Cross-references: UNIPARC:UPI0000017378D

A:Note: this sequence has the G1m(3) marker, 97-Arg

R:Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.  
Biochemistry 9, 3171-3181, 1970

A:Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid sequen

A:Reference number: A90564; MUID:71064025; PMID:5530842

A:Contents: Eu

A:Accession: A90564

A:Molecule type: protein

A:Residues: 136-154, Q', 156-165, O', 167-176, Q', 178-194, N', 196-197, D', 199-238, E', 240,

A:Cross-references: UNIPARC:UPI0000017378E

A:Note: this sequence has the G1m(non-1) markers, 239-Glu and 241-Met

R:Ponstingl, H.; Hilschmann, N.

Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976  
A>Title: Die Primärstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein Nie),  
igen Primärstruktur.  
A;Reference number: A91668; MUID:77070269; PMID:826475  
A;Contents: myeloma protein Nie  
A;Accession: B91668  
A;Molecule type: protein  
A;Residues: 1-34, Q', 36-96, 'K', 98-115, 'Q', 117-197, 'D', 199-238, 'D', 240, 'L', 242-268, 'E', 27  
A;Cross-references: UNIPARC:UPI000017378F  
A;Note: This sequence has the G1m(17) and G1m(1) markers  
R;Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.  
Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983  
A>Title: Die Primärstruktur des kristallisierten monoklonalen Immunglobulins IgG1 KO  
A;Reference number: A91723; MUID:83289131; PMID:6884994  
A;Contents: myeloma protein KOL; disulfide bonds  
A;Accession: A91723  
A;Molecule type: protein  
A;Residues: 1-96, 'R', 98-197, 'D', 199-238, 'E', 240, 'M', 242-266, 'D', 268-271, 'D', 273-330 <SCH  
A;Cross-references: UNIPARC:UPI0000173790  
A;Note: this sequence has the G1m(3) and G1m(non-1) markers  
R;Gall, W.E.; Edelman, G.M.  
Biochemistry 9, 3188-3196, 1970  
A>Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfid  
A;Reference number: A90565; MUID:71064027; PMID:4923144  
A;Contents: annotation; disulfide bonds  
R;Dreker, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.  
Hoppe-Seyler's Z. Physiol. Chem. 357, 1515-1540, 1976  
A>Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunoglob  
enbrimide cleavage products, and the disulfide bridges.  
A;Reference number: A91667; MUID:77070267; PMID:1003129  
A;Contents: annotation; disulfide bonds  
C;Genetics: GDB:IGHG1  
A;Cross-references: GDB:120085; OMIM:147100  
A;Map position: 14q32.33-14q32.33  
A;Introns: 99/1; 114/1; 224/1  
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap  
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1a  
C;Superfamily: immunoglobulin C region; immunoglobulin homology  
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin  
F;20-85/Domain: immunoglobulin homology <IM2>  
F;137-206/Domain: immunoglobulin homology <IM3>  
F;243-310/Domain: immunoglobulin homology <IM3>  
F;27-83,144-204,250-308/Disulfide bonds: #status experimental  
F;103/Disulfide bonds: interchain (to light chain) #status experimental  
F;109,112/Disulfide bonds: interchain (to heavy chain) #status experimental  
F;180/Binding site: carbohydrate (Asn) (covalent) #status experimental  
Query Match 57.5%; Score 1767; DB 1; Length 330;  
Best Local Similarity 100.0%; Pred. No. 1.4e-92; Mismatches 0; Indels 0; Gaps 0;  
Matches 330; Conservative 0;  
Qy 120 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 179  
Db 1 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60  
Qy 180 GLYSLSSVTVVPSSSLGTQYICNVNHKPSNTKVDKVEKVELTKPLGDTHTTCRCPEPKSC 217  
Db 61 GLYSLSSVTVVPSSSLGTQYICNVNHKPSNTKVDKVEKVELTKPLGDTHTTCRCPEPKSC 120  
Qy 218 -----EPKSCDTHTCPCPAPELLGGPSVFLFPPPKPDT 252  
Db 121 DTPPPCPCPEPKSCDTPPPCPCPEPKSCDTPPPCPCPEPKSCDTPPPCPCPEPKPDT 180  
Qy 253 LMTSRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREQYNSTYRVVSVLTVLH 312  
Db 181 LMTSRTPEVTCVVDVSHEDPEVQFKWYVDGVEVHNAKTKPREQYNSTYRVVSVLTVLH 240  
Qy 313 QDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPOVYTLPPSRDELTKNQVSLTCLVK 372  
Db 241 QDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPOVYTLPPSRDELTKNQVSLTCLVK 300  
Qy 373 GFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFPLYSKLTVDKSRWQQGNVFCSSVMHE 432  
Db 301 GFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFPLYSKLTVDKSRWQQGNVFCSSVMHE 360  
Qy 433 ALHNHYTQKSLSLSPGK 449  
Db 361 ALHNRFYTKSLSLSPGK 377  
RESULT 3  
A60764  
Ig gamma-3 chain C region, form LAT - human  
C;Species: Homo sapiens (man)  
C;Date: 14-May-1993 #sequence\_revision 14-May-1993 #text\_change 31-Dec-2004  
C;Accession: A60764  
R;Huck, S.; Lefranc, G.; Lefranc, M.P.  
Immunogenetics 30, 250-257, 1989  
A>Title: A human immunoglobulin IGHG3 allele (Gmb0, b1, c3, c5, u) with an IGH4 convert  
A;Reference number: A60764; MUID:90007613; PMID:2571587  
A;Accession: A60764  
A;Status: preliminary  
A;Molecule type: DNA

Db 301 QQGNVFCSCVMHEALHNHYTKSLSLSPGK 330  
|||||  
RESULT 2  
A23511  
Ig gamma-3 chain C region (allotype G3m(b)) - human  
C;Species: Homo sapiens (man)  
C;Date: 28-Dec-1987 #sequence\_revision 28-Dec-1987 #text\_change 23-Jul-1999  
C;Accession: A23511  
R;Huck, S.; Fort, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G.  
Nucleic Acids Res. 14, 1779-1789, 1986  
A>Title: Sequence of a human immunoglobulin gamma 3 heavy chain constant region  
A;Reference number: A23511; MUID:86148507; PMID:3081877  
A;Accession: A23511  
A;Molecule type: DNA  
A;Residues: 1-377 <HUC>  
A;Cross-references: UNIPARC:UPI000004718F; GB:X03604; GB:M12958; NID:933070; PIDN:CAA272;  
C;Genetics: GDB:IGHG3  
A;Cross-references: GDB:119339; OMIM:147120  
A;Map position: 14q32.33-14q32.33  
A;Introns: 98/3; 115/3; 130/3; 145/3; 160/3; 270/3  
C;Superfamily: immunoglobulin C region; immunoglobulin homology  
C;Keywords: immunoglobulin  
F;20-85/Domain: immunoglobulin homology <IM>  
Query Match 53.1%; Score 1630.5; DB 2; Length 377;  
Best Local Similarity 82.0%; Pred. No. 7.8e-85;  
Matches 309; Conservative 10; Mismatches 11; Indels 47; Gaps 1;  
Qy 120 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 179  
Db 1 ASTKGPSVFPPLAPCSRSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60  
Qy 180 GLYSLSSVTVVPSSSLGTQYICNVNHKPSNTKVDKVV----- 217  
Db 61 GLYSLSSVTVVPSSSLGTQYICNVNHKPSNTKVDKVELTKPLGDTHTTCRCPEPKSC 120  
Qy 218 -----EPKSCDTHTCPCPAPELLGGPSVFLFPPPKPDT 252  
Db 121 DTPPPCPCPEPKSCDTPPPCPCPEPKSCDTPPPCPCPEPKSCDTPPPCPCPEPKPDT 180  
Qy 253 LMTSRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREQYNSTYRVVSVLTVLH 312  
Db 181 LMTSRTPEVTCVVDVSHEDPEVQFKWYVDGVEVHNAKTKPREQYNSTYRVVSVLTVLH 240  
Qy 313 QDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPOVYTLPPSRDELTKNQVSLTCLVK 372  
Db 241 QDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPOVYTLPPSRDELTKNQVSLTCLVK 300  
Qy 373 GFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFPLYSKLTVDKSRWQQGNVFCSSVMHE 432  
Db 301 GFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFPLYSKLTVDKSRWQQGNVFCSSVMHE 360  
Qy 433 ALHNHYTQKSLSLSPGK 449  
Db 361 ALHNRFYTKSLSLSPGK 377  
RESULT 3  
A60764  
Ig gamma-3 chain C region, form LAT - human  
C;Species: Homo sapiens (man)  
C;Date: 14-May-1993 #sequence\_revision 14-May-1993 #text\_change 31-Dec-2004  
C;Accession: A60764  
R;Huck, S.; Lefranc, G.; Lefranc, M.P.  
Immunogenetics 30, 250-257, 1989  
A>Title: A human immunoglobulin IGHG3 allele (Gmb0, b1, c3, c5, u) with an IGH4 convert  
A;Reference number: A60764; MUID:90007613; PMID:2571587  
A;Accession: A60764  
A;Status: preliminary  
A;Molecule type: DNA





Ig gamma-4 chain C region - human  
C:Species: Homo sapiens (man)  
C:Date: 02-Apr-1982 #sequence\_revision 02-Apr-1982 #text\_change 09-Jul-2004  
C:Accession: A30933; A90249; A02150  
R:Ellison, J.; Buxbaum, J.; Hood, L.  
DNA 1, 11-18, 1981  
A:Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.  
A:Reference number: A30933; MUID:83157104; PMID:6299662  
A:Accession: A30933  
A:Molecule type: DNA  
A:Residues: 1-327 <ELL>  
A:Cross-references: UNIPROT:P01861; UNIPARC:UPI0000047190  
A:Note: the sequence was determined from the germline gene  
R:Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C.  
Biochem. J. 117, 33-47, 1970  
A:Title: Human immunoglobulin subclasses. Partial amino acid sequence of the constant  
A:Reference number: A30249; MUID:70207560; PMID:4192699  
A:Accession: A30249  
A:Molecule type: protein  
A:Residues: 1-30; 81-326 <PIN>  
A:Cross-references: UNIPARC:UPI0000173795; UNIPARC:UPI0000173796  
C:Genetics:  
A:Gene: GDB:IGHG4  
A:Cross-references: GDB:119340; OMIM:147130  
A:Map position: 14q32.33-14q32.33  
A:Introns: 99/1; 111/1; 221/1  
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger disulfide bonds. interchain (to heavy chain) #status experimental  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin  
F:20-85/Domain: immunoglobulin homology <IM1>  
F:99-110/Region: hinge  
F:134-203/Domain: immunoglobulin homology <IM2>  
F:240-307/Domain: immunoglobulin homology <IM3>  
F:14/Disulfide bonds: interchain (to light chain) #status experimental  
F:27-83, 141-201, 247-305/Disulfide bonds: #status predicted  
F:106, 109/Disulfide bonds: interchain (to heavy chain) #status experimental  
F:177/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 51.8%; Score 1590.5; DB 1; Length 327;  
Best Local Similarity 90.9%; Pred. No. 1.2e-82;  
Matches 300; Conservative 12; Mismatches 15; Indels 3; Gaps 1;

QY 120 ASTKGPSVFPPLAPSKSTSGGTAALGCLVKDYFPPPTVSNWNSGALTSGVHTFPAVLQSS 179  
DB 1 ASTKGPSVFPPLAPCSRSTSESTAALGCLVKDYFPPPTVSNWNSGALTSGVHTFPAVLQSS 60

QY 180 GLYSLSVVTVFPSSSLGTQTYICNVNPKSNTKVDKVPKSCDKTHTCPPCPAPELAGG 239  
DB 61 GLYSLSVVTVFPSSSLGTQTYICNVNPKSNTKVDKVPKSCDKTHTCPPCPAPELAGG 117

QY 240 PSVLFPPPKDXTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVVEVHNATKPREEQYN 299  
DB 118 PSVLFPPPKDXTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVVEVHNATKPREEQFN 177

QY 300 STYRVVSVLTVLHQDLNGKEYCKVSNKALPAPIETKISKAKGQPREPQVYTLPPSRDE 359  
DB 178 STYRVVSVLTVLHQDLNGKEYCKVSNKALPAPIETKISKAKGQPREPQVYTLPPSQEE 237

QY 360 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 419  
DB 238 MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 297

QY 420 QQGNVFCVSNVMEALHNHYTQKSLSLSPGK 449  
DB 298 QQGNVFCVSNVMEALHNHYTQKSLSLSPGK 327

RESULT 6  
PC4436  
monoclonal antibody 13-1 heavy chain - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 04-Feb-1998 #sequence\_revision 13-Mar-1998 #text\_change 21-Jan-2000

C:Accession: PC4436  
R:Akashi, S.; Kato, K.; Torizawa, T.; Dohmae, N.; Yamaguchi, H.; Kamachi, M.; Harada, A.  
Biochem. Biophys. Res. Commun. 240, 566-572, 1997  
A:Title: Structural characterization of mouse monoclonal antibody 13-1 against a porphyrin  
A:Reference number: JC5810; MUID:98063277; PMID:9398605  
A:Accession: PC4436  
A:Molecule type: protein  
A:Residues: 1-444 <AKA>  
A:Cross-references: UNIPARC:UPI0000176F41  
C:Comment: This catalytic antibody has peroxidase activity. It is directed against  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
F:251-320/Domain: immunoglobulin homology <IMM>  
F:22/Disulfide bonds: interchain (to 98) #status predicted  
F:99/Disulfide bonds: interchain (to 109) #status predicted

Query Match 49.1%; Score 1508.5; DB 2; Length 444;  
Best Local Similarity 61.1%; Pred. No. 7.1e-78;  
Matches 277; Conservative 73; Mismatches 90; Indels 13; Gaps 6;

QY 1 EVQLVESGGDFVQPGGSLRVSCAASGFAFSAHYAMSWRQAPGKLEWVAIIS--SGSGT 58  
DB 1 EVQVETGGGLVRPGNSLKLSCLTSGFTFSNRYMRHLRQPPGKLEWIAVIIVKSDNYGA 60

QY 59 YYSVSVKGRPTISRDNSTKNTLYLQMRSLRAEDSAVYFCTRVKLTGYTFDSWGQGLTLTVS 118  
DB 61 KYAESVGRFTISRDDSKSVYLQWNLREEDTATYYCCRTP-WYAMDCKGQSTSVIS 119

QY 119 SASTKGPSVFPPLAPSKSTSGGTAALGCLVKDYFPPPTVSNWNSGALTSGVHTFPAVLQSS 178  
DB 120 SAKTTPPSVYPLAPGSAATNSMVTGLCLVKGFYPPPTVSNWNSGALTSGVHTFPAVLQSS 179

QY 179 SGLYSLSVVTVFPSSSLGTQTYICNVNPKSNTKVDKVPKSCDKTHTCPP--CPAPEL 236  
DB 180 D-LYTLSSSVTVFPSSSTWPESETVTCTVAHPASSTKVDKXIIVPRDCG----CKPCICTVPEV 234

QY 237 LGGSPVLFPPPKDXTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVVEVHNATKPREE 296  
DB 235 ---SSVFIFFPKPKDXTLTITPKVTCVVDVSHEDPEVKFNWYVDGVVEVHTAQTPREE 291

QY 297 QYNSTYRVVSVLTVLHQDLNGKEYCKVSNKALPAPIETKISKAKGQPREPQVYTLPPS 356  
DB 292 QFNSTFRSVSELPIMHQDLNGKEYCKVSNKALPAPIETKISKAKGQPREPQVYTLPPP 351

QY 357 RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDK 416  
DB 352 KEQMAKDKVSLTMITDFFPEDITVEQWNGQPAENYKNTQPIIMDTDGSYFVSKLVNQK 411

QY 417 SRWQGNVFCVSNVMEALHNHYTQKSLSLSPGK 449  
DB 412 SNWEAGNTFTCSVLHSEGLHNHTKLSLSHSPGK 444

RESULT 7  
S22080  
Ig heavy chain precursor (B/MT-4A.17.H5.A5) - bovine  
A:Alternate names: Ig gamma-1 chain C region (clone 8.10)  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 23-Jul-1999  
C:Accession: S22080; S06610; A31303  
R:Sanders, P.G.  
submitted to the EMBL Data Library, November 1991  
A:Reference number: S22080  
A:Accession: S22080  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-470 <SAN>  
A:Cross-references: UNIPARC:UPI0000116007; EMBL:X62916; NID:9439; PID:CAA44699.1; PID:9  
R:Symons, D.B.A.; Clarkson, C.A.; Beale, D.  
Mol. Immunol. 26, 841-850, 1989  
A:Title: Structure of bovine immunoglobulin constant region heavy chain gamma 1 and gamma  
A:Reference number: S06610; MUID:90097956; PMID:2513487  
A:Accession: S06610  
A:Molecule type: DNA

A;Residues: 142-470 <SYM>  
A;Cross-References: UNIPARC:UPI0000176F36; EMBL:X16701  
A;Note: the sequence was determined from the germline gene  
C;Genetics:  
A;Gene: Ig CH gamma-1  
A;Introns: 98/1; 111/1; 221/1  
C;Superfamily: immunoglobulin C region; immunoglobulin homology  
C;Keywords: glycoprotein; heterotetramer; immunoglobulin; membrane protein  
F;161-225/Domain: immunoglobulin homology <IMM>  
F;318/Binding site: carbohydrate (Asn) #status predicted

Query Match 48.4%; Score 1487; DB 2; Length 470;  
Best Local Similarity 62.4%; Pred. No. 1.2e-76;  
Matches 284; Conservative 60; Mismatches 101; Indels 10; Gaps 6;

QY 1 EVLVESGGDFVOPGSLRVSCAASGFAFASHYAMSVWRQAPGKLEWVAYISSGGSGTY 60  
DB 20 QVLRSGPSLVKPKGQTLSTCTVSGFSLSSVYALTWRQAPGKLEWVGGITSGGT-TY 78

QY 61 SDSVKGRFTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLTGTY----YFDSWGQTLT 116  
DB 79 NPALKSRLSITKENSQSVLSVSTPEDTATYYCARSTYGEVGDGAIDAMWGQLLVT 138

QY 117 VSSASTKGPSVPLAPSSKSTSGGTAALGCLVKDYFPEPVTVMNSGALTSGVHTFPAVL 176  
DB 139 VSSASTTAPKVTPLSSCCGDKSSVTILGCLVSSNPPEPVTVMNSGALKSGVHTFPAVL 198

QY 177 QSSGLYSLSVVTPVSSSLGTQTYICNVNHPKNTKVDKVPKSCDKTHTCPPEL 236  
DB 199 QSSGLYSLSVMVTPVSGTSG-QTFCTCNAHPASSTKVDKAVDP-TC-KPSPCDCPPPEL 255

QY 237 LGGPSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 296  
DB 256 PGGPSVFIFPPPKKDTLISGTPEVTCVVVDVGHDDPEVKESWFDVDDVEVNTATTKPREE 315

QY 297 QYNSTRYRVSVLTVLHQDLNGKEYCKVSKNKAIPAPIETISKAKGQPREPOVYTLPPS 356  
DB 316 QFNSTRYRVSVLRIQHDMWTEGKEPKCKVHNEGFLPAPIRTISRTKGPARBPQVYVLAPP 375

QY 357 RDELTKNQVSLTCLVKGFYPSDIAVEWESNGOP--ENNYKTTTPPVLDSDGFFLYSKLT 414  
DB 376 QEELSKSTVSLTCMTVSYFPDYIAVEWQBNQGPESDKYGTTPQLDADSSVFLYSLRV 435

QY 415 DKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 449  
DB 436 DRNSHQEGDTYTCVMVHEALHNHYTQKSLSGAGK 470

RESULT 8  
S37483  
Ig gamma-2a chain - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 23-Jul-1999  
C;Accession: S37483  
R;Ducancel, F.F.D.  
submitted to the EMBL Data Library, February 1993  
A;Reference number: S37483  
A;Accession: S37483  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-469 <DUC>  
A;Cross-References: UNIPARC:UPI00002FB47; EMBL:X70423; NID:g406252; PIDN:CAA49868.1; PI  
C;Superfamily: immunoglobulin C region; immunoglobulin homology  
C;Keywords: immunoglobulin

Query Match 46.9%; Score 1440.5; DB 2; Length 469;  
Best Local Similarity 59.1%; Pred. No. 5.2e-74;  
Matches 267; Conservative 72; Mismatches 108; Indels 5; Gaps 4;

QY 1 EVLVESGGDFVOPGSLRVSCAASGFAFASHYAMSVWRQAPGKLEWVAYISSGGSGTY 60  
DB 20 QIQLQQSGPELVKPGASVKISCKSGYTFDYIYNWVKQKQGLKIGWIYPASGNTKY 79

A;Residues: 142-470 <SYM>  
A;Cross-References: UNIPARC:UPI0000176F36; EMBL:X16701  
A;Note: the sequence was determined from the germline gene  
C;Genetics:  
A;Gene: Ig CH gamma-1  
A;Introns: 98/1; 111/1; 221/1  
C;Superfamily: immunoglobulin C region; immunoglobulin homology  
C;Keywords: glycoprotein; heterotetramer; immunoglobulin; membrane protein  
F;161-225/Domain: immunoglobulin homology <IMM>  
F;318/Binding site: carbohydrate (Asn) #status predicted

Query Match 46.8%; Score 1437; DB 2; Length 446;  
Best Local Similarity 59.3%; Pred. No. 7.7e-74;  
Matches 267; Conservative 70; Mismatches 107; Indels 6; Gaps 4;

QY 1 EVLVESGGDFVOPGSLRVSCAASGFAFASHYAMSVWRQAPGKLEWVAYISSGGSGTY 60  
DB 1 QIQLQQSGPELVKPGASVKISCKSGYTFDYIYNWVKQKQKQGLKIGWIYPASGNTKY 60

QY 61 SDSVKGRFTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLTGTYFYFDSWGQTLT 120  
DB 61 NEKFKGKATLTVDTSSTAYNQLSSLTSEDSAVYFCARG--GKFAMDYWGQTSVT 118

A;Residues: 142-470 <SYM>  
A;Cross-References: UNIPARC:UPI0000176F38  
A;Note: the sequence was determined from the germline gene  
C;Genetics:  
A;Gene: Ig CH gamma-1  
A;Introns: 98/1; 111/1; 221/1  
C;Superfamily: immunoglobulin C region; immunoglobulin homology  
C;Keywords: glycoprotein; heterotetramer; immunoglobulin; membrane protein  
F;161-225/Domain: immunoglobulin homology <IMM>  
F;318/Binding site: carbohydrate (Asn) #status predicted

Query Match 46.8%; Score 1437; DB 2; Length 446;  
Best Local Similarity 59.3%; Pred. No. 7.7e-74;  
Matches 267; Conservative 70; Mismatches 107; Indels 6; Gaps 4;

QY 1 EVLVESGGDFVOPGSLRVSCAASGFAFASHYAMSVWRQAPGKLEWVAYISSGGSGTY 60  
DB 1 QIQLQQSGPELVKPGASVKISCKSGYTFDYIYNWVKQKQKQGLKIGWIYPASGNTKY 60

QY 61 SDSVKGRFTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLTGTYFYFDSWGQTLT 120  
DB 61 NEKFKGKATLTVDTSSTAYNQLSSLTSEDSAVYFCARG--GKFAMDYWGQTSVT 118



C:Species: Mus musculus (house mouse)  
C:Date: 31-Mar-1980 #sequence\_revision 01-Dec-2000 #text\_change 09-Jul-2004  
C:Accession: S25057; A02157; A26235; A26232; A26233; A53598  
R:Fischer, R.; Voss, A.; Niersbach, M.; Munziker, W.; Hirsch, H.J.; Kreuzaler, F.  
submitted to the EMBL Data Library, July 1992  
A:Description: Production of a Tobacco mosaic virus (TMV) inactivating neotop specific m  
A:Reference number: S25057  
A:Accession: S25057  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-474 <FIS>  
A:Cross-references: UNIPROT:P01866; UNIPARC:UPI0000116095; EMBL:X67210; NID:G54826; PIDN  
R.Yanawaki-Kataoka, Y.; Kataoka, T.; Takahashi, N.; Obata, M.; Honjo, T.  
Nucleic Acids Res. 1980; 8:789-798  
A:Title: Complete nucleotide sequence of immunoglobulin gamma2b chain gene cloned from m  
A:Reference number: A02157; MUID:80120716; PMID:6766534  
A:Contents: a allele  
A:Accession: A02157  
A:Molecule type: DNA  
A:Residues: 138-161, 'L', 163-189, 'FP', 193-474 <YAM>  
A:Cross-references: UNIPARC:UPI00000272D2; GB:J00461  
A:Note: the sequence was determined from the germline gene  
R:Tucker, P.W.; Marcu, K.B.; Slightom, J.L.; Blattner, F.R.  
Science 206, 1299-1303, 1979  
A:Title: Structure of the constant and 3' untranslated regions of the murine gamma2b hea  
A:Reference number: A26235; MUID:80081501; PMID:117548  
A:Contents: MPC 11  
A:Accession: A26235  
A:Molecule type: mRNA  
A:Residues: 138-172, 'P', 174-189, 'FP', 193-376, 'T', 378-474 <TU1>  
A:Cross-references: UNIPARC:UPI00001737AF  
A:Note: Lys-474 is probably removed posttranslationally  
R:Tucker, P.W.; Marcu, K.B.; Newell, N.; Richards, J.; Blattner, F.R.  
Science 206, 1303-1306, 1979  
A:Title: Sequence of the cloned gene for the constant region of murine gamma2b immunoglob  
A:Reference number: A26232; MUID:80081502; PMID:117549  
A:Accession: A26232  
A:Molecule type: DNA  
A:Residues: 138-172, 'P', 174-189, 'FP', 193-376, 'T', 378-474 <TU2>  
A:Cross-references: UNIPARC:UPI00001737AF  
R:Ollo, R.; Rougeon, F.  
Nucleic Acids Res. 1982; 10:763-768  
A:Title: Mouse immunoglobulin allotypes: post-duplication divergence of gamma2a and gamma  
A:Reference number: A26233; MUID:82173203; PMID:6803173  
A:Contents: b allele  
A:Accession: A26233  
A:Molecule type: DNA  
A:Residues: 138-161, 'L', 163-189, 'FP', 193-300, 'R', 302-331, 'A', 333-437, 'DI', 440-474 <OLL>  
A:Cross-references: UNIPARC:UPI00001737B0; GB:J00461  
R:Kim, H.; Yamaguchi, Y.; Masuda, K.; Matsunaga, C.; Yamamoto, K.; Irimura, T.; Takahashi  
J. Biol. Chem. 269, 12345-12350, 1994  
A:Title: O-glycosylation in hinge region of mouse immunoglobulin G2b.  
A:Reference number: A53598; MUID:94216359; PMID:7512967  
A:Accession: A53598  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 234-251 <KIM>  
A:Cross-references: UNIPARC:UPI00001737B1  
C:Comment: The a allele sequence is shown.  
C:Genetics:  
A:Introns: 138/1; 236/1; 258/1; 368/1  
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap  
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglob  
F:157-222/Domain: immunoglobulin homology <IMI>  
F:236-257/Region: hinge  
F:281-350/Domain: immunoglobulin homology <IM2>  
F:387-454/Domain: immunoglobulin homology <IM3>  
F:152/Disulfide bonds: interchain (to light chain) #status predicted  
F:164-220, 228-348, 394-452/Disulfide bonds: #status predicted  
F:247, 250, 253, 256/Disulfide bonds: interchain (to heavy chain) #status predicted  
F:324/Binding site: carbohydrate (Aen) (covalent) #status predicted

Query Match 45.3%; Score 1390; DB 1; Length 474;  
Best Local Similarity 56.6%; Pred. No. 3.7e-71; Indels 14; Gaps 4;  
Matches 260; Conservative 72; Mismatches 113;  
QY 1 EVQLVESGGGVDPQGGSLRVSCAASGFAFSAFHYAMSWVRQAPKGLEWVAYISSGGSGTY 60  
DB 20 EVQLQQSGPELVNPGASVKMSCKASGYTFITVYVHMHWKQKPGQGLEWIGYINPNKGTKF 79  
QY 61 SDSVKGRFTISRDNKNTLYLQMRSRAEDSAVYFCFTRVKLTGY---YFDSWGGQGLLT 117  
DB 80 NEKFKGRATLTSDKSSNTAYMELSSLTSEDSAVYFCAR----DYDYDFWFAFWGGTTLTV 135  
QY 118 SSAETKGPSVPLAPSSKTSISGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHPFPAVLQ 177  
DB 136 SAAKTTTPSVVPLAPGCGDITGSSVTGCLVKGYFPPESVTVWNSGSLSSVHTLSQALL 195  
QY 178 SSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSTNKVDKVPKSCDKT-HTCPP----- 230  
DB 196 QSGLYTWSSSVTVSSWTPSQTVTCVAHPASSITVDKLEPSPGISTINFCPCCKECHK 255  
QY 231 CPAPELLGGPSVFLFPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK 290  
DB 256 CPAPNLGGPSVFLFPPNPKDKVLSLTPTKVTCTVVDVSEDDPDVQISWFMVNNVEVHTAQ 315  
QY 291 TKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPRPOV 350  
DB 316 TQTHREDYNTIRVSVTLPIQHQDMSGKEPKCKVNNKDLSPFIERTISKIKGLVRAPQV 375  
QY 351 YTLPPSRDELTKNOVSLTCLVKGFVPSDIAVEWESNGQPENNYKTPPVLDSDGSFFFLYS 410  
DB 376 YILPPAPAEQLSKRDKVSLTCLVGFNPGDISVWNTSGHTENYKDTAPVLSDSGSYFIYS 435  
QY 411 KLTVDKRWQOQGNFVSCSVMEALHNHYTKLSLSPOK 449  
DB 436 KLNKMTSKWEKTSFSCNVRHEGLKNVYLKKTISRSPGK 474  
RESULT 13  
S01321  
Ig gamma-2b chain precursor - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 30-Sep-1989 #sequence\_revision 30-Sep-1989 #text\_change 23-Jul-1999  
A:Accession: S01321  
R:de Waele, P.; Feys, V.; van de Voorde, A.; Moelmanns, F.; Fiers, W.  
Eur. J. Biochem. 176, 287-295, 1988  
A:Title: Expression in non-lymphoid cells of mouse recombinant immunoglobulin directed a  
A:Reference number: S01320; MUID:88323081; PMID:3138116  
A:Accession: S01321  
A:Molecule type: mRNA  
A:Residues: 1-475 <DEL>  
A:Cross-references: UNIPARC:UPI0000115DDDB; EMBL:X13188; NID:G51780; PIDN:CAA31580.1; PID  
A:Note: this sequence was determined from the differentiated gene  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: immunoglobulin  
F:1-19/Domain: signal sequence #status predicted <SIG>  
F:20-475/Product: Ig gamma-2b chain #status predicted <MAT>  
F:159-223/Domain: immunoglobulin homology <IMW>  
Query Match 44.5%; Score 1367.5; DB 2; Length 475;  
Best Local Similarity 56.2%; Pred. No. 6.8e-70;  
Matches 257; Conservative 75; Mismatches 116; Indels 9; Gaps 4;  
QY 1 EVQLVESGGGVDPQGGSLRVSCAASGFAFSAFHYAMSWVRQAPKGLEWVAYISSGGSGTY 60  
DB 20 QVQLQSGAEIARFQASVKLSCKASGYTLTSYGSWVKQRTQGGLEWIGEYIPSGNSYF 79  
QY 61 SDSVKGRFTISRDNKNTLYLQMRSRAEDSAVYFCFTRVK-LGYTFPSWGGQGLLT 119  
DB 80 NEKFKGRATLTVDKSSSTAYLHLSLTSEDSAVYFCAGPRQVGLLPFGYWGQGLTVTASA 139  
QY 120 ASTKGPSVPLAPSSKTSISGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 179

Db 140 AKTTPSVYPLAPGCGDTTGGSVTLGCLVKGYPFESVITVWNSGLSSSVHTFPALLQ-S 198

Qy 180 GLYSLSSVVTVPSSSLGTQTYICNHNKPSNTKVKVPEKSCDKT-HTCpP-----Cp 232

Db 199 GLYTHSSSVTVPSSWTPGQVTCVAHPASSITVDKLEPSPGPTSTINPCPCKECHKCP 258

Qy 233 APELLGGPSVFLFPFKPKDXTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEHNNAKT 292

Db 259 APNLGGGPSVTFPPFNKIDVLMISLTPKVTVCVVVDSDDDPDVQISWFVNNVFLTAQTQ 318

Qy 293 PREEOYNSTYRVVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTIISKAKGQPREPQVYT 352

Db 319 THREDYNSTIRVVSALP:QHQQDMSGSEKFKVNNKDLPAPIERTISIKIGIVRAPQYI 378

Qy 353 LPPSRDELTKNQVSLTCLVKGPYSDIAVEESNGQPENNYKTTTPVLDSDGSRFLYSKL 412

Db 379 LSPPEQSRKQDVSLTCLAVGSPSDISVEWTSNGHTBENYKDTAPVLDSDGSRFYISKL 438

Qy 413 TVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 449

Db 439 NMKTSKWEKTDSEFCNVRHEGLKNLYLKKTISRSPGK 475

RESULT 14

147159

Ig gamma 2a chain constant region - pig (fragment)

C:Species: Sus scrofa domestica (domestic pig)

C:Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 21-Jan-2000

C:Accession: I47159

R:Kacskovics, I.; Sun, J.; Butler, J.E.

J. Immunol. 153, 3565-3573, 1994

A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a

A:Reference number: 147159; MUID:95015845; PMID:7930579

A:Accession: I47159

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-328 <KAC>

A:Cross-references: UNIPARC:UPI0000115524; EMBL:U03779; NID:G433123; PIDN:AA52217.1; PI

C:Superfamily: immunoglobulin C region; immunoglobulin homology

F:133-202/Domain: immunoglobulin homology <IMM>

Query Match 41.1%; Score 1263; DB 2; Length 328;

Best Local Similarity 69.6%; Pred. No. 3.3e-64;

Matches 231; Conservative 43; Mismatches 52; Indels 6; Gaps 2;

Qy 120 ASTKGPSVFPPLAPSSKTSGGTAALGCLVKDYFPEPFTVSNWNSGALTSGVHTFPAVLQSS 179

Db 1 APKTAPSVYPLAPCSRDTSGPNVALGCLASSYFPEPFTVTVWNSGALSSGVHTFPSVLQPS 60

Qy 180 GLYSLSSVVTVPSSSLGTQTYICNHNKPSNTKVKVPEKSCDKTHTCPCPAPPELLGG 239

Db 61 GLYSLSSMTVPASSLSKSYTCNVNHPATTTKVDKRVGTKTKPPCPICPACESP----G 116

Qy 240 PSVFLFPKPKDXTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEHNNAKTKEEEOYN 299

Db 117 PSVFLFPKPKDXTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEHNNAKTKEEEOFN 176

Qy 300 STYRVSVSLTVLHODWLNKGEYKCKVSNKALPAPIEKTIISKAKGQPREPQVYTLPPSRDE 359

Db 177 STYRVSVSLP:QHQQDNLNGKEFKCKVNNKDLPAPIRTIISKAKGQTRPEPQVYTLPPHAE 236

Qy 360 LTKNQVSLTCLVKGPYSDIAVEESNGQ--PENNYKTTTPVLDSDGSRFLYSKLTVDKS 417

Db 237 LSRKSVSITCLVIGFPPDIDVEMQRNGQPEPEGNRYRTTPPQQVDGTYFLYSKFSVDKA 296

Qy 418 RWOQGNVFCSCVMHEALHNHYTQKSLSLSPGK 449

Db 297 SWQGGGIFQCAVMHEALHNHYTQKSISKTPGK 328

S31866

Ig gamma-1 chain C region - synthetic

C:Species: synthetic

A:Note: Homo sapiens (man) gene engineered and expressed in Escherichia coli

C:Date: 06-Jan-1995 #sequence\_revision 17-Mar-1997 #text\_change 19-May-2000

C:Accession: S31866

R:Filipula, D.

submitted to the EMBL Data Library, February 1993

A:Description: Screening method for protein-protein interactions of cloned gene products.

A:Reference number: S31866

A:Accession: S31866

A:Molecule type: mRNA

A:Residues: 1-255 <FTL>

A:Cross-references: UNIPARC:UPI000011F41F; EMBL:X70421; NID:G33068; PIDN:CAA49866.1; PID

C:Keywords: immunoglobulin

F:1-22/Region: Escherichia coli outer membrane protein A precursor

F:23-255/Region: human ig gamma-1 chain C region

Query Match 41.0%; Score 1260; DB 4; Length 255;

Best Local Similarity 97.5%; Pred. No. 3.6e-64;

Matches 233; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 211 TVVDKVKVEPKSCDKTHTCPCPAPPELLGGPSVFLFPFKPKDXTLMISRTPEVTCVVVDVSH 270

Db 17 TVAQADVESKCDKTHTCPCPAPPELLGGPSVFLFPFKPKDXTLMISRTPEVTCVVVDVSH 76

Qy 271 EDPEVKFNWYVDGVEHNNAKTKEEEOYNSTYRVVSVLTVLHODWLNKGEYKCKVSNKAL 330

Db 77 EDPEVKFNWYVDGVEHNNAKTKEEEOYNSTYRVVSVLTVLHODWLNKGEYKCKVSNKAL 136

Qy 331 PAPIEKTIISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGPYPSDIAVEESNGQPE 390

Db 137 PAPIEKTIISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGPYPSDIAVEESNGQPE 196

Qy 391 NNYKTTTPVLDSDGSRFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 449

Db 197 NNYKTTTPVLDSDGSRFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 255

Search completed: April 6, 2006, 08:54:31

Job time : 30.8299 secs



Result No.	Query			ID	Description		
	Score	Match	Length				
1	2230.5	72.6	469	2	Q569F4_HUMAN	Q569f4	homo sapien
2	2223	72.4	470	2	Q6PJ4_HUMAN	Q6pj4	homo sapien
3	2212	72.0	478	2	Q6PI81_HUMAN	Q6pi81	homo sapien
4	2211.5	72.0	475	2	Q6MZQ6_HUMAN	Q6mzq6	homo sapien
5	2191.5	71.4	473	2	Q6MZV7_HUMAN	Q6mzv7	homo sapien
6	2188.5	71.3	475	2	Q6GMW7_HUMAN	Q6gmw7	homo sapien
7	2187	71.2	466	2	Q61N78_HUMAN	Q61n78	homo sapien
8	2187	71.2	472	2	Q6N089_HUMAN	Q6n089	homo sapien
9	2184.5	71.1	544	2	Q6PJ95_HUMAN	Q6pj95	homo sapien
10	2172	70.7	480	2	Q6N094_HUMAN	Q6n094	homo sapien
11	2165.5	70.5	475	2	Q5EFES_HUMAN	Q5efes	homo sapien
12	2159	70.3	466	2	Q6N096_HUMAN	Q6n096	homo sapien
13	2158	70.3	470	2	Q725W1_HUMAN	Q725w1	homo sapien
14	2149.5	70.0	473	2	Q6P055_HUMAN	Q6p055	homo sapien
15	2134	69.5	482	2	Q72351_HUMAN	Q72351	homo sapien
16	2105.5	68.6	481	2	Q6N097_HUMAN	Q6n097	homo sapien
17	2083.5	67.8	469	2	Q727P5_HUMAN	Q727p5	homo sapien
18	2064	67.2	476	2	Q6GMX1_HUMAN	Q6gmx1	homo sapien
19	2062.5	67.2	475	2	Q6N095_HUMAN	Q6n095	homo sapien
20	2056.5	67.0	465	2	Q6GMX6_HUMAN	Q6gmx6	homo sapien
21	2045	66.6	464	2	Q6MZU6_HUMAN	Q6mzu6	homo sapien
22	2041.5	66.5	480	2	Q6EUFF_HUMAN	Q6epjf1	homo sapien
23	2041.5	66.5	465	2	Q6P6C4_HUMAN	Q6p6c4	homo sapien
24	2015.5	65.6	475	2	Q5RE17_PONPY	Q5re17	pongo pygma
25	1998.5	65.1	521	2	Q8N4Y9_HUMAN	Q8n4y9	homo sapien
26	1967	64.1	518	2	Q6N030_HUMAN	Q6n030	homo sapien
27	1955	63.7	470	2	Q6SCN4_HUMAN	Q6scn4	homo sapien
28	1945	63.3	417	2	Q6N093_HUMAN	Q6n093	homo sapien
29	1918.5	62.5	519	2	Q5SBM2_HUMAN	Q5sbm2	homo sapien
30	1841	59.9	473	2	Q8TC63_HUMAN	Q8tc63	homo sapien
31	1818	59.2	348	2	Q6PYX1_HUMAN	Q6pyx1	homo sapien





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RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ussdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Sanchez A.,
RA Faney J., Helton E., Kettner M., Madan A.C., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Groumwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RG NIH MGC Project;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC041037; AAH41037.1; -, mRNA.
DR HSSP; P01861; 1ADO.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig.cl.
DR InterPro; IPR003006; Ig.MHC.
DR InterPro; IPR003596; Ig.v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
SQ SEQUENCE 478 AA; 52667 MW; 17BED38D917970D6 CRC64;

Query Match 72.0%; Score 2212; DB 2; Length 478;
Best Local Similarity 91.3%; Pred. No. 7.2e-134;
Matches 419; Conservative 10; Mismatches 20; Indels 10; Gaps 2;

Qy 1 EVQLVESGGDFVQPGSLRVS CAASGFAFSPHYAMSVWRQAPGKLEWVAYISSGSGTY 60
Db 20 EVQLVESGGGLVQPGSLRLS CAASGFTFRYAMNVRQAPGKLEWVSGISSGVNTY 79

Qy 61 SDSVKGRFTISRDNKNTLYLQMSLR AEDSAVFCTRVKLGTY-----VKLGTYF--DSWG 110
Db 80 VDSVKGRFTISRDNKNTLYLQMSLR AEDTAVYYCARPEFSTMTTNADYYFYFMDVWG 139

Qy 111 QGTLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPPPTVSVNWSGALTSGVH 170
Db 140 KGTITVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPPPTVSVNWSGALTSGVH 199

Qy 171 TFPVAVLQSSGLYSLSVVTVPSSSLGTQTYICNVNHPKSNKTKVDPKPEKCDKTHTCPP 230
Db 200 TFPVAVLQSSGLYSLSVVTVPSSSLGTQTYICNVNHPKSNKTKVDPKPEKCDKTHTCPP 259

Qy 231 CPAPELLGGPSVFLFPPPKDPTLMISRPTVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK 290
Db 260 CPAPELLGGPSVFLFPPPKDPTLMISRPTVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK 319

Qy 291 TKPREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPQV 350
Db 320 TKPREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPQV 379

Qy 351 YTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDSGSFYLS 410
Db 380 YTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDSGSFYLS 439

Qy 411 KLTVDKSRWQGNVFCSCVMHEALHNNHYTKQSLSLSPGK 449
Db 440 KLTVDKSRWQGNVFCSCVMHEALHNNHYTKQSLSLSPGK 478
```

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RESULT 4
QM206_HUMAN
ID Q6MZQ6 HUMAN PRELIMINARY; PRT; 475 AA.
AC Q6MZQ6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein DKFZP686G11190.
GN Name=DKFZP686G11190;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Esophagus tumor;
RG The German cDNA Consortium;
RA Bahr A., Lauber J., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G.,
RA Han M., Wiemann S.;
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640947; CAB45972.1; -, mRNA.
DR HSSP; P01861; 1ADO.
DR SMR; Q6MZQ6; 20-475.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig.cl.
DR InterPro; IPR003006; Ig.MHC.
DR InterPro; IPR003596; Ig.v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
KW Hypothetical protein.
SQ SEQUENCE 475 AA; 52043 MW; B7EAE255A26F4B8E CRC64;
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Query Match 72.0%; Score 2211.5; DB 2; Length 475;
Best Local Similarity 91.2%; Pred. No. 7.7e-134;
Matches 416; Conservative 13; Mismatches 20; Indels 7; Gaps 1;

Qy 1 EVQLVESGGDFVQPGSLRVS CAASGFAFSPHYAMSVWRQAPGKLEWVAYISSGSGTY 60
Db 20 EVQLLESGGGLVQPGSLRLS CAASGFTFRYAMNVRQAPGKLEWVSGISSGVNTY 79

Qy 61 SDSVKGRFTISRDNKNTLYLQMSLR AEDSAVFCTRVKLGTY-----YFDSWGQGT 113
Db 80 ADSVKGRFTISGDISTNTLYLQMSLR AEDTAVYYCARADYRDYQVSPAYWYFDVWGRT 139

Qy 114 LLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSVNWSGALTSGVHTFP 173
Db 140 LVSVAASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSVNWSGALTSGVHTFP 199

Qy 174 AVLOSGLYSLSVVTVPSSSLGTQTYICNVNHPKSNKTKVDPKPEKCDKTHTCPPCPA 233
Db 200 AVLQSSGLYSLSVVTVPSSSLGTQTYICNVNHPKSNKTKVDPKPEKCDKTHTCPPCPA 259

Qy 234 PELLGGPSVFLFPPPKDPTLMISRPTVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 293
Db 260 PELLGGPSVFLFPPPKDPTLMISRPTVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 319

Qy 294 REEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPQVYTL 353
Db 320 REEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPQVYTL 379

Qy 354 PPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDSGSFYLSKLT 413
Db 380 PPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDSGSFYLSKLT 439

Qy 414 VDKSRWQGNVFCSCVMHEALHNNHYTKQSLSLSPGK 449
Db 440 VDKSRWQGNVFCSCVMHEALHNNHYTKQSLSLSPGK 478
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440 VDKRWQGNVFCSCVMHEGLHNHYTKQSLSLSPGK 473

Db 440 KSRWQGNVFCSCVMHEGLHNHYTKQSLSLSPGK 473

RESULT 5

Q6MZV7 HUMAN  
ID Q6MZV7 HUMAN PRELIMINARY; PRT; 473 AA.  
AC Q6MZV7  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Hypothetical protein DKFZp686C11235.  
GN Name=DKFZp686C11235;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC Tissue=Small intestine;  
RG The German cDNA Consortium;  
RA Bloecher H., Boecher M., Brandt P., Mewes H.W., Weil B., Amid C.,  
RA Osanger A., Fobo G., Han M., Wiemann S.;  
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BX640853; CAE45920.1; -; mRNA.  
DR HSSP; P01861; IADO.  
DR InterPro; IPR003599; IG.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003597; IG\_c1.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_v.  
DR Pfam; PF07654; C1-set; 3.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IGc1; 3.  
DR SMART; SM00406; IGv; 1.  
DR PROSITE; PS0835; IG LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
KW Hypothetical protein.  
SQ SEQUENCE 473 AA; 52121 MW; 9476EAE4C0BFC447 CRC64;

Query Match 71.4%; Score 2191.5; DB 2; Length 473;  
Best Local Similarity 90.1%; Pred. No. 1.5e-132;  
Matches 409; Conservative 21; Mismatches 19; Indels 5; Gaps 1;  
Qy 1 EVQLVESGGGFVQPGGSLRVSCAASGFPASHYAMSVWRQAPGKGLWVAYISSGGSGTY 60  
Db 20 EIQLVESGGGLVQPGGSLRLCAASGFTFSFEMNWRQAPGKGLWLSYITRSGNTVYY 79  
Qy 61 SDSVKGRFTISRDNKNTLYLQMSLRADSAVYFCTRVKLT-----YFDSWGQGLL 115  
Db 80 ADSLQGRFTISRDNARNSLYLQMSLRADSAVYFCTRVKLT-----YFDSWGQGLL 139  
Qy 116 TVSSASTKGPSVFFPLAPSSKSTSGTAAALGCLVKDYFPEPTVSNWNSGALTSGVHTFPAV 175  
Db 140 TVSSASTKGPSVFFPLAPSSKSTSGTAAALGCLVKDYFPEPTVSNWNSGALTSGVHTFPAV 199  
Qy 176 LQSSGLYSLSSVTVVPSSSLGTQTVICNNHKPSNTKVDKVPKSCDKHTCTPCPAP 235  
Db 200 LQSSGLYSLSSVTVVPSSSLGTQTVICNNHKPSNTKVDKVPKSCDKHTCTPCPAP 259  
Qy 236 LGGPSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNKTKPRE 295  
Db 260 LGGPSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNKTKPRE 319  
Qy 296 EQYNSTYRVSVLTIVHLDWNLNGKEYCKVSNKALPAPIETKISKAKQPREPVYTLPP 355  
Db 320 EQYNSTYRVSVLTIVHLDWNLNGKEYCKVSNKALPAPIETKISKAKQPREPVYTLPP 379  
Qy 356 SRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLKLTVD 415  
Db 380 SREMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLKLTVD 439  
Qy 416 KSRWQGNVFCSCVMHEGLHNHYTKQSLSLSPGK 449

RESULT 6

Q6GMW7 HUMAN  
ID Q6GMW7 HUMAN PRELIMINARY; PRT; 475 AA.  
AC Q6GMW7  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC Tissue=Spleen;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Faney J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butlerfield Y.S.N., Krzywinski M.I., Skaleka U., Smalls D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC Tissue=Spleen;  
RA Strausberg R.;  
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC073782; AAH73782.1; -; mRNA.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR InterPro; IPR003599; IG.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003597; IG\_c1.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_v.  
DR Pfam; PF07654; C1-set; 3.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IGc1; 3.  
DR SMART; SM00406; IGv; 1.  
DR PROSITE; PS0835; IG LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
KW Hypothetical protein.  
SQ SEQUENCE 475 AA; 51987 MW; 2A1PE55D736860F8 CRC64;

Query Match 71.3%; Score 2188.5; DB 2; Length 475;  
Best Local Similarity 91.0%; Pred. No. 2.3e-132;  
Matches 415; Conservative 11; Mismatches 23; Indels 7; Gaps 2;  
Qy 1 EVQLVESGGGFVQPGGSLRVSCAASGFPASHYAMSVWRQAPGKGLWVAYISSGGSGTY 60  
Db 20 EVQLVESGGGLVQPGGSLRLCAASGFTFSFEMNWRQAPGKGLWLSYITRSGNTVYY 79  
Qy 61 SDSVKGRFTISRDNKNTLYLQMSLRADSAVYFCTRVK-----LGTYT-FDSWGQGT 113  
Db 80 ADSVKGRFTISRDNKNTLYLQMSLRADSAVYFCTRVK-----LGTYT-FDSWGQGT 139



DR InterPro; IPR003597; Ig cl.  
 DR InterPro; IPR003006; Ig MHC.  
 DR InterPro; IPR003596; Ig v.  
 DR Pfam; PF07654; Cl-set; 3.  
 DR SMART; SM00409; IG; 2.  
 DR SMART; SM00407; IGcl; 3.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS00835; IG LIKE; 4.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
 KW Hypothetical protein.  
 SQ SEQUENCE 472 AA; 51724 MW; 26CB340D0046D279 CRC64;  
 Query Match 71.2%; Score 2187; DB 2; Length 472;  
 Best Local Similarity 91.2%; Pred. No. 2.9e-132;  
 Matches 414; Conservative 13; Mismatches 21; Indels 6; Gaps 3;  
 QY 1 EVQLVESGGDFVPGGSLRVSCAASGFAPFASHYAMSVWRQAFKGLWVAYISGGSGTYY 60  
 DB 20 EVQLVESGGGLVQPGSLRLSCAASGFTFDYAMHWVRQAPGKGLWVSGISWNSGSTAY 79  
 QY 61 SDSVKGRFTISRDNKNTLYLQMSLRADDSAVYFCTRVKLTG---YYP--DSWGQGTLL 115  
 DB 80 ADSVKGRFTISRDNKNTLYLQMSLRADDSAVYFCTRVKLTG---YYP--DSWGQGTLL 138  
 QY 116 TVSSASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAV 175  
 DB 139 TVSSASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAV 198  
 QY 176 LQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKTKVDKVEPKSCDKTHTCPCPAPE 235  
 DB 199 LQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKTKVDKVEPKSCDKTHTCPCPAPE 258  
 QY 236 LLGGPSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPRE 295  
 DB 259 LLGGPSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPRE 318  
 QY 296 EYQNSTYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP 355  
 DB 319 EYQNSTYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP 378  
 QY 356 SRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSFFLYSKLTVD 415  
 DB 379 SRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSFFLYSKLTVD 438  
 QY 416 KSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 449  
 DB 439 KSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 472

RESULT 9

ID Q6PU95 HUMAN PRELIMINARY; PRT; 544 AA.  
 AC Q6PU95;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE IGHG1 protein.  
 GN Name=IGHG1;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;  
 OC Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RC NUCLEOTIDE SEQUENCE.  
 RP TISSUE=Primary B-Cells;  
 RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.F.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,  
 RA Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.,  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Primary B-Cells;  
 RG NIH MGC Project;  
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC019046; AAH19046.1; -; mRNA.  
 DR HSP; P01861; IADQ.  
 DR SMR; Q6PU95; 20-473.  
 DR InterPro; IPR003599; Ig.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig cl.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig v.  
 DR Pfam; PF07654; Cl-set; 3.  
 DR SMART; SM00409; IG; 2.  
 DR SMART; SM00407; IGcl; 3.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS00835; IG LIKE; 4.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
 SQ SEQUENCE 544 AA; 60102 MW; 1895814B2297C668 CRC64;  
 Query Match 71.1%; Score 2184.5; DB 2; Length 544;  
 Best Local Similarity 87.4%; Pred. No. 5.1e-132;  
 Matches 418; Conservative 12; Mismatches 29; Indels 19; Gaps 2;  
 QY 1 EVQLVESGGDFVPGGSLRVSCAASGFAPFASHYAMSVWRQAPGKGLWVAYISGGSGTYY 60  
 DB 20 QAQLVESGGGVQPGSLRLSCAASGFRFSGNYGMHWVRQAPGKGLWVAVFSYDESKYY 79  
 QY 61 SDSVKGRFTISRDNKNTLYLQMSLRADDSAVYFCTRVKLTG-----YEDSWCGGT 113  
 DB 80 AASVKGRFTISRDNKNTLYLQMSLRADDSAVYFCTRVKLTG-----YEDSWCGGT 139  
 QY 114 LLTVSSASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPTVTSWNSGALTSGVHTFP 173  
 DB 140 LLTVSSASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPTVTSWNSGALTSGVHTFP 199  
 QY 174 AVLOSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKTKVDKVEPKSCDKTHTCPCPA 233  
 DB 200 AVLOSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKTKVDKVEPKSCDKTHTCPCPA 259  
 QY 234 PELLGGPSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKP 293  
 DB 260 PELLGGPSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKP 319  
 QY 294 REEYQNSTYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL 353  
 DB 320 REEYQNSTYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL 379  
 QY 354 PPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSFFLYSKLT 413  
 DB 380 PPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSFFLYSKLT 439  
 QY 414 VDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGKAPTSSSTKTKTOLLEHLLDLQ 471  
 DB 440 VDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSP-----ELQEESCAEAQ 485

ID	Q6N094_HUMAN PRELIMINARY; PRT; 480 AA.
AC	Q6N094;
DT	05-JUL-2004 (TrEMBLrel. 27, Created)
DT	05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT	05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE	Hypothetical protein DKFZp686001196.
DE	Name=DKFZp686001196;
GN	Os Homo sapiens (Human).
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC	OC Homo.
OX	NCBI_TaxID=9606;
RP	[1]
FN	NUCLEOTIDE SEQUENCE.
RC	TISSUE=Esophagus tumor;
RG	The German cDNA Consortium;
RA	Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Oeanger A.,
RA	Fobo G., Han M., Wiemann S.;
RL	Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
RL	EMBL; BX640622; CAE45776.1; -; mRNA.
DR	HSSP; P01861; IADO.
DR	InterPro; IPR003599; Ig.
DR	InterPro; IPR007110; Ig-like.
DR	InterPro; IPR003597; Ig.cl.
DR	InterPro; IPR003006; Ig_MHC.
DR	InterPro; IPR003596; Ig_v.
DR	Pfam; PF07654; C1-set; 3.
DR	SMART; SM00409; IG; 2.
DR	SMART; SM00407; IGcl; 3.
DR	SMART; SM00406; IGV; 1.
DR	PROSITE; PS0835; IG Like; 4.
DR	PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW	Hypothetical protein.
QY	SEQUENCE 480 AA; 52612 MW; 225247F3D35AEC18 CRC64;
QY	Query Match 70.7%; Score 2172; DB 2; Length 480;
DB	Best Local Similarity 88.1%; Pred. No. 2.7e-131;
DB	Matches 406; Conservative 21; Mismatches 22; Indels 12; Gaps 1;
QY	1 EVQLVESGGDVPQGGSLRVCAASGAFSPFHYAMSWVRQAPGKGLEWVAYISSGSGCTYY 60
DB	20 EEELVRSVGGGLVKGPEGLRLSCAASGFTFRSFNNWVRQAPGKLEWIAFINSRGEKYY 79
QY	61 SDSVKGRFTISRDNKNTLYLQMSLRADSAVVFCTRVK-----LGTYYPDS 108
DB	80 GESVKGRFTISRDNADNSLFLQMSLRVDDTAIYYCARGVWPAGTSTSGVPRHWFD 139
QY	109 WGQGLTLTVSSASTKGPSVFLFAPSSKTSCTGTAALGCLVKDYPPVPTVSMNSGALTSG 168
DB	140 WGQGLTLTVISSASTKGPSVFLFAPSSKTSCTGTAALGCLVKDYPPVPTVSMNSGALTSG 199
QY	169 VHTPPAVLQSSGLYSLSSVTVTPSSSLGTQYIYCNVHKPNTKVDKKVEPKSCDKTHTC 228
DB	200 VHTPPAVLQSSGLYSLSSVTVTPSSSLGTQYIYCNVHKPNTKVDKKVEPKSCDKTHTC 259
QY	229 PPCPAPELLGGPSVFLPPEPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 288
DB	260 PPCPAPELLGGPSVFLPPEPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 319
QY	289 AKTKPREEQYNSTYRVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTIISKAKGQPREP 348
DB	320 AKTKPREEQYNSTYRVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTIISKAKGQPREP 379
QY	349 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPL 408
DB	380 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPL 439
QY	409 YSKLTVDKSRVQOGNVFSCSVMHALHNHYTKSLSPGK 449
DB	440 YSKLTVDKSRVQOGNVFSCSVMHGLNHYTKSLSPGK 480

RESULT 11	
QSEFES_HUMAN	
ID QSEFES HUMAN PRELIMINARY;	PRT; 475 AA.
AC QSEFES;	
DT 10-MAY-2005 (TtEMBLrel. 30, Created)	
DT 10-MAY-2005 (TtEMBLrel. 30, Last sequence update)	
DT 10-MAY-2005 (TtEMBLrel. 30, Last annotation update)	
DE Anti-Rhd monoclonal T125 gammal heavy chain precursor.	
OS Homo sapiens (human).	
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae;	
OC Homo.	
OX NCBI_TaxID=9606;	
[1]	
RN NUCLEOTIDE SEQUENCE.	
RP Gaucher C., Klein P., Beliard R.;	
RA "Sequence determination of the recombinant human anti-RHD monoclonal antibody T125".	
RT Submitted (JAN-2005) to the EMBL/GenBank/DDBJ databases.	
RL EMBL; AY894992; AAW82028.1; -, mRNA.	
DR InterPro; IPR003599; Ig.	
DR InterPro; IPR007110; Ig-like.	
DR InterPro; IPR003597; Ig c1.	
DR InterPro; IPR003006; Ig_MHC.	
DR InterPro; IPR003596; Ig_v.	
DR Pfam; PF07654; Cl-set; 3.	
DR Pfam; PF07686; V-set; 1.	
DR SMART; SM00409; IG; 2.	
DR SMART; SM00407; IGc1; 3.	
DR SMART; SM00406; IGv; 1.	
DR PROSITE; PSS0835; IG_LIKE; 4.	
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.	
SIGNAL.	
FT SIGNAL.	1 19 Potential.
FT CHAIN	20 475 anti-RHD monoclonal T125 gammal heavy chain.
FT FT	
FT FT	
FT SQ	SEQUENCE 475 AA; 52362 MW; 1367D400DC7D2859 CRC64;
Query Match	70.5%; Score 2165.5; DB 2; Length 475;
Best Local Similarity	90.1%; Pred. No. 7e-131;
Matches 411; Conservative 13; Mismatches 25; Indels 7; Gaps 2	
Qy 1 EVLVRESGGDFVPGGSLRVSCAASGAPAFSHYAMSWVRQAPGKGLEWVAYISSGGSGTYIY 60	
Dd 20 QVLVESGGGVQPGRSLRLSCTASGTFKNYAMHWVRQAPAKGLEWVATISYDGRNIQY 79	
Qy 61 SDSVKGRFTTRNSKNLTLYQLMRSRAEDSAVVFCTR-----VKLGTY-YFDSSWGOGT 113	
Dd 80 ADSVKRGCTFSRNSQDTLYQLNSLRPEADTVAYICARPVRSRLQGLSDAFHMGOGT 139	
Qy 114 LLTVSSASTKGPSVFPLAPSCKTSSTGTAALGCLIVKDYPFPPTVSVNSGALTSGVHTFP 173	
Dd 140 MVTVSSASTKGPSVFPLAPSCKTSSTGTAALGCLIVKDYPFPPTVSVNSGALTSGVHTFP 199	
Qy 174 AVLQSSGLYSLSVVTPVPSSSLGTQTYYICNVNHKPSNTKYDKVEPKSCDKHTCPPCPA 233	
Dd 200 AVLQSSGLYSLSVVTPVPSSSLGTQTYYICNVNHKPSNTKYDKVEPKSCDKHTCPPCPA 259	
Qy 234 PELLGGSPVFLPPKPKDTLMISRTPEVTCVDVDSHEDPEVKFNWYVDGVEVHNATKTP 293	
Dd 260 PELLGGSPVFLPPKPKDTLMISRTPEVTCVDVDSHEDPEVKFNWYVDGVEVHNATKTP 319	
Qy 294 REQYNSTYRWVSVLTVLDHDLNGEKYCKVSNKALPAPIEKTISKAKGQPREPQVYTL 353	
Dd 320 REQYNSTYRWVSVLTVLDHDLNGEKYCKVSNKALPAPIEKTISKAKGQPREPQVYTL 379	
Qy 354 PPSRDELTKNQVSLTCLVKGFYPSDIAVEESNGQPENNYKTTTPPVLDSDGSFFLYSKLT 413	
Dd 380 PPSRDELTKNQVSLTCLVKGFYPSDIAVEESNGQPENNYKTTTPPVLDSDGSFFLYSKLT 439	
Qy 414 VDKSRRMOQGNVFCSCVNHEALHHNYHTOKSLSLSPGK 449	
Dd 440 VDKSRRMOQGNVFCSCVNHEALHHNYHTOKSLSLSPGK 475	





Db 137 TVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAV 196  
Qy 176 LOSSGLYSLSSVTVTPSSSLGTQTVICNVNHPKSNKVDKVKPKSCDKTHTCCPCPAPE 235  
Db 197 LQSSGLYSLSSVTVTPSSSLGTQTVICNVNHPKSNKVDKVKPKSCDKTHTCCPCPAPE 256  
Qy 236 LLGSPSVLFPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 295  
Db 257 LLGSPSVLFPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 316  
Qy 296 EGYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPP 355  
Db 317 EGYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPP 376  
Qy 356 SRDELTKNQVSLTCLVKGYFSPDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSLKLTVD 415  
Db 377 SRDELTKNQVSLTCLVKGYFSPDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSLKLTVD 436  
Qy 416 KSRWQGNVFCSCVMHEALHNNHYTKQSLSPGK 449  
Db 437 KSRWQGNVFCSCVMHEALHNNHYTKQSLSPGK 470

RESULT 14  
Q6P055\_HUMAN PRELIMINARY; PRT; 473 AA.  
AC Q6P055;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Peripheral Nervous System;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Peripheral Nervous System;  
RA Strausberg R.;  
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC065820; AAH65820.1; -; mRNA.  
DR HSSP; P01861; 1ADQ.  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig.c1.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig.v.  
DR Pfam; PF07654; C1-set; 3.

SMART; SM00409; IG; 2.  
DR SMART; SM00407; IGC1; 3.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00835; IG-LIKE; 4.  
DR PROSITE; PS00290; IG-MHC; UNKNOWN\_2.  
KW Hypothetical protein.  
SQ SEQUENCE 473 AA; 51344 MW; 9816D56A7129B57 CRC64;  
Query Match Similarity 70.0%; Score 2149.5; DB 2; Length 473;  
Best Local Similarity 89.6%; Pred. No. 7.5e-130;  
Matches 407; Conservative 12; Mismatches 30; Indels 5; Gaps 2;  
Qy 1 EVQLVESGGDPVQPGSGSLRVSCAASGAFSHYAMSWRQAPGKGLEWVAYISS--GSGGT 58  
Db 20 EAHLVESGGGLVRPGGSLTSLCTSGGTFFSAWLSWRQAPGKGLEWVARLTEDDGGTT 79  
Qy 59 YYSDSVGRFTISRDNKNTLYLQWRSIRAEADSAVYFCTRVKLGTY---YFDSMGQGTLL 115  
Db 80 HYGIAGVGRFTVSRDSDSNTLYLQMSDLRTEDTAFYFCATGSMNTVGLTGFDSMGQGTLL 139  
Qy 116 TVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAV 175  
Db 140 TVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAV 199  
Qy 176 LOSSGLYSLSSVTVTPSSSLGTQTVICNVNHPKSNKVDKVKPKSCDKTHTCCPCPAPE 235  
Db 200 LQSSGLYSLSSVTVTPSSSLGTQTVICNVNHPKSNKVDKVKPKSCDKTHTCCPCPAPE 259  
Qy 236 LLGSPSVLFPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 295  
Db 260 LLGSPSVLFPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 319  
Qy 296 EGYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPP 355  
Db 320 EGYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPP 379  
Qy 356 SRDELTKNQVSLTCLVKGYFSPDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSLKLTVD 415  
Db 380 SRDELTKNQVSLTCLVKGYFSPDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSLKLTVD 439  
Qy 416 KSRWQGNVFCSCVMHEALHNNHYTKQSLSPGK 449  
Db 440 KSRWQGNVFCSCVMHEALHNNHYTKQSLSPGK 473

RESULT 15  
Q72351\_HUMAN PRELIMINARY; PRT; 482 AA.  
ID Q72351\_HUMAN PRELIMINARY;  
AC Q72351;  
DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Hypothetical protein DKFZp686N02209.  
GN Name=DRFZp686N02209;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Rectum tumor;  
RG The German cDNA Consortium;  
RA Bloeker H., Boecker M., Brandt P., Mewes H.W., Weill B., Amid C.,  
RA Osanger A., Fobbo G., Han M., Wiemann S.;  
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BX538118; CAD98026.1; -; mRNA.  
DR HSSP; P01857; 1HZH.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig.c1.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig.v.  
DR Pfam; PF07654; C1-set; 3.





GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: April 6, 2006, 08:50:25 ; Search time 36.1767 Seconds  
(without alignments)  
1330.063 Million cell updates/sec

Title: US-10-089-500-53

Perfect score: 3071

Sequence: 1 EVQLVESGGDFVPGGSLRV.....IVEFLNRWTFQSIISTLT 562

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*

- 1: /cgn2\_6/ptodata/1/iaa/5.COMB.pep.\*
- 2: /cgn2\_6/ptodata/1/iaa/6.COMB.pep.\*
- 3: /cgn2\_6/ptodata/1/iaa/H.COMB.pep.\*
- 4: /cgn2\_6/ptodata/1/iaa/PCTUS.COMB.pep.\*
- 5: /cgn2\_6/ptodata/1/iaa/RE.COMB.pep.\*
- 6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2220	72.3	474	2	US-09-848-832-3
2	2194.5	71.5	452	2	US-09-027-449-71
3	2194.5	71.5	452	2	US-09-026-985-71
4	2194.5	71.5	452	2	US-09-121-352A-71
5	2194.5	71.5	452	2	US-09-234-340A-71
6	2194.5	71.5	452	2	US-09-355-014-71
7	2194.5	71.5	459	1	US-08-157-101A-7
8	2169	70.6	453	2	US-08-466-151-8
9	2169	70.6	453	2	US-08-466-163B-8
10	2169	70.6	453	2	US-09-802-096-8
11	2169	70.6	453	2	US-09-802-077-8
12	2169	70.6	453	2	US-09-925-179-8
13	2167	70.6	451	1	US-08-887-352B-14
14	2167	70.6	451	1	US-08-887-352B-16
15	2167	70.6	451	2	US-08-466-151-65
16	2167	70.6	451	2	US-09-109-207C-14
17	2167	70.6	451	2	US-09-109-207C-16
18	2167	70.6	451	2	US-09-296-005-14
19	2167	70.6	451	2	US-09-296-005-16
20	2167	70.6	451	2	US-09-920-171-14
21	2167	70.6	451	2	US-09-920-171-16
22	2167	70.6	451	2	US-09-716-028-14
23	2167	70.6	451	2	US-09-716-028-16
24	2167	70.6	451	2	US-10-113-996-14
25	2167	70.6	451	2	US-10-113-996-16
26	2167	70.6	451	2	US-09-925-179-65
27	2164	70.5	451	2	US-09-925-179-66

28	2163	70.4	451	1	US-08-887-352B-18	Sequence 18, Appl
29	2163	70.4	451	2	US-09-109-207C-18	Sequence 18, Appl
30	2163	70.4	451	2	US-09-282-505-2	Sequence 2, Appl
31	2163	70.4	451	2	US-09-054-255-2	Sequence 2, Appl
32	2163	70.4	451	2	US-09-296-005-18	Sequence 18, Appl
33	2163	70.4	451	2	US-09-282-846-2	Sequence 2, Appl
34	2163	70.4	451	2	US-09-680-145-2	Sequence 18, Appl
35	2163	70.4	451	2	US-09-920-171-18	Sequence 18, Appl
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37	2163	70.4	451	2	US-09-483-588-2	Sequence 2, Appl
38	2163	70.4	451	2	US-10-113-996-18	Sequence 10, Appl
39	2160.5	70.4	449	2	US-09-679-397-2	Sequence 2, Appl
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41	2160.5	70.4	449	2	US-09-304-465A-2	Sequence 2, Appl
42	2160.5	70.4	449	2	US-10-356-974-2	Sequence 2, Appl
43	2155	70.2	451	2	US-09-925-179-68	Sequence 68, Appl
44	2140	69.7	478	2	US-08-487-550-8	Sequence 8, Appl
45	2140	69.7	478	2	US-09-526-098-8	Sequence 8, Appl

## ALIGNMENTS

RESULT 1

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US-09-848-832-3
; Sequence 3, Application US/09848832
; Patent No. 6890532
; GENERAL INFORMATION:
; APPLICANT: Hooper, Douglas
; APPLICANT: Dietzschold, Bernhard
; TITLE OF INVENTION: RABIES VIRUS-SPECIFIC NEUTRALIZING HUMAN
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES AND NUCLEIC ACIDS AND RELATED METHODS
; FILE REFERENCE: H0001.NP0002
; CURRENT APPLICATION NUMBER: US/09/848,832
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: 60/204,518
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 474
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-848-832-3

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Query Match 72.3%; Score 2220; DB 2; Length 474;
Best Local Similarity 91.9%; Pred. No. 6.1e-163;
Matches 418; Conservative 14; Mismatches 17; Indels 6; Gaps 1;

Qy 1 EVQLVESGGDFVPGGSLRVSCAASGFAFASHYAMSWRQAPGKLEWVAYISSGGSTYY 60
Db 20 EVQLLESGLVQPGGSLRLSCAASGFTFSNYSAMSWRQAPGKLEWVSAISAGHSTYL 79
Qy 61 SDSVKGRFTISRDNSKNTLYLQWRSRLRSDSAVYFCTRVKLGITYY-----PDSWGQGLT 114
Db 80 ADSVKGRFTISRDNSKNTLYLQWRSRLRSDTAIVYCAKOREVTNIVLVNGGFDYWGQGT 139
Qy 115 LTVSSASTKGPSVFPLAPSSKSTSGGTAALGLCLVKDYFPEPVTVSVNSGALTSGVHTFPA 174
Db 140 VTVSSASTKGPSVFPLAPSSKSTSGGTAALGLCLVKDYFPEPVTVSVNSGALTSGVHTFPA 199
Qy 175 VLOSGLYSLSSVTVVPSSSLGTQTYICNNHKPSNTKVDKVPKPSCKDTHTCPCPCAP 234
Db 200 VLOSGLYSLSSVTVVPSSSLGTQTYICNNHKPSNTKVDKVPKPSCKDTHTCPCPCAP 259
Qy 235 ELIIGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPR 294
Db 260 ELIIGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPR 319
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Db 320 EEQYNSTYRVSVLTVLDHQLNGKEYKCKVSNKALPAPIETKTISKAKGQPREPQVYVTL 379

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Qy 118 SSASTKGPSVFLPAPSSKSTSGTAAALGCLVKDYFPBPVTVSNWNGALTSVHTFPAVLQ 177  
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Db 181 SSGLYSLSSVVTVFSSSLGTQYICNVNHPKSNTKVDKVEPKSCDKTHTCPPCPAPPELL 240  
Qy 238 GGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQ 297  
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Qy 298 YNSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYVTLPPSR 357  
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Qy 358 DELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGDSFFLYSKLTVDKS 417  
Db 361 BEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGDSFFLYSKLTVDKS 420  
Qy 418 RWOQGNVFCSCVMHEALHNYTKQSLSPGK 449  
Db 421 RWOQGNVFCSCVMHEALHNYTKQSLSPGK 452

## RESULT 4

US-09-121-952A-71  
; Sequence 71, Application US/09121952A  
; Patent No. 6458355  
; GENERAL INFORMATION:  
; APPLICANT: Genentech, Inc., Hsei, Vanessa  
; APPLICANT: Komenis, Iphigenia  
; APPLICANT: Leong, Steven R.  
; APPLICANT: Presta, Leonard G.  
; APPLICANT: Shahrokh, Zahra  
; APPLICANT: Zapata, Gerardo A.  
; TITLE OF INVENTION: METHODS OF TREATING INFLAMMATORY DISEASES  
; TITLE OF INVENTION: WITH ANTI-IL-8 ANTIBODY FRAGMENT-POLYMER CONJUGATES  
; NUMBER OF SEQUENCES: 72  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/121,952A  
; FILING DATE: 24-Jul-1998  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/074330  
; FILING DATE: 22-JAN-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/075467  
; FILING DATE: 20-FEB-1998  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Love, Richard B.  
; REGISTRATION NUMBER: 34,659  
; REFERENCE/DOCKET NUMBER: P1085R4  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-5530  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 71:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 452 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear

## US-09-121-952A-71

Query Match 71.5%; Score 2194.5; DB 2; Length 452;  
Best Local Similarity 90.9%; Pred. No. 5.3e-161;  
Matches 411; Conservative 14; Mismatches 24; Indels 3; Gaps 1;  
Qy 1 EVOLVESGGDFVOPGSLRVSCAASGPAFSPHAYMSVVRQAPGKGLWVAYISSGSGSTYY 60  
Db 1 EVOLVSGGGLVOPGSLRVSCAASGYSPSSHVMHVRQAPGKGLWVYIDPSNGETTY 60  
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Db 121 SSASTKGPSVFLPAPSSKSTSGTAAALGCLVKDYFPBPVTVSNWNGALTSVHTFPAVLQ 180  
Qy 178 SSGLYSLSSVVTVFSSSLGTQYICNVNHPKSNTKVDKVEPKSCDKTHTCPPCPAPPELL 237  
Db 181 SSGLYSLSSVVTVFSSSLGTQYICNVNHPKSNTKVDKVEPKSCDKTHTCPPCPAPPELL 240  
Qy 238 GGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQ 297  
Db 241 GGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQ 300  
Qy 298 YNSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYVTLPPSR 357  
Db 301 YNSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYVTLPPSR 360  
Qy 358 DELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGDSFFLYSKLTVDKS 417  
Db 361 BEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGDSFFLYSKLTVDKS 420  
Qy 418 RWOQGNVFCSCVMHEALHNYTKQSLSPGK 449  
Db 421 RWOQGNVFCSCVMHEALHNYTKQSLSPGK 452

## RESULT 5

US-09-234-340A-71  
; Sequence 71, Application US/09234340A  
; Patent No. 6468532  
; GENERAL INFORMATION:  
; APPLICANT: Genentech, Inc., Hsei, Vanessa  
; APPLICANT: Komenis, Iphigenia  
; APPLICANT: Leong, Steven R.  
; APPLICANT: Presta, Leonard G.  
; APPLICANT: Shahrokh, Zahra  
; APPLICANT: Zapata, Gerardo A.  
; TITLE OF INVENTION: METHODS OF TREATING INFLAMMATORY DISEASES  
; TITLE OF INVENTION: WITH ANTI-IL-8 ANTIBODY FRAGMENT-POLYMER CONJUGATES  
; NUMBER OF SEQUENCES: 72  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/234,340A  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/121,952  
; FILING DATE: 24-Jul-1998  
; APPLICATION NUMBER: 60/074330

; FILING DATE: 22-JAN-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/075467  
; FILING DATE: 20-FEB-1998  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Love, Richard B.  
; REGISTRATION NUMBER: 34,659  
; REFERENCE/DOCKET NUMBER: P1085R4  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-5530  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 71:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 452 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
; US-09-234-340A-71

Query Match 71.5%; Score 2194.5; DB 2; Length 452;  
Best Local Similarity 90.9%; Pred. No. 5.3e-161;  
Matches 411; Conservative 14; Mismatches 24; Indels 3; Gaps 1;

Qy 1 EVQLVESGGDFVQPGSLRVCAASGFAFASHYAMVWRQAPGKLEWVAYISSGSGTYY 60  
Db 1 EVQLVQSGGGLVQPGSLRLSCAASGYFSFSSHYMHVWRQAPGKLEWVGVIDPSNGETTY 60  
Qy 61 SDSVKGRFTISRDNKNTLYLQMSRLRAEDSAVYFCTRVKL---GTYYFDSWGQGLTLTV 117  
Db 61 NQKFKGRFTLSRDNSKNTAYLQMSRLRAEDTAVVYCARGDYRYNGDWFDFVWGQGLTLTV 120  
Qy 118 SSASTKGPSVFPFLAPSSKTSGGTAALGCLVKDYFPEPTVTVSNWGALTSGVHTFPAVLQ 177  
Db 121 SSASTKGPSVFPFLAPSSKTSGGTAALGCLVKDYFPEPTVTVSNWGALTSGVHTFPAVLQ 180  
Qy 178 SSGLYSLSSVVTVFSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKHTHTCPPCPAPELL 237  
Db 181 SSGLYSLSSVVTVFSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKHTHTCPPCPAPELL 240  
Qy 238 GGPSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQ 297  
Db 241 GGPSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQ 300  
Qy 298 YNSTYRVSVLTVLHQDLNGKEYCKVSNKALPAPIEKTIISKAKGQPREPQVYVTLPPSR 357  
Db 301 YNSTYRVSVLTVLHQDLNGKEYCKVSNKALPAPIEKTIISKAKGQPREPQVYVTLPPSR 360  
Qy 358 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKS 417  
Db 361 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKS 420  
Qy 418 RWQOGNVFSCVMHEALHNHYTQKSLSLSPGK 449  
Db 421 RWQOGNVFSCVMHEALHNHYTQKSLSLSPGK 452

RESULT 6  
US-09-355-014-71  
; Sequence 71, Application US/09355014  
; Patent No. 6870033  
; GENERAL INFORMATION:  
; APPLICANT: Genentech, Inc., Haei, Vanessa  
; Koumenis, Iphigenia  
; Leong, Steven R.  
; Presta, Leonard G.  
; Shahrokh, Zahra  
; Zapata, Gerardo A.  
; TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and  
; Humanized Anti-IL-8 Monoclonal Antibodies  
; NUMBER OF SEQUENCES: 72  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco

; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Winpatin (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/355,014  
; FILING DATE: 21-Jul-1999  
; CLASSIFICATION: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Love, Richard B.  
; REGISTRATION NUMBER: 34,659  
; REFERENCE/DOCKET NUMBER: P1085R3PCT  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-5530  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 71:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 452 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
; SEQUENCE DESCRIPTION: SEQ ID NO: 71:  
; US-09-355-014-71

Query Match 71.5%; Score 2194.5; DB 2; Length 452;  
Best Local Similarity 90.9%; Pred. No. 5.3e-161;  
Matches 411; Conservative 14; Mismatches 24; Indels 3; Gaps 1;

Qy 1 EVQLVESGGDFVQPGSLRVCAASGFAFASHYAMVWRQAPGKLEWVAYISSGSGTYY 60  
Db 1 EVQLVQSGGGLVQPGSLRLSCAASGYFSFSSHYMHVWRQAPGKLEWVGVIDPSNGETTY 60  
Qy 61 SDSVKGRFTISRDNKNTLYLQMSRLRAEDSAVYFCTRVKL---GTYYFDSWGQGLTLTV 117  
Db 61 NQKFKGRFTLSRDNSKNTAYLQMSRLRAEDTAVVYCARGDYRYNGDWFDFVWGQGLTLTV 120  
Qy 118 SSASTKGPSVFPFLAPSSKTSGGTAALGCLVKDYFPEPTVTVSNWGALTSGVHTFPAVLQ 177  
Db 121 SSASTKGPSVFPFLAPSSKTSGGTAALGCLVKDYFPEPTVTVSNWGALTSGVHTFPAVLQ 180  
Qy 178 SSGLYSLSSVVTVFSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKHTHTCPPCPAPELL 237  
Db 181 SSGLYSLSSVVTVFSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKHTHTCPPCPAPELL 240  
Qy 238 GGPSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQ 297  
Db 241 GGPSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQ 300  
Qy 298 YNSTYRVSVLTVLHQDLNGKEYCKVSNKALPAPIEKTIISKAKGQPREPQVYVTLPPSR 357  
Db 301 YNSTYRVSVLTVLHQDLNGKEYCKVSNKALPAPIEKTIISKAKGQPREPQVYVTLPPSR 360  
Qy 358 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKS 417  
Db 361 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKS 420  
Qy 418 RWQOGNVFSCVMHEALHNHYTQKSLSLSPGK 449  
Db 421 RWQOGNVFSCVMHEALHNHYTQKSLSLSPGK 452

RESULT 7  
US-08-157-101A-7  
; Sequence 7, Application US/08157101A  
; Patent No. 5808032  
; GENERAL INFORMATION:  
; APPLICANT: KURIHARA, TATSUYA  
; APPLICANT: MATSUKURA, SHIGEKAZU  
; APPLICANT: TSURUOKA, NOBUO  
; APPLICANT: ARIMA, KENJI

APPLICANT: NISHIHARA, TATSURO  
 TITLE OF INVENTION: ANTI-HBS ANTIBODY GENES AND EXPRESSION  
 NUMBER OF SEQUENCES: 9  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: PILLBURY, MADISON & SUTRO  
 STREET: 1100 NEW YORK AVENUE, N.W.  
 CITY: WASHINGTON  
 STATE: D.C.  
 COUNTRY: USA  
 ZIP: 20005  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/157,101A  
 FILING DATE: 05-APR-1994  
 CLASSIFICATION: 530  
 ATTORNEY/AGENT INFORMATION:  
 NAME: TITUS, MARLANA K  
 REGISTRATION NUMBER: 35843  
 REFERENCE/DOCKET NUMBER: 9437/204199  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-861-3711  
 TELEFAX: 202-822-0944  
 TELEX: 6714627 CUCH  
 INFORMATION FOR SEQ ID NO: 7:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 459 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 US-08-157-101A-7

Query Match 71.5%; Score 2194.5; DB 1; Length 459;  
 Best Local Similarity 91.8%; Pred. No. 5.4e-161;  
 Matches 413; Conservative 15; Mismatches 21; Indels 1; Gaps 1;

Qy	1	EVLVESGGDFVOPGSLRVSCAASGFAFASHYAMSWROAPGKLEWVAVISSGSGTYY	60
Db	10	QVQLVESGGGVVQGRSLRLSCAASGFTSSNHWVRQAPGKLEWVAVILYDGNHKKY	69
Qy	61	SDSVKGRFTISRDNKNTLYLQMSRAEDSAVYFCTRVK-LGTYYPDSWGQGLTLTVSS	119
Db	70	ADSVKGRFTISRDNKNTLYLQMSRAEDSAVYFCTRVK-LGTYYPDSWGQGLTLTVSS	129
Qy	120	ASTKGPSVFPPLAPSSKTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTTFAVLQSS	179
Db	130	ASTKGPSVFPPLAPSSKTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTTFAVLQSS	189
Qy	180	GLYSLSVSVTPSSSLGTQYICNVNHPKSNKTKVDKVPKSCDKTHTCCPCAPPELLGG	239
Db	190	GLYSLSVSVTPSSSLGTQYICNVNHPKSNKTKVDKVPKSCDKTHTCCPCAPPELLGG	249
Qy	240	PSVFLFPKPKDLMISRTPEVTCVVDVSHEDPEVKFNWVDGVEVHNAKTKPREQYN	299
Db	250	PSVFLFPKPKDLMISRTPEVTCVVDVSHEDPEVKFNWVDGVEVHNAKTKPREQYN	309
Qy	300	STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE	359
Db	310	STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE	369
Qy	360	LTKNQVSLTCLVKGFYPSDIAVEHESNGQPENNYKTPPVLDSDGSFPLYSKLTVDKSRW	419
Db	370	LTKNQVSLTCLVKGFYPSDIAVEHESNGQPENNYKTPPVLDSDGSFPLYSKLTVDKSRW	429
Qy	420	QQGNVFSCSVMHEALHNHYTQKSLSLSPGK	449
Db	430	QQGNVFSCSVMHEALHNHYTQKSLSLSPGK	459

RESULT 8  
 US-08-466-151-8  
 ; Sequence 8, Application US/08466151  
 ; Patent No. 6037453  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Jardieu, Paula M.  
 ; APPLICANT: Presta, Leonard G.  
 ; TITLE OF INVENTION: Immunoglobulin Variants  
 ; NUMBER OF SEQUENCES: 65  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Genentech, Inc.  
 ; STREET: 1 DNA Way  
 ; CITY: South San Francisco  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 94080  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: WinPatIn (Genentech)  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/466,151  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/466163  
 ; FILING DATE: 06-Jun-1995  
 ; APPLICATION NUMBER: 08/405617  
 ; FILING DATE: 15-MAR-1995  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/185899  
 ; FILING DATE: 26-JAN-1994  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 07/879495  
 ; FILING DATE: 07-MAY-1992  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 07/744768  
 ; FILING DATE: 14-AUG-1991  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Svoboda, Craig G.  
 ; REGISTRATION NUMBER: 39,044  
 ; REFERENCE/DOCKET NUMBER: P0718P2C1D1  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 650/225-1489  
 ; TELEFAX: 650/952-9881  
 ; INFORMATION FOR SEQ ID NO: 8:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 453 amino acids  
 ; TYPE: Amino Acid  
 ; TOPOLOGY: Linear  
 ; US-08-466-151-8

Query Match 70.6%; Score 2169; DB 2; Length 453;  
 Best Local Similarity 91.0%; Pred. No. 4.9e-159;  
 Matches 413; Conservative 16; Mismatches 19; Indels 6; Gaps 4;

Qy	1	EVLVESGGDFVOPGSLRVSCAASGFAF-SHYAMSWROAPGKLEWVAVISSGSGTYY	59
Db	1	EVLVESGGGVVQGRSLRLSCAASGFTSSNHWVRQAPGKLEWVAVILYDGNHKKY	59
Qy	60	YDSVKGRFTISRDNKNTLYLQMSRAEDSAVYFCTRVK--LGTYYPDSWGQGLTLTV	117
Db	60	YDSVKGRFTISRDNKNTLYLQMSRAEDSAVYFCTRVK--LGTYYPDSWGQGLTLTV	119
Qy	118	SSAST--KGPSVFPPLAPSSKTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTTFAV	175
Db	120	SSASTKGPSVFPPLAPSSKTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTTFAV	179
Qy	176	LQSSGLYSLSVSVTPSSSLGTQYICNVNHPKSNKTKVDKVPKSCDKTHTCCPCAPE	235
Db	180	LQSSGLYSLSVSVTPSSSLGTQYICNVNHPKSNKTKVDKVPKSCDKTHTCCPCAPE	239

QY 236 LLGSPSVFLPPPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 295  
 ||:|||||  
 Db 240 LLGSPSVFLPPPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 299  
 ||:|||||  
 QY 296 EQNSTYRVVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP 355  
 ||:|||||  
 Db 300 EQNSTYRVVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP 359  
 ||:|||||  
 QY 356 SRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD 415  
 ||:|||||  
 Db 360 SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD 419  
 ||:|||||  
 QY 416 KSRWQOGNVFSCSVMEALHNNHYTKQSLSLSPGK 449  
 ||:|||||  
 Db 420 KSRWQOGNVFSCSVMEALHNNHYTKQSLSLSPGK 453  
 ||:|||||  
 RESULT 9  
 US-08-466-163B-8  
 ; Sequence 8, Application US/08466163B  
 ; Patent No. 6329509  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Presta, Paula M.  
 ; TITLE OF INVENTION: Immunoglobulin Variants  
 ; FILE REFERENCE: P0718P2C1D1  
 ; CURRENT APPLICATION NUMBER: US/08/466,163B  
 ; PRIOR FILING DATE: 1995-06-06  
 ; PRIOR FILING DATE: 1995-03-15  
 ; PRIOR FILING DATE: 1995-03-15  
 ; PRIOR FILING DATE: 1994-01-26  
 ; PRIOR FILING DATE: 1992-05-07  
 ; PRIOR FILING DATE: 1991-08-14  
 ; NUMBER OF SEQ ID NOS: 64  
 ; SEQ ID NO 8  
 ; LENGTH: 453  
 ; TYPE: PRT  
 ; ORGANISM: Artificial sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: humanized mae11, version 1 heavy chain  
 US-08-466-163B-8  
 Query Match 70.6%; Score 2169; DB 2; Length 453;  
 Best Local Similarity 91.0%; Pred. No. 4.9e-159;  
 Matches 413; Conservative 16; Mismatches 19; Indels 6; Gaps 4;  
 QY 1 EVOLVESGGDFVQPGGSLRVSCAASGAPF-SHYAMSVVROAPGKGLWVAYISGGSGTY 59  
 ||:|||||  
 Db 1 EVOLVESGGGLVQPGGSLRLSCAASVGSITSGYSVNWIRQAPGKGLWVASITYDGS-TN 59  
 ||:|||||  
 QY 60 YSDSVKGRFTISRDNKNTLYLQMRSLRAEDSAVYFCTRVK--LGTYFDSWGQGLTLTV 117  
 ||:|||||  
 Db 60 YADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYICARGSHYFGHHFAVMQGLTLTV 119  
 ||:|||||  
 QY 118 SSAST--KGPSVFLPAPSSKTSGGTAALGCLVKDYFPEPTVTVSNWNSGALTSGVHTFP 175  
 ||:|||||  
 Db 120 SSASTKGGPSVFLPAPSSKTSGGTAALGCLVKDYFPEPTVTVSNWNSGALTSGVHTFP 179  
 ||:|||||  
 QY 176 LQSSGLYSLSSVTVPPSSSLGTQTYICNVNHNKPSNTKVDKVEPKSCDKTHTCCPCPA 235  
 ||:|||||  
 Db 180 LQSSGLYSLSSVTVPPSSSLGTQTYICNVNHNKPSNTKVDKVEPKSCDKTHTCCPCPA 239  
 ||:|||||  
 QY 236 LLGSPSVFLPPPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 295  
 ||:|||||  
 Db 240 LLGSPSVFLPPPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 299  
 ||:|||||  
 QY 296 EQNSTYRVVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP 355  
 ||:|||||  
 Db 300 EQNSTYRVVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP 359  
 ||:|||||

QY 356 SRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD 415  
 ||:|||||  
 Db 360 SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD 419  
 ||:|||||  
 QY 416 KSRWQOGNVFSCSVMEALHNNHYTKQSLSLSPGK 449  
 ||:|||||  
 Db 420 KSRWQOGNVFSCSVMEALHNNHYTKQSLSLSPGK 453  
 ||:|||||  
 RESULT 10  
 US-09-802-096-8  
 ; Sequence 8, Application US/09802096  
 ; Patent No. 6685939  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Jardieu, Paula M.  
 ; APPLICANT: Presta, Leonard G.  
 ; TITLE OF INVENTION: Method of Preventing the Onset of Allergic Disorders (as amended)  
 ; FILE REFERENCE: P0718P2C3US  
 ; CURRENT APPLICATION NUMBER: US/09/802,096  
 ; CURRENT FILING DATE: 2001-03-08  
 ; PRIOR APPLICATION NUMBER: US 08/405,617  
 ; PRIOR FILING DATE: 1995-03-15  
 ; PRIOR APPLICATION NUMBER: US 08/185,899  
 ; PRIOR FILING DATE: 1994-01-26  
 ; PRIOR APPLICATION NUMBER: PCT/US92/06860  
 ; PRIOR FILING DATE: 1992-08-14  
 ; PRIOR APPLICATION NUMBER: US 07/879,495  
 ; PRIOR FILING DATE: 1992-05-07  
 ; PRIOR APPLICATION NUMBER: US 07/744,768  
 ; PRIOR FILING DATE: 1991-08-14  
 ; NUMBER OF SEQ ID NOS: 64  
 ; SEQ ID NO 8  
 ; LENGTH: 453  
 ; TYPE: PRT  
 ; ORGANISM: Artificial sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: humanized mae11, version 1 heavy chain  
 US-09-802-096-8  
 Query Match 70.6%; Score 2169; DB 2; Length 453;  
 Best Local Similarity 91.0%; Pred. No. 4.9e-159;  
 Matches 413; Conservative 16; Mismatches 19; Indels 6; Gaps 4;  
 QY 1 EVOLVESGGDFVQPGGSLRVSCAASGAPF-SHYAMSVVROAPGKGLWVAYISGGSGTY 59  
 ||:|||||  
 Db 1 EVOLVESGGGLVQPGGSLRLSCAASVGSITSGYSVNWIRQAPGKGLWVASITYDGS-TN 59  
 ||:|||||  
 QY 60 YSDSVKGRFTISRDNKNTLYLQMRSLRAEDSAVYFCTRVK--LGTYFDSWGQGLTLTV 117  
 ||:|||||  
 Db 60 YADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYICARGSHYFGHHFAVMQGLTLTV 119  
 ||:|||||  
 QY 118 SSAST--KGPSVFLPAPSSKTSGGTAALGCLVKDYFPEPTVTVSNWNSGALTSGVHTFP 175  
 ||:|||||  
 Db 120 SSASTKGGPSVFLPAPSSKTSGGTAALGCLVKDYFPEPTVTVSNWNSGALTSGVHTFP 179  
 ||:|||||  
 QY 176 LQSSGLYSLSSVTVPPSSSLGTQTYICNVNHNKPSNTKVDKVEPKSCDKTHTCCPCPA 235  
 ||:|||||  
 Db 180 LQSSGLYSLSSVTVPPSSSLGTQTYICNVNHNKPSNTKVDKVEPKSCDKTHTCCPCPA 239  
 ||:|||||  
 QY 236 LLGSPSVFLPPPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 295  
 ||:|||||  
 Db 240 LLGSPSVFLPPPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 299  
 ||:|||||  
 QY 296 EQNSTYRVVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP 355  
 ||:|||||  
 Db 300 EQNSTYRVVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP 359  
 ||:|||||  
 QY 356 SRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD 415  
 ||:|||||  
 Db 360 SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD 419  
 ||:|||||  
 QY 416 KSRWQOGNVFSCSVMEALHNNHYTKQSLSLSPGK 449  
 ||:|||||

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|||||
Db 420 KSRWQGNVFCSCVMHEALHNHYTKSLSPGK 453

RESULT 11
US-09-802-077-8
; Sequence 8, Application US/09802077
; Patent No. 6699472
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Method of Treating Allergic Disorders (as amended)
; FILE REFERENCE: P0718P2C2US
; CURRENT APPLICATION NUMBER: US/09/802,077
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 8
; LENGTH: 453
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: humanized maell, version 1 heavy chain
US-09-802-077-8

Query Match 70.6%; Score 2169; DB 2; Length 453;
Best Local Similarity 91.0%; Pred. No. 4.9e-159;
Matches 413; Conservative 16; Mismatches 19; Indels 6; Gaps 4;

Qy 1 EVLVESGGDFVQPGGSLRVSCAASGFAP-SHYAMSWRQAPGKGLWVAYISGGSGTY 59
Db 1 EVLVESGGGLVQPGGSLRVSCAASGVSYTSYGSYVWIRQAPGKGLWVASYTYDGS-TN 59
Qy 60 YDSVKGRTISRDNKNTLYLQMSLRADSDSAVYFCTRVK--LGTYYFDSWQGGTLTV 117
Db 60 YADSVKGRFTISRDDSKNTFYLMNSLRADSDTAVYYCARGSHYFGHWHFAVMQGGTLTV 119
Qy 118 SSAST--KGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVYSWNSGALTSGVHTFPAV 175
Db 120 SSASTKGKPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVYSWNSGALTSGVHTFPAV 179
Qy 176 LQSSGLYSLSVVTVPSSSLGTQTYICNVNHPKSNPKVDKKVEPKSCDKTHTCPPCPAPE 235
Db 180 LQSSGLYSLSVVTVPSSSLGTQTYICNVNHPKSNPKVDKKVEPKSCDKTHTCPPCPAPE 239
Qy 236 LLGGPSVFLPFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 295
Db 240 LLGGPSVFLPFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 299
Qy 296 EQNSTYRVVSVLTVLDHQLMNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP 355
Db 300 EQNSTYRVVSVLTVLDHQLMNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP 359
Qy 356 SRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVD 415
Db 360 SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVD 419
Qy 416 KSRWQGNVFCSCVMHEALHNHYTKSLSPGK 449
Db 420 KSRWQGNVFCSCVMHEALHNHYTKSLSPGK 453

RESULT 12
US-09-925-179-8
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; Sequence 8, Application US/09925179
; Patent No. 6914129
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Anti-IGE Antibodies (as amended)
; FILE REFERENCE: P0718P2C1D1US
; CURRENT APPLICATION NUMBER: US/09/925,179
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 08/466,163
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 68
; SEQ ID NO 8
; LENGTH: 453
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: humanized maell, version 1 heavy chain
US-09-925-179-8

Query Match 70.6%; Score 2169; DB 2; Length 453;
Best Local Similarity 91.0%; Pred. No. 4.9e-159;
Matches 413; Conservative 16; Mismatches 19; Indels 6; Gaps 4;

Qy 1 EVLVESGGDFVQPGGSLRVSCAASGFAP-SHYAMSWRQAPGKGLWVAYISGGSGTY 59
Db 1 EVLVESGGGLVQPGGSLRVSCAASGVSYTSYGSYVWIRQAPGKGLWVASYTYDGS-TN 59
Qy 60 YDSVKGRTISRDNKNTLYLQMSLRADSDSAVYFCTRVK--LGTYYFDSWQGGTLTV 117
Db 60 YADSVKGRFTISRDDSKNTFYLMNSLRADSDTAVYYCARGSHYFGHWHFAVMQGGTLTV 119
Qy 118 SSAST--KGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVYSWNSGALTSGVHTFPAV 175
Db 120 SSASTKGKPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVYSWNSGALTSGVHTFPAV 179
Qy 176 LQSSGLYSLSVVTVPSSSLGTQTYICNVNHPKSNPKVDKKVEPKSCDKTHTCPPCPAPE 235
Db 180 LQSSGLYSLSVVTVPSSSLGTQTYICNVNHPKSNPKVDKKVEPKSCDKTHTCPPCPAPE 239
Qy 236 LLGGPSVFLPFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 295
Db 240 LLGGPSVFLPFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 299
Qy 296 EQNSTYRVVSVLTVLDHQLMNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP 355
Db 300 EQNSTYRVVSVLTVLDHQLMNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP 359
Qy 356 SRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVD 415
Db 360 SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVD 419
Qy 416 KSRWQGNVFCSCVMHEALHNHYTKSLSPGK 449
Db 420 KSRWQGNVFCSCVMHEALHNHYTKSLSPGK 453

RESULT 13
US-08-887-352B-14
; Sequence 14, Application US/08887352B
; Patent No. 5994511
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
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;; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of  
;; TITLE OF INVENTION: Improving Polypeptides  
;; NUMBER OF SEQUENCES: 26  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Genentech, Inc.  
;; STREET: 1 DNA Way  
;; CITY: South San Francisco  
;; STATE: California  
;; COUNTRY: USA  
;; ZIP: 94080

;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: WinPatIn (Genentech)  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/887,352B  
;; FILING DATE: 03-Jul-1997  
;; CLASSIFICATION: 530  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Svoboda, Craig G.  
;; REGISTRATION NUMBER: 39,044  
;; REFERENCE/DOCKET NUMBER: P1123  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 650/225-1489  
;; TELEFAX: 650/952-9881  
;; INFORMATION FOR SEQ ID NO: 14:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 451 amino acids  
;; TYPE: Amino Acid  
;; TOPOLOGY: Linear

US-08-887-352B-14

Query Match 70.6%; Score 2167; DB 1; Length 451;

Best Local Similarity 90.9%; Pred. No. 7e-159;

Matches 411; Conservative 16; Mismatches 21; Indels 4; Gaps 3;

QY 1 EVLVESGGDFVQPGSLRVSCAAGPAP-SHYAMSWVROAPGKGLEWVAYISSGGSGTY 59

Db 1 EVLVESGGGLVQPGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWASITYDGS-TN 59

QY 60 YSDSVKGRITISRDNSKNTLYLQMSLRADSNAVYFCTRVK--LGTYYFDSMGQGLTIV 117

Db 60 YNPSVKGRITISRDNSKNTLYLQMSLRADTAIVYICARGSHYFGHHFAVWGQGLTIV 119

QY 118 SSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQ 177

Db 120 SSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQ 179

QY 178 SGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPCPAPELL 237

Db 180 SGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPCPAPELL 239

QY 238 GGPSVFLFPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQ 297

Db 240 GGPSVFLFPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQ 299

QY 298 YNSTYRVSVSLTVLHQDLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSR 357

Db 300 YNSTYRVSVSLTVLHQDLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSR 359

QY 358 DELTKNQVSLTCLVKGPYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKS 417

Db 360 EEMTKNQVSLTCLVKGPYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKS 419

QY 418 RWOQGNVFCSCVMHEALHNHYTQKSLSLSPGK 449

Db 420 RWOQGNVFCSCVMHEALHNHYTQKSLSLSPGK 451

RESULT 14

US-08-887-352B-16

; Sequence 16, Application US/08887352B

; Patent No. 5994511

; GENERAL INFORMATION:

; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe

; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of

; TITLE OF INVENTION: Improving Polypeptides

; NUMBER OF SEQUENCES: 26

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.

; STREET: 1 DNA Way

; CITY: South San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94080

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: WinPatIn (Genentech)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/887,352B

; FILING DATE: 03-Jul-1997

; CLASSIFICATION: 530

; ATTORNEY/AGENT INFORMATION:

; NAME: Svoboda, Craig G.

; REGISTRATION NUMBER: 39,044

; REFERENCE/DOCKET NUMBER: P1123

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 650/225-1489

; TELEFAX: 650/952-9881

; INFORMATION FOR SEQ ID NO: 16:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 451 amino acids

; TYPE: Amino Acid

; TOPOLOGY: Linear

US-08-887-352B-16

Query Match 70.6%; Score 2167; DB 1; Length 451;

Best Local Similarity 90.9%; Pred. No. 7e-159;

Matches 411; Conservative 16; Mismatches 21; Indels 4; Gaps 3;

QY 1 EVLVESGGDFVQPGSLRVSCAAGPAP-SHYAMSWVROAPGKGLEWVAYISSGGSGTY 59

Db 1 EVLVESGGGLVQPGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWASITYDGS-TN 59

QY 60 YSDSVKGRITISRDNSKNTLYLQMSLRADSNAVYFCTRVK--LGTYYFDSMGQGLTIV 117

Db 60 YNPSVKGRITISRDNSKNTLYLQMSLRADTAIVYICARGSHYFGHHFAVWGQGLTIV 119

QY 118 SSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQ 177

Db 120 SSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQ 179

QY 178 SGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPCPAPELL 237

Db 180 SGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPCPAPELL 239

QY 238 GGPSVFLFPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQ 297

Db 240 GGPSVFLFPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQ 299

QY 298 YNSTYRVSVSLTVLHQDLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSR 357

Db 300 YNSTYRVSVSLTVLHQDLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSR 359

QY 358 DELTKNQVSLTCLVKGPYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKS 417

Db 360 EEMTKNQVSLTCLVKGPYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKS 419

QY 418 RWOQGNVFCSCVMHEALHNHYTQKSLSLSPGK 449

Db 420 RWOQGNVFCSCVMHEALHNHYTQKSLSLSPGK 451



RESULT 15  
US-08-466-151-65  
; Sequence 65, Application US/08466151  
; Patent No. 6037453  
; GENERAL INFORMATION:  
; APPLICANT: Jardiou, Paula M.  
; APPLICANT: Presta, Leonard G.  
; TITLE OF INVENTION: Immunoglobulin Variants  
; NUMBER OF SEQUENCES: 65  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Winpatin (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/466.151  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/466163  
; FILING DATE: 06-Jun-1995  
; APPLICATION NUMBER: 08/405617  
; FILING DATE: 15-MAR-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/185899  
; FILING DATE: 26-JAN-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/879495  
; FILING DATE: 07-MAY-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/744768  
; FILING DATE: 14-AUG-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Svoboda, Craig G.  
; REGISTRATION NUMBER: 39,044  
; REFERENCE/DOCKET NUMBER: P0718P2C1D1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-1489  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 65:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 451 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear

Search completed: April 6, 2006, 08:51:33  
Job time : 38.1767 secs

Query Match 70.6%; Score 2167; DB 2; Length 451;  
Best Local Similarity 90.9%; Pred. No. 7e-159;  
Matches 411; Conservative 16; Mismatches 21; Indels 4; Gaps 3;  
Qy 1 EVQLVESGGGVQPGGSLRVSCTASGPAF-SHYAMSWVROAPGKLEWVAYISGGSGTY 59  
Db 1 EVQLVESGGGLVQPGGSLRLSCAVSISITSGYSWNIROAPGKLEWVASITYDGS-TN 59  
Qy 60 YSDSVKGRFTISRDNSKNTLYLQMRSLRAEDSAVYFCTRVK--LGTYYPDSWGQGLLTV 117  
Db 60 YNPVSKGRITIRSDSKNTLYLQMRSLRAEDTAVYFCARGSHVFGHHFAVWGQGLTV 119  
Qy 118 SSASTKGPSVFPPLAPSSKSTSGTAAALCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQ 177  
Db 120 SSASTKGPSVFPPLAPSSKSTSGTAAALCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQ 179  
Qy 178 SSGLYSLSSVVTVPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKHTCTCPCPAPELL 237  
Db 180 SSGLYSLSSVVTVPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKHTCTCPCPAPELL 239

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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 6, 2006, 08:53:30 ; Search time 104.087 Seconds  
(without alignments)  
2336.277 Million cell updates/sec

Title: US-10-089-500-53  
Perfect score: 3071  
Sequence: 1 EVQLVSGGDFVPGGSLRV.....IVEFLNRWTFQSIISTLT 582

Scoring table: Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA.Main:  
1: /cgn2\_5/ptodata/1/pubpa/US07\_PUBCOMB.pep:  
2: /cgn2\_6/ptodata/1/pubpa/US08\_PUBCOMB.pep:  
3: /cgn2\_6/ptodata/1/pubpa/US09\_PUBCOMB.pep:  
4: /cgn2\_6/ptodata/1/pubpa/US10A\_PUBCOMB.pep:  
5: /cgn2\_6/ptodata/1/pubpa/US10B\_PUBCOMB.pep:  
6: /cgn2\_6/ptodata/1/pubpa/US11\_PUBCOMB.pep:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2750.5	89.6	579	4	US-10-138-727A-41
2	2750.5	89.6	579	4	US-10-310-719-32
3	2719.5	88.6	575	4	US-10-737-208A-6
4	2621	85.3	580	4	US-10-310-719-37
5	2589	84.3	580	4	US-10-310-719-35
6	2246.5	73.2	447	4	US-10-474-832-4
7	2240.5	73.0	447	4	US-10-474-832-5
8	2238.5	72.9	663	4	US-10-412-406-32
9	2238.5	72.9	4852	4	US-10-412-406-33
10	2236.5	72.8	447	4	US-10-474-832-6
11	2236	72.8	464	5	US-10-938-353-102
12	2234.5	72.8	445	4	US-10-320-231A-79
13	2234.5	72.8	445	5	US-10-867-506-79
14	2233	72.7	449	5	US-10-476-265-12
15	2233	72.7	468	5	US-10-476-265-20
16	2231.5	72.7	444	4	US-10-150-475A-6
17	2231.5	72.7	444	4	US-10-704-522-6
18	2231.5	72.7	444	4	US-10-645-215-6
19	2231.5	72.7	444	6	US-11-136-538-7
20	2229	72.6	470	5	US-10-938-353-98
21	2226	72.5	449	3	US-09-736-371B-21
22	2226	72.5	449	4	US-10-463-442-21
23	2225.5	72.4	477	4	US-10-291-265-395
24	2221.5	72.3	446	4	US-10-408-901-38
25	2220	72.3	474	3	US-09-848-832-3
26	2220	72.3	474	4	US-10-225-108A-3
27	2220	72.3	474	4	US-10-461-148-1

28	2216.5	72.2	442	4	US-10-226-435A-12	Sequence 12, Appl
29	2216.5	72.2	442	5	US-10-487-326-12	Sequence 12, Appl
30	2216.5	72.2	442	5	US-10-486-908-12	Sequence 12, Appl
31	2216.5	72.2	442	5	US-10-512-527-12	Sequence 12, Appl
32	2216	72.2	451	3	US-09-822-698A-26	Sequence 26, Appl
33	2216	72.2	457	5	US-10-778-915-1	Sequence 1, Appl
34	2215	72.1	449	5	US-10-985-584-10	Sequence 10, Appl
35	2213	72.1	449	6	US-11-056-776-5	Sequence 5, Appl
36	2213	72.1	468	6	US-11-056-776-6	Sequence 5, Appl
37	2212	72.0	445	4	US-10-408-901-34	Sequence 34, Appl
38	2209.5	71.9	442	4	US-10-487-322-12	Sequence 12, Appl
39	2209.5	71.9	442	5	US-10-487-326-21	Sequence 21, Appl
40	2209.5	71.9	442	5	US-10-486-908-16	Sequence 16, Appl
41	2209.5	71.9	442	5	US-10-512-527-21	Sequence 21, Appl
42	2207	71.9	453	5	US-10-891-658-41	Sequence 41, Appl
43	2202.5	71.7	446	4	US-10-408-901-46	Sequence 46, Appl
44	2202.5	71.7	469	5	US-10-858-186-14	Sequence 14, Appl
45	2198.5	71.6	469	4	US-10-656-769-26	Sequence 26, Appl

# ALIGNMENTS

RESULT 1

US-10-138-727A-41

; Sequence 41, Application US/10138727A

; Publication No. US20030157054A1

; GENERAL INFORMATION:

; APPLICANT: Gillies, Stephen

; APPLICANT: Lo, Kin-Ming

; APPLICANT: Qian, Susan

; TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof

; FILE REFERENCE: LEX-019

; CURRENT APPLICATION NUMBER: US/10/138,727A

; PRIOR FILING DATE: 2002-05-03

; PRIOR APPLICATION NUMBER: US 60/288,564

; PRIOR FILING DATE: 2001-05-03

; NUMBER OF SEQ ID NOS: 42

; SOFTWARE: Patent version 3.0

; SEQ ID NO 41

; LENGTH: 579

; TYPE: PRT

; ORGANISM: Artificial sequence

; FEATURE:

; OTHER INFORMATION: heavy chain-IL2

US-10-138-727A-41

Query Match 89.6%; Score 2750.5; DB 4; Length 579;

Best Local Similarity 88.5%; Pred. No. 6.8e-166;

Matches 516; Conservative 32; Mismatches 30; Indels 5; Gaps 2;

Qy 1 EVQLVSGGDFVPGGSLRVCAAGFAPFSHYAMSVVRQAPGKLEWVAYISSGGSGTYY 60

Db 1 QIQLVSGAEVKKPGETVKISKASGYTFNYGMNVKQTPGKLGKMGWINTYTGEPY 60

Qy 61 SDSVKGRFTISRDNKNTLYLQMRSLRADSAVYFCTR-VKLGTYVFDWGQGLTLTVSS 119

Db 61 ADDFKGRFAPSLFTSTSTAFQLQNNLRSDTATYFCVRFISKGDY----WGQGSTVTVSS 116

Qy 120 ASTKGPSVPLAPSSKSTSGTAAALGCLVKDYPEPEVTVSWNSGALTSGVHTFPVQLQSS 179

Db 117 ASTKGPSVPLAPSSKSTSGTAAALGCLVKDYPEPEVTVSWNSGALTSGVHTFPVQLQSS 176

Qy 180 GLYSLSVTVTPSSSLGTQTYICNVNHPKSNKTKVDKKVBPSPKSCDKTHTCCPPCAPPELLGG 239

Db 240 PSVFLPPPKKDTLMI SRTPETVTCVVVDVSHEDPEVKFNWYVDGVEVHNKATKPREQYN 299

Db 237 PSVFLPPPKKDTLMI SRTPETVTCVVVDVSHEDPEVKFNWYVDGVEVHNKATKPREQYN 296

Qy 300 STYRVVSVLTVTHODLNGKKEVKCKYKNKALPAIEKTIISKAKGQPREPOVYTLPPSRDE 359





Db 537 NVIVLBKSGTTFMCEYADETATVEFLNRWITFQSIISTLT 580  
|||||

RESULT 6  
US-10-474-832-4  
; Sequence 4, Application US/10474832  
; Publication No. US20040081651A1  
; GENERAL INFORMATION:  
; APPLICANT: BIOGEN, INC.  
; TITLE OF INVENTION: ANTIBODIES TO VLA-1  
; FILE REFERENCE: A101 PCT  
; CURRENT APPLICATION NUMBER: US/10/474,832  
; CURRENT FILING DATE: 2003-10-14  
; PRIOR APPLICATION NUMBER: 60/283,794  
; PRIOR FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: 60/303,689  
; PRIOR FILING DATE: 2001-07-06  
; NUMBER OF SEQ ID NOS: 70  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 447  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: polypeptide  
US-10-474-832-4

Query Match 73.2%; Score 2246.5; DB 4; Length 447;  
Best Local Similarity 95.1%; Pred. No. 4.2e-134;  
Matches 426; Conservative 4; Mismatches 17; Indels 1; Gaps 1;  
QY 1 EVQLVESGGDFVOPGSLRVSCAASGFPAPSHYAMSWVRQAPGKLEWVAIISGGSGTYY 60  
Db 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSRYTMSWVRQAPGKLEWVAIISGGGH-TYY 59  
QY 61 SDSVKGRFTISRDNKNTLYLQMSLRRAEDSAVYFCTRVKLGTYYPDSWGQGTLLTVSSA 120  
Db 60 LDSVKGRTISRDNKNTLYLQMSLRRAEDTAVYCTRGFGDGGYFDVWGQGTLLTVSSA 119  
QY 121 STKGPSVFPFLAPSSKSTSGTAAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSSG 180  
Db 120 STKGPSVFPFLAPSSKSTSGTAAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSSG 179  
QY 181 LYSLSVTVTPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPPCPAPELGGP 240  
Db 180 LYSLSVTVTPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPPCPAPELGGP 239  
QY 241 SVFLFPPPKDITLMSRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYNS 300  
Db 240 SVFLFPPPKDITLMSRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYNS 299  
QY 301 TYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL 360  
Db 300 TYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL 359  
QY 361 TKQVSLTCLVKGFPYPSDIAVEHESNGQPENNYKTPPVLDSDGSFPLYSKLTVDKSRWQ 420  
Db 360 TKQVSLTCLVKGFPYPSDIAVEHESNGQPENNYKTPPVLDSDGSFPLYSKLTVDKSRWQ 419  
QY 421 QGNVFSCSVNHEALHNHYTQKSLSLSPG 448  
Db 420 QGNVFSCSVNHEALHNHYTQKSLSLSPG 447

RESULT 7  
US-10-474-832-5  
; Sequence 5, Application US/10474832  
; Publication No. US20040081651A1  
; GENERAL INFORMATION:  
; APPLICANT: BIOGEN, INC.  
; TITLE OF INVENTION: ANTIBODIES TO VLA-1

; FILE REFERENCE: A101 PCT  
; CURRENT APPLICATION NUMBER: US/10/474,832  
; CURRENT FILING DATE: 2003-10-14  
; PRIOR APPLICATION NUMBER: 60/283,794  
; PRIOR FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: 60/303,689  
; PRIOR FILING DATE: 2001-07-06  
; NUMBER OF SEQ ID NOS: 70  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 5  
; LENGTH: 447  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: polypeptide  
US-10-474-832-5

Query Match 73.0%; Score 2240.5; DB 4; Length 447;  
Best Local Similarity 94.9%; Pred. No. 1e-133;  
Matches 425; Conservative 4; Mismatches 18; Indels 1; Gaps 1;

QY 1 EVQLVESGGDFVOPGSLRVSCAASGFPAPSHYAMSWVRQAPGKLEWVAIISGGSGTYY 60  
Db 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSRYTMSWVRQAPGKLEWVAIISGGGH-TYY 59  
QY 61 SDSVKGRFTISRDNKNTLYLQMSLRRAEDSAVYFCTRVKLGTYYPDSWGQGTLLTVSSA 120  
Db 60 LDSVKGRTISRDNKNTLYLQMSLRRAEDTAVYCTRGFGDGGYFDVWGQGTLLTVSSA 119  
QY 121 STKGPSVFPFLAPSSKSTSGTAAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSSG 180  
Db 120 STKGPSVFPFLAPSSKSTSGTAAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSSG 179  
QY 181 LYSLSVTVTPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPPCPAPELGGP 240  
Db 180 LYSLSVTVTPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPPCPAPELGGP 239  
QY 241 SVFLFPPPKDITLMSRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYNS 300  
Db 240 SVFLFPPPKDITLMSRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYNS 299  
QY 301 TYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL 360  
Db 300 TYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL 359  
QY 361 TKQVSLTCLVKGFPYPSDIAVEHESNGQPENNYKTPPVLDSDGSFPLYSKLTVDKSRWQ 420  
Db 360 TKQVSLTCLVKGFPYPSDIAVEHESNGQPENNYKTPPVLDSDGSFPLYSKLTVDKSRWQ 419  
QY 421 QGNVFSCSVNHEALHNHYTQKSLSLSPG 448  
Db 420 QGNVFSCSVNHEALHNHYTQKSLSLSPG 447

RESULT 8  
US-10-412-406-32  
; Sequence 32, Application US/10412406  
; Publication No. US20040058394A1  
; GENERAL INFORMATION:  
; APPLICANT: BIOGEN, INC.  
; APPLICANT: GARBER, Ellen  
; APPLICANT: LYNE, Paul  
; APPLICANT: SALDHANA, Jose W.  
; TITLE OF INVENTION: HUMANIZED ANTI-LT-BETA-R ANTIBODIES  
; FILE REFERENCE: B1A100CN  
; CURRENT APPLICATION NUMBER: US/10/412,406  
; CURRENT FILING DATE: 2003-04-10  
; PRIOR APPLICATION NUMBER: 60/240,285  
; PRIOR FILING DATE: 2000-10-13  
; PRIOR APPLICATION NUMBER: 60/275,289  
; PRIOR FILING DATE: 2001-03-13  
; PRIOR APPLICATION NUMBER: 60/299,987

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; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: PCT/US01/32140
; PRIOR FILING DATE: 2001-10-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 663
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-412-406-32

Query Match      72.9%; Score 2238.5; DB 4; Length 663;
Best Local Similarity 94.0%; Pred. No. 2.1e-133;
Matches 422; Conservative 8; Mismatches 18; Indels 1; Gaps 1;

Qy 1 EVQLVESGGDFVQPGGSLRVSCAASGFPAPSHYAMSVWRQAPGKGLEWVAIISGGSGTTY 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 215 EVQLVESGGGLVPGGSLRLSCLAAAGFTFSFYMYMFRQAPGKGLEWVAIISGGSYTY 274
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 61 SDSVKGRFTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLG-YYFDSWGQGLTLTVSS 119
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 275 PDSVKGRFTISRDNKNSLYLQMSLRAEDTAVYICAREENGNFYFDYWGQGLTVTVSS 334
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 120 ASTKGPSVFLPAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTTTPAVLQSS 179
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 335 ASTKGPSVFLPAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTTTPAVLQSS 394
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 180 GLYSLSVSVTVPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKTHCTCPCPAPPELLGG 239
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 395 GLYSLSVSVTVPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKTHCTCPCPAPPELLGG 454
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 240 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 299
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 455 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 514
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 300 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPOVYITLPPSRDE 359
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 515 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPOVYITLPPSRDE 574
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 360 LTRNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSGFFLYSKLTVDKSRW 419
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 575 LTRNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSGFFLYSKLTVDKSRW 634
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 420 QQGNVFSCSVMEALHNHYTQKSLSLSPG 448
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 635 QQGNVFSCSVMEALHNHYTQKSLSLSPG 663
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 9
US-10-412-406-33
; Sequence 33, Application US/10412406
; Publication No. US20040058394A1
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC.
; APPLICANT: GARBER, Ellen
; APPLICANT: LYNE, Paul
; APPLICANT: SALDHANA, Jose W.
; TITLE OF INVENTION: HUMANIZED ANTI-LT-BETA-R ANTIBODIES
; FILE REFERENCE: BINALOCCN
; CURRENT APPLICATION NUMBER: US/10/412,406
; CURRENT FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: 60/240,285
; PRIOR FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: 60/275,289
; PRIOR FILING DATE: 2001-03-13
; PRIOR APPLICATION NUMBER: 60/299,987
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: PCT/US01/32140
; PRIOR FILING DATE: 2001-10-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 4852

Query Match      72.9%; Score 2238.5; DB 4; Length 4852;
Best Local Similarity 94.0%; Pred. No. 2.2e-132;
Matches 422; Conservative 8; Mismatches 18; Indels 1; Gaps 1;

Qy 1 EVQLVESGGDFVQPGGSLRVSCAASGFPAPSHYAMSVWRQAPGKGLEWVAIISGGSGTTY 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 4404 EVQLVESGGGLVPGGSLRLSCLAAAGFTFSFYMYMFRQAPGKGLEWVAIISGGSYTY 4463
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 61 SDSVKGRFTISRDNKNTLYLQMRSLRAEDSAVYFCTRVKLG-YYFDSWGQGLTLTVSS 119
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 4464 PDSVKGRFTISRDNKNSLYLQMSLRAEDTAVYICAREENGNFYFDYWGQGLTVTVSS 4523
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 120 ASTKGPSVFLPAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTTTPAVLQSS 179
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 4524 ASTKGPSVFLPAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTTTPAVLQSS 4583
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 180 GLYSLSVSVTVPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKTHCTCPCPAPPELLGG 239
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 4584 GLYSLSVSVTVPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKTHCTCPCPAPPELLGG 4643
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 240 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 299
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 4644 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 4703
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 300 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPOVYITLPPSRDE 359
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 4704 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPOVYITLPPSRDE 4763
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 360 LTRNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSGFFLYSKLTVDKSRW 419
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 4764 LTRNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSGFFLYSKLTVDKSRW 4823
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 420 QQGNVFSCSVMEALHNHYTQKSLSLSPG 448
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 4824 QQGNVFSCSVMEALHNHYTQKSLSLSPG 4852
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 10
US-10-474-832-6
; Sequence 6, Application US/10474832
; Publication No. US20040081651A1
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC.
; TITLE OF INVENTION: ANTIBODIES TO VLA-1
; FILE REFERENCE: A101 PCT
; CURRENT APPLICATION NUMBER: US/10/474,832
; CURRENT FILING DATE: 2003-10-14
; PRIOR APPLICATION NUMBER: 60/283,794
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/303,689
; PRIOR FILING DATE: 2001-07-06
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 447
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: polypeptide
US-10-474-832-6

Query Match      72.8%; Score 2236.5; DB 4; Length 447;
Best Local Similarity 94.6%; Pred. No. 1.8e-133;
Matches 424; Conservative 4; Mismatches 19; Indels 1; Gaps 1;

Qy 1 EVQLVESGGDFVQPGGSLRVSCAASGFPAPSHYAMSVWRQAPGKGLEWVAIISGGSGTTY 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 EVQLVESGGGLVQPGGSLRLSCLAAAGFTFSRYTMSVWRQAPGKGLEWVAIISGGH-TYY 59
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
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QY 61 SDSVKGRTISRDNKNTLYLQMSLRRAEDSAVYFCTRVKLGTYTFDSWGQGLLTVSSA 120  
Db 60 LDSVKGRTISRDNKNTLYLQMSLRRAEDTAAYYCTRGFGDGGYFDVWGQGLTIVSSA 119  
QY 121 STKGPSVFPPLAPSKSTSGGTAALGCLVKDYFPEPVTVSNWNSGALTSVHTFPFVAVLQSSG 180  
Db 120 STKGPSVFPPLAPSKSTSGGTAALGCLVKDYFPEPVTVSNWNSGALTSVHTFPFVAVLQSSG 179  
QY 181 LYSLSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPPELLGGP 240  
Db 180 LYSLSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPPEAAGGP 239  
QY 241 SVFLFPPKPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 300  
Db 240 SVFLFPPKPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 299  
QY 301 TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPSRDEL 360  
Db 300 TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPSRDEL 359  
QY 361 TKNOVSLTCLVKGFPYSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQ 420  
Db 360 TKNOVSLTCLVKGFPYSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQ 419  
QY 421 QGNVFSCSVNHEALHNHYTQKSLSLSPG 448  
Db 420 QGNVFSCSVNHEALHNHYTQKSLSLSPG 447

## RESULT 11

US-10-938-353-102  
; Sequence 102, Application US/10938353  
; Publication No. US20050059113A1  
; GENERAL INFORMATION:  
; APPLICANT: BEDIAN, VAHE  
; APPLICANT: DEVALARAJA, MADHAV NARASIMHA  
; APPLICANT: FOLTZ, IAN  
; APPLICANT: HAAK-PRENDSCO, MARY  
; APPLICANT: KELLERMANN, SIRID-AIMEE  
; APPLICANT: LOW, JOSEPH EDWIN  
; APPLICANT: MOBLEY, JAMES LESLIE  
; TITLE OF INVENTION: ANTIBODIES TO M-CSF  
; FILE REFERENCE: ABX-PF4  
; CURRENT APPLICATION NUMBER: US/10/938,353  
; CURRENT FILING DATE: 2004-09-09  
; PRIOR APPLICATION NUMBER: 60/502,163  
; PRIOR FILING DATE: 2003-09-10  
; NUMBER OF SEQ ID NOS: 117  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 102  
; LENGTH: 464  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-938-353-102

Query Match 72.8%; Score 2236; DB 5; Length 464;  
Best Local Similarity 93.5%; Pred. No. 2e-133;  
Matches 420; Conservative 11; Mismatches 14; Indels 4; Gaps 1;

QY 1 EVQLVESGGGFVQPGGSLRVSCAASGFAPFASHYAMSWVRQAPGKGLEWYAISSGSGSTYY 60  
Db 20 QVQLVESGGGLVQPGGSLRLSCAASGFTFSDYIMSWIRQAPGKLEWVYISSGSGTIYY 79  
QY 61 SDSVKGRTISRDNKNTLYLQMSLRRAEDSAVYFCTRVKLGTYTFDSWGQGLLTVSSA 120  
Db 80 ADSVKGRTISRDNKNTLYLQMSLRRAEDTAAYYCARGLTGDY----WGQGLTIVSSA 135  
QY 121 STKGPSVFPPLAPSKSTSGGTAALGCLVKDYFPEPVTVSNWNSGALTSVHTFPFVAVLQSSG 180  
Db 136 STKGPSVFPPLAPSKSTSGGTAALGCLVKDYFPEPVTVSNWNSGALTSVHTFPFVAVLQSSG 195  
QY 181 LYSLSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPPELLGGP 240

Db 196 LYSLSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPPELLGGP 255  
QY 241 SVFLFPPKPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 300  
Db 256 SVFLFPPKPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 315  
QY 301 TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPSRDEL 360  
Db 316 TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPSRDEL 375  
QY 361 TKNOVSLTCLVKGFPYSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQ 420  
Db 376 TKNOVSLTCLVKGFPYSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQ 435  
QY 421 QGNVFSCSVNHEALHNHYTQKSLSLSPG 449  
Db 436 QGNVFSCSVNHEALHNHYTQKSLSLSPG 464

## RESULT 12

US-10-320-231A-79  
; Sequence 79, Application US/10320231A  
; Publication No. US20030194405A1  
; GENERAL INFORMATION:  
; APPLICANT: Neben, Steven  
; APPLICANT: Takeuchi, Toshihiko  
; APPLICANT: Tomkinson, Adrian  
; TITLE OF INVENTION: Antibody Inhibiting Stem Cell Factor Activity And Use For  
; TITLE OF INVENTION: Treatment Of Asthma  
; FILE REFERENCE: 7430\*163  
; CURRENT APPLICATION NUMBER: US/10/320,231A  
; CURRENT FILING DATE: 2002-12-19  
; PRIOR APPLICATION NUMBER: US 60/342,174  
; PRIOR FILING DATE: 2001-12-17  
; NUMBER OF SEQ ID NOS: 85  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 79  
; LENGTH: 445  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: synthetic sequence  
US-10-320-231A-79

Query Match 72.8%; Score 2234.5; DB 4; Length 445;  
Best Local Similarity 94.4%; Pred. No. 2.4e-133;  
Matches 421; Conservative 7; Mismatches 17; Indels 1; Gaps 1;

QY 4 LVESGGDFVQPGGSLRVSCAASGFAPFASHYAMSWVRQAPGKLEWYAISSGSGSTYSDS 63  
Db 1 LVESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKLEWYAISSGSGSTYADS 60  
QY 64 VKGRFTISRDNKNTLYLQMSLRRAEDSAVYFCTRVKLGTYTFDSWGQGLTIVSSASTK 123  
Db 61 VKGRFTISRDNKNTLYLQMSLRRAEDTAAYYCARRDFFA-HFDVWGQGLTIVSSASTK 119  
QY 124 GPSVPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSNWNSGALTSVHTFPFVAVLQSSGLYS 183  
Db 120 GPSVPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSNWNSGALTSVHTFPFVAVLQSSGLYS 179  
QY 184 LYSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPPELLGSPSVF 243  
Db 180 LYSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPPELLGSPSVF 239  
QY 244 LFPFPPKPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSYR 303  
Db 240 LFPFPPKPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSYR 299  
QY 304 VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPSRDELTKN 363  
Db 300 VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPSRDELTKN 359



QY 364 QVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTTTPPVLDSGSPFLYXSKLTVDKSRWQGN 423  
Db 360 QVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTTTPPVLDSGSPFLYXSKLTVDKSRWQGN 419  
QY 424 VFSCSVNHEALHNHYTKQSLSLSPGK 449  
Db 420 VFSCSVNHEALHNHYTKQSLSLSPGK 445

RESULT 13  
US-10-867-506-79  
; Sequence 79, Application US/10867506  
; Publication No. US20050112698A1  
; GENERAL INFORMATION:  
; APPLICANT: Neben, Steven  
; APPLICANT: Takeuchi, Toshihiko  
; APPLICANT: Tomkinson, Adrian  
; APPLICANT: Delaria, Kathy  
; APPLICANT: Yan, Kelly  
; APPLICANT: Wong, Teresa  
; APPLICANT: Longphre, Malinda  
; TITLE OF INVENTION: Antibody Inhibiting Stem Cell Factor Activity And Use For  
; TITLE OF INVENTION: Treatment Of Asthma  
; FILE REFERENCE: 11334\*10  
; CURRENT APPLICATION NUMBER: US/10/867,506  
; CURRENT FILING DATE: 2004-06-14  
; PRIOR APPLICATION NUMBER: US 10/320,231  
; PRIOR FILING DATE: 2002-12-16  
; PRIOR APPLICATION NUMBER: US 60/342,174  
; PRIOR FILING DATE: 2001-12-17  
; NUMBER OF SEQ ID NOS: 101  
; SOFTWARE: Patentin version 3.2  
; SEQ ID NO 79  
; LENGTH: 445  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: synthetic sequence  
US-10-867-506-79

Query Match 72.8%; Score 2234.5; DB 5; Length 445;  
Best Local Similarity 94.4%; Pred. No. 2.4e-133;  
Matches 421; Conservative 7; Mismatches 17; Indels 1; Gaps 1;

QY 4 LVESGGDFVQPGSLRVSCAASGFAFSHYAMSVROAPGKGLEWVAYISGGSGTYSDS 63  
Db 1 LVESGGGLVQPGSLRLSCAASGFTFSSYAMSVROAPGKGLEWVSAISGGSGTYADS 60  
QY 64 VKGRFTISRDNKNTLYLQWRSRAEDSAVYFCTRVKLGTYYPDSGQGTLLTVSSASTK 123  
Db 61 VKGRFTISRDNKNTLYLQWNSRAEDTAVYYCARRDFFA-HPDVWGQGTLLTVSSASTK 119  
QY 124 GPSVFPLAPSSKTSSTGTAALGCLVKDYRPEPTVTSWNSGALTSGVHTTTPAVLQSSGLYS 183  
Db 120 GPSVFPLAPSSKTSSTGTAALGCLVKDYRPEPTVTSWNSGALTSGVHTTTPAVLQSSGLYS 179  
QY 184 LSSVVTVPSSSLGTQTYICNVNHPKSNKTKVDKKEPKSCDKTHCTCPCPAPELGGPSVF 243  
Db 180 LSSVVTVPSSSLGTQTYICNVNHPKSNKTKVDKKEPKSCDKTHCTCPCPAPELGGPSVF 239  
QY 244 LFPPPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKTPRBEQYNSTYR 303  
Db 240 LFPPPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKTPRBEQYNSTYR 299  
QY 304 VVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDELTKN 363  
Db 300 VVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDELTKN 359  
QY 364 QVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTTTPPVLDSGSPFLYXSKLTVDKSRWQGN 423  
Db 360 QVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTTTPPVLDSGSPFLYXSKLTVDKSRWQGN 419  
QY 424 VFSCSVNHEALHNHYTKQSLSLSPGK 449

Db 420 VFSCSVNHEALHNHYTKQSLSLSPGK 445

RESULT 14  
US-10-476-265-12  
; Sequence 12, Application US/10476265  
; Publication No. US20050090648A1  
; GENERAL INFORMATION:  
; APPLICANT: Eli Lilly and Company  
; TITLE OF INVENTION: Humanized Antibodies  
; FILE REFERENCE: X14958  
; CURRENT APPLICATION NUMBER: US/10/476,265  
; CURRENT FILING DATE: 2003-10-22  
; PRIOR APPLICATION NUMBER: 60/287539  
; PRIOR FILING DATE: 2001-04-30  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 12  
; LENGTH: 449  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: humanized antibody  
US-10-476-265-12

Query Match 72.7%; Score 2233; DB 5; Length 449;  
Best Local Similarity 93.5%; Pred. No. 3e-133;  
Matches 420; Conservative 10; Mismatches 19; Indels 0; Gaps 0;

QY 1 EVLVESGGDFVQPGSLRVSCAASGFAFSHYAMSVROAPGKGLEWVAYISGGSGTY 60  
Db 1 EVLVESGGGLVQPGSLRLSCAASGFTFSGMSVROAPGKGLEWVASIRSGGRTY 60  
QY 61 SDSVKGRTISRDNKNTLYLQWRSRAEDSAVYFCTRVKLGTYYPDSGQGTLLTVSSA 120  
Db 61 SDNVKGRFTISRDNKNTLYLQWNSRAEDTAVYYCVRDHYSGSSDYWGQGTLLTVSSA 120  
QY 121 STKGPSVFPFLAPSSKTSSTGTAALGCLVKDYRPEPTVTSWNSGALTSGVHTTTPAVLQSSG 180  
Db 121 STKGPSVFPFLAPSSKTSSTGTAALGCLVKDYRPEPTVTSWNSGALTSGVHTTTPAVLQSSG 180  
QY 181 LYSLSGVVTVPPSSSLGTQTYICNVNHPKSNKTKVDKKEPKSCDKTHCTCPCPAPELGGP 240  
Db 181 LYSLSGVVTVPPSSSLGTQTYICNVNHPKSNKTKVDKKEPKSCDKTHCTCPCPAPELGGP 240  
QY 241 SVFLPPPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKTPRBEQYNS 300  
Db 241 SVFLPPPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKTPRBEQYNS 300  
QY 301 TYRVVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDEL 360  
Db 301 TYRVVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDEL 360  
QY 361 TKQVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTTTPPVLDSGSPFLYXSKLTVDKSRWQ 420  
Db 361 TKQVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTTTPPVLDSGSPFLYXSKLTVDKSRWQ 420  
QY 421 QGNVFSCSVNHEALHNHYTKQSLSLSPGK 449  
Db 421 QGNVFSCSVNHEALHNHYTKQSLSLSPGK 449

RESULT 15  
US-10-476-265-20  
; Sequence 20, Application US/10476265  
; Publication No. US20050090648A1  
; GENERAL INFORMATION:  
; APPLICANT: Eli Lilly and Company  
; TITLE OF INVENTION: Humanized Antibodies  
; FILE REFERENCE: X14958  
; CURRENT APPLICATION NUMBER: US/10/476,265  
; CURRENT FILING DATE: 2003-10-22

; PRIOR APPLICATION NUMBER: 60/287539  
; PRIOR FILING DATE: 2001-04-30  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 20  
; LENGTH: 468  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: humanized antibody  
US-10-476-265-20

Query Match		72.7%;	Score 2233;	DB 5;	Length 468;
Best Local Similarity		91.5%;	Pred. No. 3.2e-133;		
Matches	420;	Conservative	10;	Mismatches	19;
				Indels	0;
				Gaps	0;
Qy	1	EVQLVESGGGVQPGGSLRVS	CAASGFAF	SHYAMSV	RQAPGKLEWVAYISSGGSGTYY 60
Db	20	EVQLVESGGGLVQPGGSLRL	SCAGSGFTF	SNYGMV	RQAPGKLEWVASIRSGGRTYY 79
Qy	61	SDSVKGRFTISRDNKNTLY	LQMSRAED	SAVYFCT	RVKLGTTYFDSNGOGTLLTVSSA 120
Db	80	SDNVKGRFTISRDNKNTLY	LQMSRAED	TAIVYCV	RDYHSGSSDYNGQGTLTVSSA 139
Qy	121	STKGPSVFPPLAPSKSTSG	GTAAALG	CLVKDY	PEPTVSNVNSGALTSGVHTFPAVLQSSG 180
Db	140	STKGPSVFPPLAPSKSTSG	GTAAALG	CLVKDY	PEPTVSNVNSGALTSGVHTFPAVLQSSG 199
Qy	181	LYSLSSVTVTPSSSLGTQ	TYICNVN	HKPSN	TKVDKVEPKSCDKTHTCPPCPAPPELLGGP 240
Db	200	LYSLSSVTVTPSSSLGTQ	TYICNVN	HKPSN	TKVDKVEPKSCDKTHTCPPCPAPPELLGGP 259
Qy	241	SVFLFPPKPKDTLMISRT	PEVTCV	VDVSH	EDPEVKFNWYVDGVEVHNAKTKPREEQYNS 300
Db	260	SVFLFPPKPKDTLMISRT	PEVTCV	VDVSH	EDPEVKFNWYVDGVEVHNAKTKPREEQYNS 319
Qy	301	TYRWSVLTVLHODWLN	GKEYCK	CVSNK	ALPAPIEKTISKAKGQPREPQVYTLPPSRDEL 360
Db	320	TYRWSVLTVLHODWLN	GKEYCK	CVSNK	ALPAPIEKTISKAKGQPREPQVYTLPPSRDEL 379
Qy	361	TKNQVSLTCLVKGFYPS	SDIAVE	WESNGQ	PENNYKTTTPVLDSDGSPFLYSKLTVDKSRWQ 420
Db	380	TKNQVSLTCLVKGFYPS	SDIAVE	WESNGQ	PENNYKTTTPVLDSDGSPFLYSKLTVDKSRWQ 439
Qy	421	QGNVFSCSVNHEALHN	HYTK	OKSL	SLSPGK 449
Db	440	QGNVFSCSVNHEALHN	HYTK	OKSL	SLSPGK 468

Search completed: April 6, 2006, 08:56:24  
Job time : 105.087 sec8



Qy	300	STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPPVYTLPDSRDR	359
Db	297	STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPPVYTLPDSRBE	356
Qy	360	LTQKVSLTCLVKGFVPSDIAVEHESNQGPENNYKTPPVLDSDGSFPLYSKLTVDKSRW	419
Db	357	MTQKVSLTCLVKGFVPSDIAVEHESNQGPENNYKTPPVLDSDGSFPLYSKLTVDKSRW	416
Qy	420	QQGNVFSCSVMHEALHNHYTQKSLSLSPGKAPTSSSTKKTQLQLEHLLLDLQMLNGINN	479
Db	417	QQGNVFSCSVMHEALHNHYTQKSLSLSPGKAPTSSSTKKTQLQLEHLLLDLQMLNGINN	476
Qy	480	YKNPKLTRMLTFKFPYMPKATELKHQLCCEELKPLBEVLNLAQSKNFHLRPRDLISNTN	539
Db	477	YKNPKLTRMLTFKFPYMPKATELKHQLCCEELKPLBEVLNLAQSKNFHLRPRDLISNTN	536
Qy	540	VIVLELKGSETTFMCEYADETATIVFELNRRWITFCQSIISTLT	582
Db	537	VIVLELKGSETTFMCEYADETATIVFELNRRWITFCQSIISTLT	579

```

RESULT 2
US-11-172-320-6
; Sequence 6, Application US/11172320
; Publication No. US2005024413A1
; GENERAL INFORMATION:
; APPLICANT: Adolf, Guenther
; APPLICANT: Baum, Anke
; APPLICANT: Heider, Karl-Heinz
; TITLE OF INVENTION: Compositions and Methods for Treating Cancer using
; TITLE OF INVENTION: Cytotoxic CD44 Antibody Immunoconjugates and
; TITLE OF INVENTION: Chemotherapeutic Agents
; FILE REFERENCE: 1/1383
; CURRENT APPLICATION NUMBER: US/11/172,320
; CURRENT FILING DATE: 2005-06-30
; PRIOR APPLICATION NUMBER: US/10/645,215
; PRIOR FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: EP 02 018 686.2
; PRIOR FILING DATE: August 21, 2002
; PRIOR APPLICATION NUMBER: US 60/405,956
; PRIOR FILING DATE: August 26, 2002
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanised Murine Antibody BIWA 4 Heavy Chain
US-11-172-320-6

```

Query Match	72.7%	Score 2231.5	DB 7	Length 444
Best Local Similarity	93.8%	Pred. No. 8.1e-131		
Matches 421	Conservative 10	Mismatches 13	Indels 5	Gaps 1
Qy	1	EVQLVESGGDVPQCGSLRVS	CAASGFATFSVAMSWRQAPKGL	EWAVYISSGSGCTYY 60
Db	1	EVQLVESGGGLVLPQGSURLS	CAASGFTFSYDMSWRQAPKGL	EWVSTISSGGSYYT 60
Qy	61	SDSVKGRFTISRDNKNTLYLQ	MRSLRAEDSAVFTCTRVKLTGY	YFDSWGQGTLLTVSSA 120
Db	61	LDSIKGRFTISRDNAKNSLYLQ	MNSLRAEDTAVYYCAEQGL----	DYWGKGTLLTVSSA 115
Qy	121	STKGPSVFPFLAPSSKSTGGT	AAALGCLVKDYFPPPVTVSMNSG	ALTSQVHTFPFVLOSGG 180
Db	116	STKGPSVFPFLAPSSKSTGGT	AAALGCLVKDYFPEPVTVMNSG	ALTSQVHTFPFVLOSGG 175
Qy	181	LYSLSSVTVTPSSSLGTQTYI	CNNHKEPNTKVDKKEPKSCDK	THTCPCCPAPPELLGGP 240
Db	176	LYSLSSVTVTPSSSLGTQTYI	CNNHKEPNTKVDKKEPKSCDK	THTCPCCPAPPELLGGP 235
Qy	241	SVFLFPKPKDITLMSIRTPET	VCVVVDVSHEDPEVKFNWYDGV	GEVHNAKTKPREEQVNS 300

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Db      236  SVFLFPKPKDITLMSITPEVTCVVDSHSDPEVKFNWYVDGVGVHNAKTKPREQVNS 299
Qy      301  TYRVSVLTVLVHQDLWGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL 360
Db      296  TYRVSVLTVLVHQDLWGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL 355
Qy      361  TKQVSLTCLVKGPYPGSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQ 420
Db      356  TKQVSLTCLVKGPYPGSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQ 415
Qy      421  QGNVFSCVMHEALHNHYTQKSLSLSPGK 449
Db      416  QGNVFSCVMHEALHNHYTQKSLSLSPGK 444

RESULT 3
US-11-173-969-6
; Sequence 6, Application US/11173969
; Publication No. US20050271672A1
; GENERAL INFORMATION:
; APPLICANT: Adolf, G. et al.
; TITLE OF INVENTION: Cytotoxic CD44 Antibody Immunoconjugates
; FILE REFERENCE: 1/1211
; CURRENT APPLICATION NUMBER: US/11/173,969
; CURRENT FILING DATE: 2005-07-01
; PRIOR APPLICATION NUMBER: US/10/150,475
; PRIOR FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: US 60/307,451
; PRIOR FILING DATE: 2001-07-24
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Humanised
; OTHER INFORMATION: Murine Antibody B1WA 4 Heavy Chain SEQ ID NO: 6
US-11-173-969-6

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Query Match	72.7%	Score	2231.5	DB	7	Length	444
Best Local Similarity	93.8%	Pred. No.	8.1e-131				
Matches	421	Conservative	10	Mismatches	13	Indels	5
Gaps	1						
Qy	1	EVQLVESGGGDFVPGGSLRVISCAASGAFPSHYAMSWVRQAPGKGLIEWAVYISSGGSGTY	60				
Db	1	EVQLVESGGGLVPGGSLRLISCAASGRTFSSYDMSWRQAPGKGLIEWYSTISSGGSYTY	60				
Qy	61	SDSVKGFRTISRDNSSKNLTLYLQMSLRRAEDSAVVFCTRVKLTGYTFYFDSWGQGTLLTVSSA	120				
Db	61	LDSIKGRFTISRDNKAGLSYLQMSLRRAEDPAVYCARQGL-----DYWGRGTLTVSSA	115				
Qy	121	STKGPSVFPFLAPSSKTSGGTAAUGCGLVKDYFPPEPVTVSMNSGALTSGVHFPFVQLQSG	180				
Db	116	STKGPSVFPFLAPSSKTSGGTAAUGCGLVKDYFPPEPVTVSMNSGALTSGVHFPFVQLQSG	175				
Qy	181	LYSLSSVTVTPSSSLGTQYICNVNHKPSNTKVDKKVEPKSCDKTHTCPCPAPPELLGCP	240				
Db	176	LYSLSSVTVTPSSSLGTQYICNVNHKPSNTKVDKKVEPKSCDKTHTCPCPAPPELLGCP	235				
Qy	241	SVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKATKPREEQYNS	300				
Db	236	SVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKATKPREEQYNS	295				
Qy	301	TYRVVSVLTVLHQDLNKGKEYCKCSNKALPAPIEKTIISKAGQPREPQVYTLPPSRDEL	360				
Db	296	TYRVVSVLTVLHQDLNKGKEYCKCSNKALPAPIEKTIISKAGQPREPQVYTLPPSRDEL	355				
Qy	361	TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGDSFFLYSKLTVDKSRWQ	420				
Db	356	TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGDSFFLYSKLTVDKSRWQ	415				
Qy	421	QGNFYSCSVMEALHNHYTQKSLSLSPK	449				

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Db 416 QGNVFCSCVMHEALHNHYTKLSLSLSPGK 444
|||||
RESULT 4
US-11-158-505-33
; Sequence 33, Application US/11158505
; Publication No. US20060002921A1
; GENERAL INFORMATION:
; APPLICANT: WINSOR-HINES, DAWN
; APPLICANT: RAO, PATRICIA
; APPLICANT: RINGLER, DOUGLAS J
; APPLICANT: PONATH, PAUL
; TITLE OF INVENTION: OPTIMIZED DOSING OF ANTI-CD4 ANTIBODIES FOR TOLERANCE
; TITLE OF INVENTION: INDUCTION IN PRIMATES
; FILE REFERENCE: TLN-031
; CURRENT APPLICATION NUMBER: US/11/158,505
; CURRENT FILING DATE: 2005-06-21
; PRIOR APPLICATION NUMBER: 60/582,181
; PRIOR FILING DATE: 2004-06-22
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: Patent in Ver. 3.3
; SEQ ID NO 33
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Humanized CD8
; OTHER INFORMATION: antibody heavy chain construct
US-11-158-505-33

Query Match 72.6%; Score 2229; DB 7; Length 451;
Best Local Similarity 93.1%; Pred. No. 1.2e-130;
Matches 420; Conservative 10; Mismatches 19; Indels 2; Gaps 1;

Qy 1 EVQLVESGGDFVQPGGSLRVSCAASGFAPFASHYAMSVWRQAPGKLEWVAYISSGSGTYY 60
Db 1 QVQLVESGGGVVQPGSLRLSCAASGFTFSDFGMNWRQAPGKLEWVALLIYDGSKFY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 61 SDSVKGRTTISRDNKNTLYLQMSLRADSAVYFCTRVKLGTY--FDSMGQGTLLTVS 118
Db 61 ADSVKGRTTISRDNKNTLYLQMSLRADSAVYFCTRVKLGTY--FDSMGQGTLLTVS 120
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 119 SASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQS 178
Db 121 SASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQS 180
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 179 SGLYSLSVTVTPSSSLGTQYICNVNHPKSNTRYKDKVPEKSCDKTHCTCPCPAPELIG 238
Db 181 SGLYSLSVTVTPSSSLGTQYICNVNHPKSNTRYKDKVPEKSCDKTHCTCPCPAPELIG 240
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 239 GPSVFLPPPKDPTLMISRTEPVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQY 298
Db 241 GPSVFLPPPKDPTLMISRTEPVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQY 300
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 299 NSTYRVSVLTCLVKGFPSPDIADVESNGQPNNTKTPPVLDSDGSGFFLYSKLTVDKSR 358
Db 301 NSTYRVSVLTCLVKGFPSPDIADVESNGQPNNTKTPPVLDSDGSGFFLYSKLTVDKSR 360
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 359 ELTKNQVSLTCLVKGFPSPDIADVESNGQPNNTKTPPVLDSDGSGFFLYSKLTVDKSR 418
Db 361 ELTKNQVSLTCLVKGFPSPDIADVESNGQPNNTKTPPVLDSDGSGFFLYSKLTVDKSR 420
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 419 WQGNVFCSCVMHEALHNHYTKLSLSLSPGK 449
Db 421 WQGNVFCSCVMHEALHNHYTKLSLSLSPGK 451
|||||
RESULT 5
US-11-049-536-701
; Sequence 701, Application US/11049536
; Publication No. US20060024297A1
; GENERAL INFORMATION:
; APPLICANT: Wood, Clive R.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Pieters, Henk
; APPLICANT: Hufton, Simon E.
; TITLE OF INVENTION: TIE COMPLEX BINDING PROTEINS
; FILE REFERENCE: 10280-135001
; CURRENT APPLICATION NUMBER: US/11/199,739
```

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; APPLICANT: Wood, Clive R.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Pieters, Henk
; APPLICANT: Hufton, Simon E.
; TITLE OF INVENTION: TIE COMPLEX BINDING PROTEINS
; FILE REFERENCE: 10280-128001
; CURRENT APPLICATION NUMBER: US/11/049,536
; CURRENT FILING DATE: 2005-02-02
; PRIOR APPLICATION NUMBER: US 10/916,840
; PRIOR FILING DATE: 2004-08-12
; PRIOR APPLICATION NUMBER: US 60/494,713
; PRIOR FILING DATE: 2003-08-12
; NUMBER OF SEQ ID NOS: 721
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 701
; LENGTH: 450
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antibody
; US-11-049-536-701

Query Match 72.5%; Score 2225.5; DB 7; Length 450;
Best Local Similarity 93.3%; Pred. No. 1.9e-130;
Matches 420; Conservative 9; Mismatches 20; Indels 1; Gaps 1;

Qy 1 EVQLVESGGDFVQPGGSLRVSCAASGFAPFASHYAMSVWRQAPGKLEWVAYISSGSGTYY 60
Db 1 EVQLLESGGGLVQPGGSLRLSCAASGFTFSFMYGMVWRQAPGKLEWVISPSPGNTGY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 61 SDSVKGRTTISRDNKNTLYLQMSLRADSAVYFCTRVKLG-TYFDSMGQGTLLTVSS 119
Db 61 ADSVKGRTTISRDNKNTLYLQMSLRADSAVYFCTRVKLG-TYFDSMGQGTLLTVSS 120
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 120 ASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQS 179
Db 121 ASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQS 180
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 180 GLYSLSVTVTPSSSLGTQYICNVNHPKSNTRYKDKVPEKSCDKTHCTCPCPAPELIG 239
Db 181 GLYSLSVTVTPSSSLGTQYICNVNHPKSNTRYKDKVPEKSCDKTHCTCPCPAPELIG 240
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 240 PSVFLPPPKDPTLMISRTEPVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 299
Db 241 PSVFLPPPKDPTLMISRTEPVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 300
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 300 STYRVSVSLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 359
Db 301 STYRVSVSLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 360
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 360 LTKNQVSLTCLVKGFPSPDIADVESNGQPNNTKTPPVLDSDGSGFFLYSKLTVDKSRW 419
Db 361 LTKNQVSLTCLVKGFPSPDIADVESNGQPNNTKTPPVLDSDGSGFFLYSKLTVDKSRW 420
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 420 QQGNVFCSCVMHEALHNHYTKLSLSLSPGK 449
Db 421 QQGNVFCSCVMHEALHNHYTKLSLSLSPGK 450
|||||
RESULT 6
US-11-199-739-701
; Sequence 701, Application US/11199739
; Publication No. US20060057138A1
; GENERAL INFORMATION:
; APPLICANT: Wood, Clive R.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Pieters, Henk
; APPLICANT: Hufton, Simon E.
; TITLE OF INVENTION: TIE COMPLEX BINDING PROTEINS
; FILE REFERENCE: 10280-135001
; CURRENT APPLICATION NUMBER: US/11/199,739
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; CURRENT FILING DATE: 2005-08-09
; PRIOR APPLICATION NUMBER: US 11/049,536
; PRIOR FILING DATE: 2005-02-02
; PRIOR APPLICATION NUMBER: US 10/916,840
; PRIOR FILING DATE: 2004-08-12
; PRIOR APPLICATION NUMBER: US 60/494,713
; PRIOR FILING DATE: 2003-08-12
; NUMBER OF SEQ ID NOS: 726
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 701
; LENGTH: 450
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antibody
; US-11-199-739-701

Query Match          72.5%; Score 2225.5; DB 7; Length 450;
Best Local Similarity 93.3%; Pred. No. 1.9e-130; Indels 1; Gaps 1;
Matches 420; Conservative 9; Mismatches 20;

Qy 1 EVQLVESGGGVQPGGSLRVSRCASGFAFPAHYSWVRQAPGKGLWVAYISSGGSGTYY 60
Db 1 EVQLVESGGGLVQPGGSLRLSCLASGFTFSYMGVMVVRQAPGKGLWVVISPSGGNTGY 60
Qy 61 SDSVKGRTTISRDNKNTLYLQMSLRADSAVYFCTRVKLG-TYYFDSWQGGTLTVSS 119
Db 61 ADSVKGRTTISRDNKNTLYLQMSLRADSAVYFCTRVKLG-TYYFDSWQGGTLTVSS 120
Qy 120 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 179
Db 121 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 180
Qy 180 GLYSLSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHITCPCPAPELGG 239
Db 181 GLYSLSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHITCPCPAPELGG 240
Qy 240 PSVFLPPPKKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPRRQYN 299
Db 241 PSVFLPPPKKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPRRQYN 300
Qy 300 STYRWSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 359
Db 301 STYRWSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 360
Qy 360 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSKLTVDKSRW 419
Db 361 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSKLTVDKSRW 420
Qy 420 QQGNVFSCVMEALHNHYTQKSLSLSPGK 449
Db 421 QQGNVFSCVMEALHNHYTQKSLSLSPGK 450

RESULT 7
US-11-000-463-395
; Sequence 395, Application US/11000463
; Publication No. US20050266423A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Chen, Rui-hong
; APPLICANT: Qian, Xiaohong B.
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhang, Jie
; APPLICANT: Zhou, Ping
; APPLICANT: Cao, Yi-Cheng
; APPLICANT: Drmanac, Radjoe T.
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; FILE REFERENCE: 785CIP4CN
; CURRENT APPLICATION NUMBER: US/11/000,463
```

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; CURRENT FILING DATE: 2004-11-29
; PRIOR APPLICATION NUMBER: 10/291,265
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/922,279
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 395
; LENGTH: 477
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-000-463-395

Query Match          72.4%; Score 2222.5; DB 7; Length 477;
Best Local Similarity 91.7%; Pred. No. 3.2e-130; Indels 9; Gaps 2;
Matches 420; Conservative 12; Mismatches 17;

Qy 1 EVQLVESGGGVQPGGSLRVSRCASGFAFPAHYSWVRQAPGKGLWVAYISSGGSGTYY 60
Db 20 QVQLVESGGGVQPGGSLRSLSCASGFTFSYMGVMVVRQAPGKGLWVAAIWYDGSNKYY 79
Qy 61 SDSVKGRTTISRDNKNTLYLQMSLRADSAVYFCTR---VKLGF-----YYFDSWQ 111
Db 80 ADSVKGRTTISRDNKNTLYMQMNSLRADSAVYFCTR---VKLGF-----YYFDPYWG 139
Qy 112 GTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHT 171
Db 140 GTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHT 199
Qy 172 FPAVLQSSGLYSLSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHITCPPC 231
Db 200 FPAVLQSSGLYSLSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHITCPPC 259
Qy 232 PAPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATK 291
Db 260 PAPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATK 319
Qy 292 KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY 351
Db 320 KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY 379
Qy 352 TLPSPRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSK 411
Db 380 TLPSPREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSK 439
Qy 412 LTVDKSRWQQGNVFSCVMEALHNHYTQKSLSLSPGK 449
Db 440 LTVDKSRWQQGNVFSCVMEALHNHYTQKSLSLSPGK 477

RESULT 8
US-11-224-623-12
; Sequence 12, Application US/11224623
; Publication No. US20060039906A1
; GENERAL INFORMATION:
; APPLICANT: ELI LILLY AND COMPANY AND WASHINGTON UNIVERSITY
; TITLE OF INVENTION: Humanized Antibodies that Sequester Amyloid Beta Peptide
; FILE REFERENCE: 8792/293
; CURRENT APPLICATION NUMBER: US/11/224,623
; CURRENT FILING DATE: 2005-09-12
; PRIOR APPLICATION NUMBER: US/10/226,435
; PRIOR FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: PCT/US01/06191
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; PRIOR FILING DATE: 2001-02-26  
 ; PRIOR APPLICATION NUMBER: 60/184,601  
 ; PRIOR FILING DATE: 2000-02-24  
 ; PRIOR APPLICATION NUMBER: 60/254,465  
 ; PRIOR FILING DATE: 2000-12-08  
 ; PRIOR APPLICATION NUMBER: 60/254,498  
 ; PRIOR FILING DATE: 2000-12-08  
 ; NUMBER OF SEQ ID NOS: 16  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 12  
 ; LENGTH: 442  
 ; TYPE: PRT  
 ; ORGANISM: Artificial sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Humanized antibodies  
 ; US-11-224-623-12  
  
 Query Match 72.2%; Score 2216.5; DB 7; Length 442;  
 Best Local Similarity 93.5%; Pred. No. 6.8e-130;  
 Matches 420; Conservative 9; Mismatches 13; Indels 7; Gaps 2;  
  
 Qy 1 EVQLVESGGDFVPGGSLRVS CAASGFAFHYAMSWVRQAPGKGLEWVAISSGSGTYY 60  
 Db 1 EVQLVESGGGLVQPGGSLRLS CAASGFTFSRYMSWVRQAPGKGLELVAQINSVGNSTYY 60  
 Qy 61 SDSVKGRTTISRDN SKNTLYLQMSLR AEDSAVYFCTRVKLG-TYYFDSNCGOGLTLTVSSA 120  
 Db 61 PDTVKGRFTISRDN SKNTLYLQMSLR AEDTA VYICAS---WGQGLTLTVSSA 113  
 Qy 121 STKGPSVFP LAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSG 180  
 Db 114 STKGPSVFP LAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSG 173  
 Qy 181 LYSLSVVTVPPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPPCPAPELLGGP 240  
 Db 174 LYSLSVVTVPPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPPCPAPELLGGP 233  
 Qy 241 SVFLPPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKRREEQYN 300  
 Db 234 SVFLPPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKRREEQYN 293  
 Qy 301 TYRVSVLTVLH QDWLNGKEYCKVSNKALPAPIEKTIISKAKGQPREPQVYTLPPSRDEL 360  
 Db 294 TYRVSVLTVLH QDWLNGKEYCKVSNKALPAPIEKTIISKAKGQPREPQVYTLPPSRDEL 353  
 Qy 361 TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSFFLYSKLTVDKSRWQ 420  
 Db 354 TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSFFLYSKLTVDKSRWQ 413  
 Qy 421 QGNVFSCSVMEALHNHYTQKSLSLSPGK 449  
 Db 414 QGNVFSCSVMEALHNHYTQKSLSLSPGK 442

RESULT 9  
 US-11-199-739-723  
 ; Sequence 723, Application US/11199739  
 ; Publication No. US20060057138A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wood, Clive R.  
 ; APPLICANT: Dransfield, Daniel T.  
 ; APPLICANT: Pieters, Henk  
 ; APPLICANT: Hoet, Rene  
 ; APPLICANT: Hufton, Simon E.  
 ; TITLE OF INVENTION: TIE COMPLEX BINDING PROTEINS  
 ; FILE REFERENCE: 10280-135001  
 ; CURRENT APPLICATION NUMBER: US/11/199,739  
 ; CURRENT FILING DATE: 2005-08-09  
 ; PRIOR APPLICATION NUMBER: US 11/049,536  
 ; PRIOR FILING DATE: 2005-02-02  
 ; PRIOR APPLICATION NUMBER: US 10/916,840  
 ; PRIOR FILING DATE: 2004-08-12  
 ; PRIOR APPLICATION NUMBER: US 60/494,713

; PRIOR FILING DATE: 2003-08-12  
 ; NUMBER OF SEQ ID NOS: 726  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 723  
 ; LENGTH: 450  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Synthetically generated peptide  
 ; US-11-199-739-723  
  
 Query Match 72.2%; Score 2216.5; DB 7; Length 450;  
 Best Local Similarity 92.7%; Pred. No. 6.9e-130;  
 Matches 417; Conservative 12; Mismatches 20; Indels 1; Gaps 1;  
  
 Qy 1 EVQLVESGGDFVPGGSLRVS CAASGFAFHYAMSWVRQAPGKGLEWVAISSGSGTYY 60  
 Db 1 EVQLLESGGGLVQPGGSLRLS CAASGFTFSYMGVWVRQAPGKGLEWVSVISPSGNTGY 60  
 Qy 61 SDSVKGRTTISRDN SKNTLYLQMSLR AEDSAVYFCTRVKLG-TYYFDSNCGOGLTLTVSS 119  
 Db 61 ADSVKGRTTISRDN SKNTLYLQMSLR AEDTA VYICARPRGYSYGYIYWGQGLTLTVSS 120  
 Qy 120 ASTKGPSVFP LAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 179  
 Db 121 ASTKGPSVFP LAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 180  
 Qy 180 GLYSLSVVTVPPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPPCPAPELLGG 239  
 Db 181 GLYSLSVVTVPPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPPCPAPELLGG 240  
 Qy 240 PSVFLPPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKRREEQYN 299  
 Db 241 PSVFLPPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKRREEQYN 300  
 Qy 300 STYRVSVLTVLH QDWLNGKEYCKVSNKALPAPIEKTIISKAKGQPREPQVYTLPPSRDE 359  
 Db 301 STYRVSVLTVLH QDWLNGKEYCKVSNKALPAPIEKTIISKAKGQPREPQVYTLPPSRDE 360  
 Qy 360 LTRNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSFFLYSKLTVDKSRW 419  
 Db 361 MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSFFLYSKLTVDKSRW 420  
 Qy 420 QGNVFSCSVMEALHNHYTQKSLSLSPGK 449  
 Db 421 QGNVFSCSVMEALHNHYTQKSLSLSPGK 450

RESULT 10  
 US-10-981-356A-25  
 ; Sequence 25, Application US/10981356A  
 ; Publication No. US20060015952A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: FILVAROFF, ELLEN H.  
 ; TITLE OF INVENTION: SCREENING ASSAYS AND METHODS OF TUMOR TREATMENT  
 ; FILE REFERENCE: E2068R1  
 ; CURRENT APPLICATION NUMBER: US/10/981,356A  
 ; CURRENT FILING DATE: 2004-11-04  
 ; PRIOR APPLICATION NUMBER: US 60/520,398  
 ; PRIOR FILING DATE: 2003-11-13  
 ; PRIOR APPLICATION NUMBER: US 60/557,951  
 ; PRIOR FILING DATE: 2004-03-31  
 ; NUMBER OF SEQ ID NOS: 45  
 ; SEQ ID NO 25  
 ; LENGTH: 666  
 ; TYPE: PRT  
 ; ORGANISM: Artificial sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Sequence is synthesized  
 ; US-10-981-356A-25  
  
 Query Match 71.9%; Score 2208; DB 6; Length 666;  
 Best Local Similarity 91.8%; Pred. No. 3.6e-129;



Matches 412; Conservative 16; Mismatches 19; Indels 2; Gaps 1;  
Qy 1 EVQLVESGGDFVQPGGSLRVSQAASGFAFHYAMSWRQAPGKLEWVAISSGGSTYY 60  
Db 220 EVQLVESGGGLVQPGGSLRLSQAASGVAFTNYLIIEWRQAPGKLEWIGVNNPGSGSNY 279  
Qy 61 SDSVKGRFTISRDNKNTLYLQMSLRADSAVVFCTRVKLTGYTFDSWGGTLLTVSSA 120  
Db 280 NEKFGRFTISADNSKNTLYLQMSLRADTAIYCAR--SGGFYFDYWGQGLTVTVSSA 337  
Qy 121 STKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSG 180  
Db 338 STKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSG 397  
Qy 181 LYSLSVVTVPSSSLGTQTYICNVNHPKPSNTKVDKVEPKSCDKTHTCPPCPAPPELLGGP 240  
Db 398 LYSLSVVTVPSSSLGTQTYICNVNHPKPSNTKVDKVEPKSCDKTHTCPPCPAPPELLGGP 457  
Qy 241 SVFLFPPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 300  
Db 458 SVFLFPPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 517  
Qy 301 TYRVSVLTVLHQLDNLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYVTLPPSRDEL 360  
Db 518 TYRVSVLTVLHQLDNLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYVTLPPSRDEM 577  
Qy 361 TKQVSLTCLVKGYFSPDSIAVEWESNGOPENNYKTTTPVLDSDGSPFLYSKLTVDKSRWQ 420  
Db 578 TKQVSLTCLVKGYFSPDSIAVEWESNGOPENNYKTTTPVLDSDGSPFLYSKLTVDKSRWQ 637  
Qy 421 QGNVFSCVMHEALHNHYTOKLSLSLSPGK 449  
Db 638 QGNVFSCVMHEALHNHYTOKLSLSLSPGK 666

## RESULT 11

US-11-096-046-25  
; Sequence 25, Application US/11096046  
; Publication No. US20050276802A1  
; GENERAL INFORMATION:  
; APPLICANT: ADAMS, CAMELLIA W.  
; APPLICANT: FERRARA, NAPOLEONE  
; APPLICANT: FILVAROFF, ELLEN H.  
; APPLICANT: MAO, WEIGUANG  
; APPLICANT: PRESTA, LEONARD G.  
; APPLICANT: TEJADA, MAX L.  
; TITLE OF INVENTION: Humanized Anti-TGF-Beta Antibodies  
; FILE REFERENCE: PI954R1US  
; CURRENT APPLICATION NUMBER: US/11/096.046  
; CURRENT FILING DATE: 2005-03-31  
; PRIOR APPLICATION NUMBER: US 60/558,290  
; PRIOR FILING DATE: 2004-03-31  
; NUMBER OF SEQ ID NOS: 47  
; SEQ ID NO 25  
; LENGTH: 667  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: sequence is synthesized  
; NAME/KEY: Unsure  
; LOCATION: 220  
; OTHER INFORMATION: Unknown amino acid  
US-11-096-046-25  
Query Match 71.9%; Score 2208; DB 7; Length 667;  
Best Local Similarity 91.8%; Pred. No. 3.6e-129;  
Matches 412; Conservative 16; Mismatches 19; Indels 2; Gaps 1;  
Qy 1 EVQLVESGGDFVQPGGSLRVSQAASGFAFHYAMSWRQAPGKLEWVAISSGGSTYY 60  
Db 221 EVQLVESGGGLVQPGGSLRLSQAASGVAFTNYLIIEWRQAPGKLEWIGVNNPGSGSNY 280

Qy 61 SDSVKGRFTISRDNKNTLYLQMSLRADSAVVFCTRVKLTGYTFDSWGGTLLTVSSA 120  
Db 281 NEKFGRFTISADNSKNTLYLQMSLRADTAIYCAR--SGGFYFDYWGQGLTVTVSSA 338  
Qy 121 STKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSG 180  
Db 339 STKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSG 398  
Qy 181 LYSLSVVTVPSSSLGTQTYICNVNHPKPSNTKVDKVEPKSCDKTHTCPPCPAPPELLGGP 240  
Db 399 LYSLSVVTVPSSSLGTQTYICNVNHPKPSNTKVDKVEPKSCDKTHTCPPCPAPPELLGGP 458  
Qy 241 SVFLFPPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 300  
Db 459 SVFLFPPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 518  
Qy 301 TYRVSVLTVLHQLDNLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYVTLPPSRDEL 360  
Db 519 TYRVSVLTVLHQLDNLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYVTLPPSRDEM 578  
Qy 361 TKQVSLTCLVKGYFSPDSIAVEWESNGOPENNYKTTTPVLDSDGSPFLYSKLTVDKSRWQ 420  
Db 579 TKQVSLTCLVKGYFSPDSIAVEWESNGOPENNYKTTTPVLDSDGSPFLYSKLTVDKSRWQ 638  
Qy 421 QGNVFSCVMHEALHNHYTOKLSLSLSPGK 449  
Db 639 QGNVFSCVMHEALHNHYTOKLSLSLSPGK 667

## RESULT 12

US-10-981-356A-26  
; Sequence 26, Application US/10981356A  
; Publication No. US20060015952A1  
; GENERAL INFORMATION:  
; APPLICANT: FILVAROFF, ELLEN H.  
; TITLE OF INVENTION: SCREENING ASSAYS AND METHODS OF TUMOR TREATMENT  
; FILE REFERENCE: P2068R1  
; CURRENT APPLICATION NUMBER: US/10/981,356A  
; CURRENT FILING DATE: 2004-11-04  
; PRIOR APPLICATION NUMBER: US 60/520,398  
; PRIOR FILING DATE: 2003-11-13  
; PRIOR APPLICATION NUMBER: US 60/557,951  
; PRIOR FILING DATE: 2004-03-31  
; NUMBER OF SEQ ID NOS: 45  
; SEQ ID NO 26  
; LENGTH: 692  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Sequence is synthesized  
US-10-981-356A-26

Query Match 71.9%; Score 2208; DB 6; Length 692;  
Best Local Similarity 92.0%; Pred. No. 3.7e-129;  
Matches 413; Conservative 15; Mismatches 19; Indels 2; Gaps 1;  
Qy 1 EVQLVESGGDFVQPGGSLRVSQAASGFAFHYAMSWRQAPGKLEWVAISSGGSTYY 60  
Db 220 EVQLVESGGGLVQPGGSLRLSQAASGVAFTNYLIIEWRQAPGKLEWVGINPGSGSNY 279  
Qy 61 SDSVKGRFTISRDNKNTLYLQMSLRADSAVVFCTRVKLTGYTFDSWGGTLLTVSSA 120  
Db 280 NEKFGRFTISADNSKNTLYLQMSLRADTAIYCAR--SGGFYFDYWGQGLTVTVSSA 337  
Qy 121 STKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSG 180  
Db 338 STKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSG 397  
Qy 181 LYSLSVVTVPSSSLGTQTYICNVNHPKPSNTKVDKVEPKSCDKTHTCPPCPAPPELLGGP 240  
Db 398 LYSLSVVTVPSSSLGTQTYICNVNHPKPSNTKVDKVEPKSCDKTHTCPPCPAPPELLGGP 457  
Qy 241 SVFLFPPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 300



Db 458 SVFLPPPKPDKTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQNS 517  
Qy 301 TYRVVSVLTVLHODWLNKSKYCKKVSNNKALPAPIEKTISKAKGQPRPQVYTLPPSRDEL 360  
Db 518 TYRVVSVLTVLHODWLNKSKYCKKVSNNKALPAPIEKTISKAKGQPRPQVYTLPPSRDEM 577  
Qy 361 TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRWQ 420  
Db 578 TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRWQ 637  
Qy 421 QGNVFSCSVMEALHNHYTQKSLSLSPGK 449  
Db 638 QGNVFSCSVMEALHNHYTQKSLSLSPGK 666  
RESULT 13  
US-11-096-046-26  
; Sequence 26, Application US/11096046  
; Publication No. US20050276802A1  
; GENERAL INFORMATION:  
; APPLICANT: ADAMS, CAMELLIA W.  
; APPLICANT: FERRARA, NAPOLEONE  
; APPLICANT: FILVAROFF, ELLEN H.  
; APPLICANT: MAO, WEIGUANG  
; APPLICANT: PRESTA, LEONARD G.  
; APPLICANT: TEJADA, MAX L.  
; TITLE OF INVENTION: Humanized Anti-TGF-Beta Antibodies  
; FILE REFERENCE: P1954R1US  
; CURRENT APPLICATION NUMBER: US/11/096,046  
; PRIOR FILING DATE: 2005-03-31  
; PRIOR FILING DATE: 2004-03-31  
; NUMBER OF SEQ ID NOS: 47  
; SEQ ID NO 26  
; LENGTH: 695  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: sequence is synthesized  
; NAME/KEY: Unsure  
; LOCATION: 220, 668, 673  
; OTHER INFORMATION: Unknown amino acid  
US-11-096-046-26  
Query Match 71.9%; Score 2208; DB 7; Length 695;  
Best Local Similarity 92.0%; Pred. No. 3.7e-129;  
Matches 413; Conservative 15; Mismatches 19; Indels 2; Gaps 1;  
Qy 1 EVQLVESGGDFVQPGSLRVSCAASGFAFASHYAMSWVRQAPGKGLWVAYISSGGSGTY 60  
Db 221 EVQLVESGGGLVQPGSLRLSCAASGVAFTNLYIEWVRQAPGKGLWGVINPGSGSNY 280  
Qy 61 SDSVKGRFTISRDNKNTLYIQMRSRAEDSAVYFCTRVKLGTY----FDSWGQGTLL 120  
Db 281 NEKFKGRATISADNSKNTLYIQMNSRAEDSAVYCAR--SCGFYFDYWGQGLTVVSSA 338  
Qy 121 STKGPSVFLAPSSKSTSGGTAALGCLVKDYFPPPTVSMNSGALTSGVHTFPAVLQSSG 180  
Db 339 STKGPSVFLAPSSKSTSGGTAALGCLVKDYFPPPTVSMNSGALTSGVHTFPAVLQSSG 398  
Qy 181 LYSLSVVTVTPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHCTCPCPAPELLGGP 240  
Db 399 LYSLSVVTVTPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHCTCPCPAPELLGGP 458  
Qy 241 SVFLPPPKPDKTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQNS 300  
Db 459 SVFLPPPKPDKTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQNS 518  
Qy 301 TYRVVSVLTVLHODWLNKSKYCKKVSNNKALPAPIEKTISKAKGQPRPQVYTLPPSRDEL 360  
Db 519 TYRVVSVLTVLHODWLNKSKYCKKVSNNKALPAPIEKTISKAKGQPRPQVYTLPPSRDEM 578

Qy 361 TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRWQ 420  
Db 579 TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRWQ 638  
Qy 421 QGNVFSCSVMEALHNHYTQKSLSLSPGK 449  
Db 639 QGNVFSCSVMEALHNHYTQKSLSLSPGK 667  
RESULT 14  
US-11-041-095-22  
; Sequence 22, Application US/11041095  
; Publication No. US20060024782A1  
; GENERAL INFORMATION:  
; APPLICANT: Lehmbeck, Jan  
; TITLE OF INVENTION: Production of a Monoclonal Antibody in a Heterokaryon Fungus or  
; FILE REFERENCE: 10453 200-US  
; CURRENT APPLICATION NUMBER: US/11/041,095  
; CURRENT FILING DATE: 2005-01-20  
; NUMBER OF SEQ ID NOS: 74  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 22  
; LENGTH: 470  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Fusion protein of the TAKA signal peptide from *Aspergillus oryzae*  
; OTHER INFORMATION: alpha-amylase and a IgG1 heavy chain from *Homo sapiens*.  
US-11-041-095-22  
Query Match 71.7%; Score 2202.5; DB 7; Length 470;  
Best Local Similarity 91.6%; Pred. No. 5.3e-129;  
Matches 416; Conservative 12; Mismatches 17; Indels 9; Gaps 3;  
Qy 1 EVQLVESGGDFVQPGSLRVSCAASGFAFASHYAMSWVRQAPGKGLWVAYISSGGSGTY 60  
Db 21 EGQLVQSGGGLVHPGGSLRLSCAGSGFTFSYGHVWRQAPGKGLWVSGIGTGG-GTYS 79  
Qy 61 SDSVKGRFTISRDNKNTLYIQMRSRAEDSAVYFCTRVKLGTY----FDSWGQGTLL 115  
Db 80 TDSVKGRFTISRDNKNTLYIQMNSRAEDSAVYCAR--GDYYGSGSFDCWGQGTLLV 136  
Qy 116 TVSSASTKGPSVFLAPSSKSTSGGTAALGCLVKDYFPPPTVSMNSGALTSGVHTFPAV 175  
Db 137 TVSSASTKGPSVFLAPSSKSTSGGTAALGCLVKDYFPPPTVSMNSGALTSGVHTFPAV 196  
Qy 176 LQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHCTCPCPAPE 235  
Db 197 LQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHCTCPCPAPE 256  
Qy 236 LGGPSVFLPPPKDKTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 295  
Db 257 LGGPSVFLPPPKDKTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 316  
Qy 296 EQYNSTYRVVSVLTVLHODWLNKSKYCKKVSNNKALPAPIEKTISKAKGQPRPQVYTLPP 355  
Db 317 EQYNSTYRVVSVLTVLHODWLNKSKYCKKVSNNKALPAPIEKTISKAKGQPRPQVYTLPP 376  
Qy 356 SRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVD 415  
Db 377 SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVD 436  
Qy 416 KSRWQGNVFSCSVMEALHNHYTQKSLSLSPGK 449  
Db 437 KSRWQGNVFSCSVMEALHNHYTQKSLSLSPGK 470  
RESULT 15  
US-11-041-095-16  
; Sequence 16, Application US/11041095  
; Publication No. US20060024782A1

; GENERAL INFORMATION:  
; APPLICANT: Lehmebeck, Jan  
; TITLE OF INVENTION: Production of a Monoclonal Antibody in a Heterokaryon Fungus or  
; FILE REFERENCE: 10453.200-US  
; CURRENT APPLICATION NUMBER: US/11/041,095  
; CURRENT FILING DATE: 2005-01-20  
; NUMBER OF SEQ ID NOS: 74  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 16  
; LENGTH: 475  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Fusion protein between the prepro sequence from lipase B from  
; OTHER INFORMATION: Candida antarctica and an Igi heavy chain from Homo sapiens  
; OTHER INFORMATION: where the native signal peptide of the heavy chain has been  
; OTHER INFORMATION: removed.  
US-11-041-095-16

Query Match 71.7%; Score 2202.5; DB 7; Length 475;  
Best Local Similarity 91.6%; Pred. No. 5.4e-129;  
Matches 416; Conservative 12; Mismatches 17; Indels 9; Gaps 3;  
  
Qy 1 EVQLVESGGDFVPGGSLRVSCAASGFAFSPHYAMSWVRQAPGKGLEWVAYISSGGSGTYY 60  
Db EGQLVQSGGGLVHPGGSLRVSQAGSGFTFSSYGMHWVRQAPGKLEWVSGIGTG-GTYS 84  
  
Qy 61 SDSVKGRFTISRDNKNTLYLQMSLRADSAVFCTRVKLGTTY-----FDSMGQGTLL 115  
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 141  
85 TDSVKGRFTISRDNKNTLYLQMSLRADSAVFCTRVKLGTTY--GDYYVSGSFFDCWQGTLLV 141  
  
Qy 116 TVSSASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV 175  
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 201  
142 TVSSASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV 201  
  
Qy 176 LQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKYDKVEPKSCDKTHCTCPCPAPE 235  
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 261  
202 LQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKYDKVEPKSCDKTHCTCPCPAPE 261  
  
Qy 236 LLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 295  
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 321  
262 LLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 321  
  
Qy 296 EYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPQVYTLPP 355  
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 381  
322 EYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPQVYTLPP 381  
  
Qy 356 SRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVD 415  
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 441  
382 SREWTNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVD 441  
  
Qy 416 KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 449  
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 475  
442 KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 475

Search completed: April 6, 2006, 08:55:08  
Job time : 21.3097 secs

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: April 6, 2006, 08:47:08 ; Search time 24.1439 Seconds  
(without alignment)  
1965.416 Million cell updates/sec

Title: US-10-089-500-54  
Perfect score: 568  
Sequence: 1 DIQWTQSPSSLSASVGRVLT.....HQYSKLPWTFQGTQKVEIKR 108

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_21.\*

- 1: Geneseqp1980s.\*
- 2: Geneseqp1990s.\*
- 3: Geneseqp2000s.\*
- 4: Geneseqp2001s.\*
- 5: Geneseqp2002s.\*
- 6: Geneseqp2003as.\*
- 7: Geneseqp2003bs.\*
- 8: Geneseqp2004s.\*
- 9: Geneseqp2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	568	100.0	108	4	AAB81988
2	568	100.0	108	9	ADZ57823
3	568	100.0	128	4	AAB81999
4	562	98.9	108	6	ABU11011 Modified
5	561	98.8	128	4	AAB81994
6	555	97.7	108	9	ADZ57822
7	555	97.7	128	4	AAB81997
8	551	97.0	128	4	AAB81993
9	548	96.5	108	4	AAB81986
10	548	96.5	108	9	ADZ57820
11	545	96.0	128	4	AAB81995
12	545	96.0	128	4	AAB81996
13	544	95.8	128	4	AAB81998
14	535	94.2	108	9	ADZ57819
15	532	93.7	128	4	AAB81992
16	514	90.5	108	4	AAB81990
17	514	90.5	108	6	ABU11013
18	514	90.5	108	3	AA057817
19	514	90.5	128	3	AA01628
20	514	90.5	128	4	AAB81978
21	514	90.5	128	6	ABU11003
22	513	90.3	128	2	AAR33257
23	507	89.3	110	2	AAW70673
24	507	89.3	110	5	ABP61242

25	507	89.3	237	2	AAW70703	AAW70703 Protein e
26	507	89.3	650	5	ABP61241	Abp61241 Phage-dig
27	506	89.1	128	2	AAW28368	AAW28368 PKM641 LA
28	505	88.9	107	2	AAW86805	AAW86805 Variable
29	505	88.9	107	2	AAW70625	AAW70625 Humanised
30	505	88.9	107	5	ABP61194	Abp61194 Humanised
31	504	88.7	110	2	AAW70675	AAW70675 Anti-VEGF
32	504	88.7	110	5	ABP61244	Abp61244 Humanised
33	503	88.6	108	5	ABP70618	Abp70618 Anti-VEGF
34	503	88.6	108	5	ABP61187	Abp61187 Humanised
35	503	88.6	108	8	ADG31782	Adg31782 V(L) doma
36	503	88.6	108	8	ADG31768	Adg31768 V(L) doma
37	503	88.6	108	8	ADG31893	Adg31893 V(L) prot
38	503	88.6	108	9	ADX80647	Adx80647 Humanized
39	503	88.6	110	3	AAB05897	Ab05897 Humanised
40	503	88.6	110	3	AAB13376	Ab13376 F(ab)-12
41	503	88.6	237	8	ADQ90721	Adq90721 Anti-VEGF
42	501	88.2	107	2	AAW86804	AAW86804 Variable
43	501	88.2	107	2	AAW70623	AAW70623 Humanised
44	501	88.2	107	5	ABP61192	Abp61192 Humanised
45	500	88.0	108	8	ADG31770	Adg31770 V(L) doma

#### ALIGNMENTS

##### RESULT 1

ID	AAAB81988	standard; protein; 108 AA.
XX	AAAB81988	
AC	AAAB81988	
XX		
DT	03-JUL-2001	(first entry)
XX		
DE	Ganglioside GD3 specific antibody related protein SEQ ID NO: 54.	
XX		
KW	Ganglioside; GD3; complementarity determining region; CDR; antibody;	
KW	cancer.	
XX		
OS	Synthetic.	
XX		
PN	WO200123432-A1.	
XX		
PD	05-APR-2001.	
XX		
PF	29-SEP-2000; 2000WO-JF006774.	
XX		
PR	30-SEP-1999; 99JP-00278291.	
XX		
PR	06-APR-2000; 2000JP-00105088.	
XX		
PA	(KYOW ) KYOWA HAKKO KOGYO KK.	
XX		
PI	Hanai N, Shitara K, Nakamura K, Niwa R;	
XX		
DR	WPI; 2001-266143/27.	
XX		
PT	New human type complementation-determining region-transplanted antibody	
XX	and derivatives against ganglioside GD3. The antibody and its derivatives are	
PT	of e.g. tumors, with low antigenicity, little side effects but potent	
XX	activity in cancer.	
XX		
PS	Claim 22; Page 172-173; 183pp; Japanese.	
XX		
CC	The present invention describes a monoclonal antibody which can react	
XX	specifically with ganglioside GD3. The antibody and its derivatives are	
CC	useful in the diagnosis and therapy of tumours, particularly cancer	
XX	diagnosis. The present sequence is a protein used in the exemplification	
XX	of the invention	
XX		
SQ	Sequence 108 AA;	
Query Match	100.0%;	Score 568; DB 4; Length 108;
Best Local Similarity	100.0%;	Pred. No. 1.4e-35;

Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQOKPKDKAVKLLIFYSSNLHSGVPS 60
Db 1 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQOKPKDKAVKLLIFYSSNLHSGVPS 60
QY 61 RFSGGSGTDYTLTISSLPEDIAITYFCHQYSKLPWTFGGQTKVEIKR 108
Db 61 RFSGGSGTDYTLTISSLPEDIAITYFCHQYSKLPWTFGGQTKVEIKR 108
```

## RESULT 2

ADZ57823  
ID ADZ57823 standard; protein; 108 AA.

AC ADZ57823;

DT 30-JUN-2005 (first entry)

DE Ganglioside GD3 binding antibody associated protein SEQ ID NO 27.

XX cytostatic; antibody engineering; cancer; neoplasm; ganglioside; GD3;

KW pharmaceutical.

OS Synthetic.

PN WO2005035577-A1.

XX 21-APR-2005.

PF 08-OCT-2004; 2004WO-JP015314.

XX 08-OCT-2003; 2003JP-00350161.

XX (KYOW ) KYOWA HAKKO KOGYO KK.

PI Iida S, Satoh M, Urakubo M, Wakitani M, Uchida K, Niwa R;  
PI Shitara K;

DR WPI; 2005-346195/35.

XX Antibody composition for treating ganglioside GD3 associated disease e.g.  
PT cancer, comprises genetically modified antibody molecule, which  
PT specifically binds to ganglioside GD3 and has N-glycoside-binding sugar  
PT chain in its Fc domain.

XX Claim 25; SEQ ID NO 27; 124pp; Japanese.

XX The invention describes an antibody composition (I), comprising a  
CC genetically modified antibody molecule which specifically binds to  
CC ganglioside GD3 and has an N-glycoside-binding complex sugar chain in its  
CC Fc domain, where the N-glycoside-binding complex sugar chain is a sugar  
CC chain having no fucose attached to N-acetylglucosamine at the reducing  
CC end of the sugar chain. Also described are: a transformant (II) capable  
CC of producing (I), obtained by introducing DNA that encodes the antibody  
CC molecule which specifically binds with ganglioside GD3, to a host cell;  
CC producing (I), involving cultivating (I) in a culture medium, such that  
CC C1 (sic) is produced and accumulated in the culture, extracting and  
CC purifying C1 from the culture medium; a pharmaceutical (III) containing  
CC C1 as an active ingredient; and a therapeutic agent (A1) for ganglioside  
CC GD3 associated disease, comprising C1 as an active ingredient. (I) is  
CC useful for treating GD3 associated disease, which involves administering  
CC (I), where the GD3 associated disease is cancer. (A1) is also useful for  
CC treating GD3 associated disease. (II) is useful for producing (I). (I) is  
CC useful for manufacturing a therapeutic agent for GD3 associated disease.  
CC This sequence represents a ganglioside GD3 binding antibody associated  
CC protein.

XX Sequence 108 AA;

Query Match 100.0%; Score 568; DB 9; Length 108;  
Best Local Similarity 100.0%; Pred. No. 1.4e-35;  
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQOKPKDKAVKLLIFYSSNLHSGVPS 60
Db 1 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQOKPKDKAVKLLIFYSSNLHSGVPS 60
QY 61 RFSGGSGTDYTLTISSLPEDIAITYFCHQYSKLPWTFGGQTKVEIKR 108
Db 61 RFSGGSGTDYTLTISSLPEDIAITYFCHQYSKLPWTFGGQTKVEIKR 108
```

## RESULT 3

AAB81999  
ID AAB81999 standard; protein; 128 AA.

AC AAB81999;

DT 03-JUL-2001 (first entry)

DE Ganglioside GD3 specific antibody related protein #8.

XX Ganglioside; GD3; complementarity determining region; CDR; antibody;

KW cancer.

OS Synthetic.

PN WO200123432-A1.

XX 05-APR-2001.

PF 29-SEP-2000; 2000WO-JP006774.

XX 30-SEP-1999; 99JP-00278291.

PR 06-APR-2000; 2000JP-00105088.

XX (KYOW ) KYOWA HAKKO KOGYO KK.

PI Hanai N, Shitara K, Nakamura K, Niwa R;

XX WPI; 2001-266143/27.  
DR N-PSDB; AAF86913.

XX New human type complementation-determining region-transplanted antibody  
PT and derivatives against ganglioside GD3, useful in diagnosis and therapy  
PT of e.g. tumors, with low antigenicity, little side effects but potent  
PT activity in cancer.

XX Example 1; Page 166; 183pp; Japanese.

XX The present invention describes a monoclonal antibody which can react  
CC specifically with ganglioside GD3. The antibody and its derivatives are  
CC useful in the diagnosis and therapy of tumors, particularly cancer  
CC diagnosis. The present sequence is a protein used in the exemplification  
CC of the invention

XX Sequence 128 AA;

Query Match 100.0%; Score 568; DB 4; Length 128;  
Best Local Similarity 100.0%; Pred. No. 1.7e-35;  
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQOKPKDKAVKLLIFYSSNLHSGVPS 60
Db 21 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQOKPKDKAVKLLIFYSSNLHSGVPS 80
QY 61 RFSGGSGTDYTLTISSLPEDIAITYFCHQYSKLPWTFGGQTKVEIKR 108
Db 81 RFSGGSGTDYTLTISSLPEDIAITYFCHQYSKLPWTFGGQTKVEIKR 128
```

## RESULT 4

ABU11011  
ID ABU11011 standard; protein; 108 AA.

XX

```
AC ABU11011;
XX
XX 04-FEB-2003 (first entry)
XX
XX Modified ganglioside GD3 antibody associated protein #4.
XX
XX Ganglioside GD3; anti-ganglioside GD3 antibody; tumour; melanoma.
XX
XX Synthetic.
XX
XX WO200278739-A1.
XX
XX 10-OCT-2002.
XX
XX 29-MAR-2002; 2002WO-JP003170.
XX
XX 29-MAR-2001; 2001JP-00097483.
XX
XX (KYOW ) KYOWA HAKKO KOGYO KK.
XX
XX Shitara K, Niwa R, Kanazawa J, Asada M;
XX
XX WPI; 2003-067410/06.
XX
XX Drugs containing genetically-modified antibody against ganglioside GD3,
XX its fragment, immunocompetent cell activators or/and antitumor agents in
XX combination, applicable in treating malignant tumor like melanoma.
XX
XX Claim 8; Page 100; 121pp; Japanese.
XX
XX The invention describes drugs contain a genetically-modified antibody
XX against ganglioside GD3 or its fragment and at least 1 of a substance
XX capable of activating immunocompetent cells and a substance having an
XX antitumor activity in combination. The drugs can be used to treat tumour
XX like melanoma and can provide a treatment with enhanced therapeutic
XX effect and little side-reactions, particularly to relieve problems of
XX side-effects during the conventional single administration. This sequence
XX represents a protein associated with the anti- ganglioside GD3 antibody
XX
XX Sequence 108 AA;

Query Match 98.9%; Score 562; DB 6; Length 108;
Best Local Similarity 99.1%; Pred. No. 4.1e-35;
Matches 107; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCSASQDISNLYNWYQOKPKAVKLLIFYSSNLHSGVPS 60
Db 1 DIQMTQSPSSLSASVGRVTITCSASQDISNLYNWYQOKPKAVKLLIFYSSNLHSGVPS 60

Qy 61 RFSGGSGTDYTLTISSLPEDIATYFCHQYSKLPWTFGGTKVEIKR 108
Db 61 RFSGGSGTDYTLTISSLPEDIATYFCHQYSKLPWTFGGTKVEIKR 108

RESULT 5
AAB81994
ID AAB81994 standard; protein; 128 AA.
XX
XX AAB81994;
XX
XX 03-JUL-2001 (first entry)
XX
XX Ganglioside GD3 specific antibody related protein #3.
XX
XX Ganglioside; GD3; complementarity determining region; CDR; antibody;
XX cancer.
XX
XX Synthetic.
XX
XX WO200123432-A1.
XX
XX 05-APR-2001.
XX
XX
```

```
PF 29-SEP-2000; 2000WO-JP006774.
XX
XX 30-SEP-1999; 99JP-00278291.
XX
XX 06-APR-2000; 2000JP-00105088.
XX
XX (KYOW ) KYOWA HAKKO KOGYO KK.
XX
XX Hanai N, Shitara K, Nakamura K, Niwa R;
XX
XX WPI; 2001-266143/27.
XX
XX N-PSDB; AAF86898.
XX
XX New human type complementation-determining region-transplanted antibody
XX and derivatives against ganglioside GD3, useful in diagnosis and therapy
XX of e.g. tumors, with low antigenicity, little side effects but potent
XX activity in cancer.
XX
XX Example 1; Page 155-156; 183pp; Japanese.
XX
XX The present invention describes a monoclonal antibody which can react
XX specifically with ganglioside GD3. The antibody and its derivatives are
XX useful in the diagnosis and therapy of tumours, particularly cancer
XX diagnosis. The present sequence is a protein used in the exemplification
XX of the invention
XX
XX Sequence 128 AA;

Query Match 98.8%; Score 561; DB 4; Length 128;
Best Local Similarity 98.1%; Pred. No. 5.7e-35;
Matches 106; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCSASQDISNLYNWYQOKPKAVKLLIFYSSNLHSGVPS 60
Db 21 DIQMTQSPSSLSASVGRVTITCSASQDISNLYNWYQOKPKAVKLLIFYSSNLHSGVPS 80

Qy 61 RFSGGSGTDYTLTISSLPEDIATYFCHQYSKLPWTFGGTKVEIKR 108
Db 81 RFSGGSGTDYTLTISSLPEDFATYFCHQYSKLPWTFGGTKVEIKR 128

RESULT 6
ADZ57822
ID ADZ57822 standard; protein; 108 AA.
XX
XX ADZ57822;
XX
XX 30-JUN-2005 (first entry)
XX
XX Ganglioside GD3 binding antibody associated protein SEQ ID NO 26.
XX
XX cytostatic; antibody engineering; cancer; neoplasm; ganglioside; GD3;
XX pharmaceutical.
XX
XX Synthetic.
XX
XX WO2005035577-A1.
XX
XX 21-APR-2005.
XX
XX 08-OCT-2004; 2004WO-JP015314.
XX
XX 08-OCT-2003; 2003JP-00350161.
XX
XX (KYOW ) KYOWA HAKKO KOGYO KK.
XX
XX Iida S, Satoh M, Urakubo M, Wakitani M, Uchida K, Niwa R;
XX Shitara K;
XX
XX WPI; 2005-346195/35.
XX
XX Antibody composition for treating ganglioside GD3 associated disease e.g.
XX cancer, comprises genetically modified antibody molecule, which
XX specifically binds to ganglioside GD3 and has N-glycoside-binding sugar
```

PT chain in its Fc domain.  
 XX  
 PS Claim 25; SEQ ID NO 26; 124pp; Japanese.  
 XX  
 CC The invention describes an antibody composition (I), comprising a  
 CC genetically modified antibody molecule which specifically binds to  
 CC ganglioside GD3 and has an N-glycoside-binding complex sugar chain in its  
 CC Fc domain, where the N-glycoside-binding complex sugar chain is a sugar  
 CC chain having no fucose attached to N-acetylglucosamine at the reducing  
 CC end of the sugar chain. Also described are: a transformant (II) capable  
 CC of producing (I), obtained by introducing DNA that encodes the antibody  
 CC molecule which specifically binds with ganglioside GD3, to a host cell;  
 CC producing (I), involving cultivating (I) in a culture medium, such that  
 CC C1 (sic) is produced and accumulated in the culture, extracting and  
 CC purifying C1 from the culture medium; a pharmaceutical (III) containing  
 CC C1 as an active ingredient; and a therapeutic agent (A1) for ganglioside  
 CC GD3 associated disease, comprising C1 as an active ingredient. (I) is  
 CC useful for treating GD3 associated disease, which involves administering  
 CC (I), where the GD3 associated disease is cancer. (A1) is also useful for  
 CC treating GD3 associated disease. (II) is useful for producing (I). (I) is  
 CC useful for manufacturing a therapeutic agent for GD3 associated disease.  
 CC This sequence represents a ganglioside GD3 binding antibody associated  
 CC protein.  
 XX  
 SQ Sequence 108 AA;

Query Match 97.7%; Score 555; DB 9; Length 108;  
 Best Local Similarity 98.1%; Pred. No. 1.4e-34;  
 Matches 106; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 DIQMTQSPSSLSASVGRVITTCASQDISNYLNWYQKPKAVKLLIFYSSNLHSGVPS 60  
 DB 1 DIQMTQSPSSLSASVGRVITTCASQDISNYLNWYQKPKAVKLLIFYSSNLHSGVPS 60  
 QY 61 RFSGGSGTDYTLTISLQPEDIATYFCHQYSKLPWTFGQGTKEIKR 108  
 DB 61 RFSGGSGTDYTLTISLQPEDIATYFCHQYSKLPWTFGQGTKEIKR 108

RESULT 7  
 AAB81997  
 ID AAB81997 standard; protein; 128 AA.  
 XX  
 AC AAB81997;  
 XX  
 XX 03-JUL-2001 (first entry)  
 DT  
 DE Ganglioside GD3 specific antibody related protein #6.  
 XX  
 XX Ganglioside; GD3; complementarity determining region; CDR; antibody;  
 KW cancer.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200123432-A1.  
 XX  
 PD 05-APR-2001.  
 XX  
 PF 29-SEP-2000; 2000WO-JP006774.  
 XX  
 PR 30-SEP-1999; 99JP-00278291.  
 XX  
 PR 06-APR-2000; 2000JP-00105088.  
 XX  
 XX (KYOW ) KYOWA HAKKO KOGYO KK.  
 PA Hanai N, Shitara K, Nakamura K, Niwa R;  
 XX WPI; 2001-266143/27.  
 DR N-PSDB; AAF86907.  
 XX  
 XX New human type complementation-determining region-transplanted antibody  
 PT and derivatives against ganglioside GD3, useful in diagnosis and therapy  
 PT of e.g. tumors, with low antigenicity, little side effects but potent

PT activity in cancer.  
 XX  
 PS Example 1; Page 161-162; 183pp; Japanese.  
 XX  
 CC The present invention describes a monoclonal antibody which can react  
 CC specifically with ganglioside GD3. The antibody and its derivatives are  
 CC useful in the diagnosis and therapy of tumours, particularly cancer  
 CC diagnosis. The present sequence is a protein used in the exemplification  
 CC of the invention  
 XX  
 SQ Sequence 128 AA;  
 Query Match 97.7%; Score 555; DB 4; Length 128;  
 Best Local Similarity 98.1%; Pred. No. 1.6e-34;  
 Matches 106; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 DIQMTQSPSSLSASVGRVITTCASQDISNYLNWYQKPKAVKLLIFYSSNLHSGVPS 60  
 DB 21 DIQMTQSPSSLSASVGRVITTCASQDISNYLNWYQKPKAVKLLIFYSSNLHSGVPS 80  
 QY 61 RFSGGSGTDYTLTISLQPEDIATYFCHQYSKLPWTFGQGTKEIKR 108  
 DB 81 RFSGGSGTDYTLTISLQPEDIATYFCHQYSKLPWTFGQGTKEIKR 128

RESULT 8  
 AAB81993  
 ID AAB81993 standard; protein; 128 AA.  
 XX  
 AC AAB81993;  
 XX  
 XX 03-JUL-2001 (first entry)  
 DT  
 DE Ganglioside GD3 specific antibody related protein #2.  
 XX  
 XX Ganglioside; GD3; complementarity determining region; CDR; antibody;  
 KW cancer.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200123432-A1.  
 XX  
 PD 05-APR-2001.  
 XX  
 PF 29-SEP-2000; 2000WO-JP006774.  
 XX  
 PR 30-SEP-1999; 99JP-00278291.  
 XX  
 PR 06-APR-2000; 2000JP-00105088.  
 XX  
 XX (KYOW ) KYOWA HAKKO KOGYO KK.  
 PA Hanai N, Shitara K, Nakamura K, Niwa R;  
 XX WPI; 2001-266143/27.  
 DR N-PSDB; AAF86895.  
 XX  
 XX New human type complementation-determining region-transplanted antibody  
 PT and derivatives against ganglioside GD3, useful in diagnosis and therapy  
 PT of e.g. tumors, with low antigenicity, little side effects but potent  
 PT activity in cancer.  
 XX  
 XX Example 1; Page 153; 183pp; Japanese.  
 PS  
 CC The present invention describes a monoclonal antibody which can react  
 CC specifically with ganglioside GD3. The antibody and its derivatives are  
 CC useful in the diagnosis and therapy of tumours, particularly cancer  
 CC diagnosis. The present sequence is a protein used in the exemplification  
 CC of the invention  
 XX  
 SQ Sequence 128 AA;  
 Query Match 97.0%; Score 551; DB 4; Length 128;  
 Best Local Similarity 97.2%; Pred. No. 3.2e-34;

Matches 105; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQKPKAVKLLIFYSSNLHSGVPS 60  
 DB 21 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQKPKAVKLLIFYSSNLHSGVPS 80

QY 61 RFSGGSGTDYTLTISLQPEDIAFYCHQYSKLPWTFGGTKVEIKR 108  
 DB 81 RFSGGSGTDYTLTISLQPEDIAFYCHQYSKLPWTFGGTKVEIKR 128

RESULT 9  
 AAB81986  
 ID AAB81986 standard; protein; 108 AA.  
 XX  
 AC AAB81986;  
 XX  
 DT 03-JUL-2001 (first entry)  
 XX  
 DE Ganglioside GD3 specific antibody related protein SEQ ID NO: 10.  
 XX  
 KW Ganglioside; GD3; complementarity determining region; CDR; antibody;  
 KW cancer.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200123432-A1.  
 XX  
 PD 05-APR-2001.  
 XX  
 PF 29-SEP-2000; 2000WO-JP006774.  
 XX  
 PR 30-SEP-1999; 99JP-00278291.  
 PR 06-APR-2000; 2000JP-00105088.  
 XX  
 PA (KYOW ) KYOWA HAKKO KOGYO KK.  
 XX  
 PI Hanai N, Shitara K, Nakamura K, Niwa R;  
 XX  
 DR WPI; 2001-266143/27.  
 XX  
 PT New human type complementation-determining region-transplanted antibody  
 PT and derivatives against ganglioside GD3, useful in diagnosis and therapy  
 PT of e.g. tumors, with low antigenicity, little side effects but potent  
 PT activity in cancer.  
 XX  
 PS Example 1; Page 143-144; 183pp; Japanese.  
 XX  
 CC The present invention describes a monoclonal antibody which can react  
 CC specifically with ganglioside GD3. The antibody and its derivatives are  
 CC useful in the diagnosis and therapy of tumors, particularly cancer  
 CC diagnosis. The present sequence is a protein used in the exemplification  
 CC of the invention  
 XX  
 SQ Sequence 108 AA;

Query Match 96.5%; Score 548; DB 4; Length 108;  
 Best Local Similarity 96.3%; Pred. No. 4.7e-34;  
 Matches 104; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQKPKAVKLLIFYSSNLHSGVPS 60  
 DB 1 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQKPKAVKLLIFYSSNLHSGVPS 60

QY 61 RFSGGSGTDYTLTISLQPEDIAFYCHQYSKLPWTFGGTKVEIKR 108  
 DB 61 RFSGGSGTDYTLTISLQPEDIAFYCHQYSKLPWTFGGTKVEIKR 108

RESULT 10  
 ADZ57820  
 ID ADZ57820 standard; protein; 108 AA.  
 XX

AC ADZ57820;  
 XX  
 DT 30-JUN-2005 (first entry)  
 XX  
 DE Ganglioside GD3 binding antibody associated protein SEQ ID NO 24.  
 XX  
 KW Cytostatic; antibody engineering; cancer; neoplasm; ganglioside; GD3;  
 KW pharmaceutical.  
 XX  
 OS Synthetic.  
 XX  
 PN WO2005035577-A1.  
 XX  
 PD 21-APR-2005.  
 XX  
 PF 08-OCT-2004; 2004WO-JP015314.  
 XX  
 PR 08-OCT-2003; 2003JP-00350161.  
 XX  
 PA (KYOW ) KYOWA HAKKO KOGYO KK.  
 XX  
 PI Iida S, Satoh M, Urakubo M, Wakitani M, Uchida K, Niwa R;  
 PI Shitara K;  
 XX  
 DR WPI; 2005-346195/35.  
 XX  
 PT Antibody composition for treating ganglioside GD3 associated disease e.g.  
 PT cancer, comprises genetically modified antibody molecule, which  
 PT specifically binds to ganglioside GD3 and has N-glycoside-binding sugar  
 PT chain in its Fc domain.  
 XX  
 PS Claim 21; SEQ ID NO 24; 124pp; Japanese.  
 XX  
 CC The invention describes an antibody composition (I), comprising a  
 CC genetically modified antibody molecule which specifically binds to  
 CC ganglioside GD3 and has an N-glycoside-binding complex sugar chain in its  
 CC Fc domain, where the N-glycoside-binding complex sugar chain is a sugar  
 CC chain having no fucose attached to N-acetylglucosamine at the reducing  
 CC end of the sugar chain. Also described are: a transformant (II) capable  
 CC of producing (I), obtained by introducing DNA that encodes the antibody  
 CC molecule which specifically binds with ganglioside GD3, to a host cell;  
 CC producing (I), involving cultivating (I) in a culture medium, such that  
 CC Cl (sic) is produced and accumulated in the culture, extracting and  
 CC purifying Cl from the culture medium; a pharmaceutical (III) containing  
 CC Cl as an active ingredient; and a therapeutic agent (A1) for ganglioside  
 CC GD3 associated disease, comprising Cl as an active ingredient. (I) is  
 CC useful for treating GD3 associated disease, which involves administering  
 CC (I), where the GD3 associated disease is cancer. (A1) is also useful for  
 CC treating GD3 associated disease. (II) is useful for producing (I). (I) is  
 CC useful for manufacturing a therapeutic agent for GD3 associated disease.  
 CC This sequence represents a ganglioside GD3 binding antibody associated  
 CC protein.  
 XX  
 SQ Sequence 108 AA;

Query Match 96.5%; Score 548; DB 9; Length 108;  
 Best Local Similarity 96.3%; Pred. No. 4.7e-34;  
 Matches 104; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQKPKAVKLLIFYSSNLHSGVPS 60  
 DB 1 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQKPKAVKLLIFYSSNLHSGVPS 60

QY 61 RFSGGSGTDYTLTISLQPEDIAFYCHQYSKLPWTFGGTKVEIKR 108  
 DB 61 RFSGGSGTDYTLTISLQPEDIAFYCHQYSKLPWTFGGTKVEIKR 108

RESULT 11  
 AAB81995  
 ID AAB81995 standard; protein; 128 AA.  
 XX  
 AC AAB81995;

```
XX 03-JUL-2001 (first entry)
DT Ganglioside GD3 specific antibody related protein #4.
DE Ganglioside; GD3; complementarity determining region; CDR; antibody;
KW cancer.
XX Synthetic.
OS WO200123432-A1.
XX
XX 05-APR-2001.
XX
XX 29-SEP-2000; 2000WO-JP006774.
XX
XX 30-SEP-1999; 99JP-00278291.
PR 06-APR-2000; 2000JP-00105088.
XX (KYOW ) KYOWA HAKKO KOGYO KK.
XX Hanai N, Shitara K, Nakamura K, Niwa R;
XX WPI; 2001-266143/27.
DR N-PSDB; AAF86901.
XX
XX New human type complementation-determining region-transplanted antibody
PT and derivatives against ganglioside GD3, useful in diagnosis and therapy
PT of e.g. tumors, with low antigenicity, little side effects but potent
PT activity in cancer.
XX
XX Example 1; Page 157-158; 183pp; Japanese.
XX
XX The present invention describes a monoclonal antibody which can react
CC specifically with ganglioside GD3. The antibody and its derivatives are
CC useful in the diagnosis and therapy of tumours, particularly cancer
CC diagnosis. The present sequence is a protein used in the exemplification
CC of the invention
XX
XX Sequence 128 AA;
XX
XX Query Match 96.0%; Score 545; DB 4; Length 128;
XX Best Local Similarity 95.4%; Pred. No. 9.2e-34;
XX Matches 103; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
XX
XX 1 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQOKPKAVKLLIFYSSNLHSGVPS 60
XX 21 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQOKPKAVKLLIFYSSNLHSGVPS 80
XX
XX 61 RFSGGSGTDYTLTISSLPEDVATYFCHQYSKLPWTFGQGTKEIKR 108
XX 81 RFSGGSGTDYTLTISSLPEDVATYFCHQYSKLPWTFGQGTKEIKR 128
XX
XX RESULT 12
XX AAB81996
XX ID AAB81996 standard; protein; 128 AA.
XX AC AAB81996;
XX
XX 03-JUL-2001 (first entry)
XX
XX Ganglioside GD3 specific antibody related protein #5.
XX
XX Ganglioside; GD3; complementarity determining region; CDR; antibody;
XX cancer.
XX Synthetic.
XX OS WO200123432-A1.
XX
XX 05-APR-2001.
XX
XX Query Match 96.0%; Score 545; DB 4; Length 128;
XX Best Local Similarity 95.4%; Pred. No. 9.2e-34;
XX Matches 103; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
XX
XX 1 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQOKPKAVKLLIFYSSNLHSGVPS 60
XX 21 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQOKPKAVKLLIFYSSNLHSGVPS 80
XX
XX 61 RFSGGSGTDYTLTISSLPEDVATYFCHQYSKLPWTFGQGTKEIKR 108
XX 81 RFSGGSGTDYTLTISSLPEDVATYFCHQYSKLPWTFGQGTKEIKR 128
XX
XX RESULT 13
XX AAB81998
XX ID AAB81998 standard; protein; 128 AA.
XX AC AAB81998;
XX
XX 03-JUL-2001 (first entry)
XX
XX Ganglioside GD3 specific antibody related protein #7.
XX
XX Ganglioside; GD3; complementarity determining region; CDR; antibody;
XX cancer.
XX Synthetic.
XX OS WO200123432-A1.
XX
XX 05-APR-2001.
XX
XX 29-SEP-2000; 2000WO-JP006774.
XX
XX 30-SEP-1999; 99JP-00278291.
PR 06-APR-2000; 2000JP-00105088.
XX (KYOW ) KYOWA HAKKO KOGYO KK.
XX Hanai N, Shitara K, Nakamura K, Niwa R;
XX WPI; 2001-266143/27.
DR N-PSDB; AAF86912.
XX
XX New human type complementation-determining region-transplanted antibody
PT and derivatives against ganglioside GD3, useful in diagnosis and therapy
```



PT of e.g. tumors, with low antigenicity, little side effects but potent  
 PT activity in cancer.  
 XX Example 3; Page 164-165; 183pp; Japanese.  
 PS The present invention describes a monoclonal antibody which can react  
 CC specifically with ganglioside GD3. The antibody and its derivatives are  
 CC useful in the diagnosis and therapy of tumors, particularly cancer  
 CC diagnosis. The present sequence is a protein used in the exemplification  
 CC of the invention  
 XX  
 SQ Sequence 128 AA;

Query Match 95.8%; Score 544; DB 4; Length 128;  
 Best Local Similarity 96.3%; Pred. No. 1.1e-33;  
 Matches 104; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 DIQMTQSPSSLSASVGRVTITCSAQDISNYLNWYQKPKAVKLLIFYSNLSHGVS 60  
 DB 21 DIQMTQSASSLPASVGRVTITCSAQDISNYLNWYQKPKAVKLLIFYSNLSHGVS 80  
 QY 61 RPSGGSGTDYTLTISSLPEDIAFYCHQYSKLPWTFGQGTKEIKR 108  
 DB 81 RPSGGSGTDYTLTISSLPEDIAFYCHQYSKLPWTFGQGTKEIKR 128

RESULT 14  
 ADZ57819  
 ID ADZ57819 standard; protein; 108 AA.  
 XX  
 AC ADZ57819;  
 XX  
 DT 30-JUN-2005 (first entry)  
 XX  
 DE Ganglioside GD3 binding antibody associated protein SEQ ID NO 23.  
 XX  
 KW cytostatic; antibody engineering; cancer; neoplasm; ganglioside; GD3;  
 KW pharmaceutical.  
 XX  
 OS Synthetic.  
 XX  
 PN WO2005035577-A1.  
 XX  
 PD 21-APR-2005.  
 XX  
 PF 08-OCT-2004; 2004WO-JP015314.  
 XX  
 PR 08-OCT-2003; 2003JP-00350161.  
 XX  
 PA (KYOW ) KYOWA HAKKO KOGYO KK.  
 XX  
 PI Iida S, Satoh M, Urakubo M, Wakitani M, Uchida K, Niwa R;  
 PI Shitara K;  
 XX  
 DR WPI; 2005-346195/35.  
 XX

Antibody composition for treating ganglioside GD3 associated disease e.g.  
 PT cancer, comprises genetically modified antibody molecule, which  
 PT specifically binds to ganglioside GD3 and has N-glycoside-binding sugar  
 PT chain in its FC domain.  
 XX  
 PS Claim 20; SEQ ID NO 23; 124pp; Japanese.  
 XX  
 CC The invention describes an antibody composition (I), comprising a  
 CC genetically modified antibody molecule which specifically binds to  
 CC ganglioside GD3 and has an N-glycoside-binding complex sugar chain in its  
 CC FC domain, where the N-glycoside-binding complex sugar chain is a sugar  
 CC chain having no fucose attached to N-acetylglucosamine at the reducing  
 CC end of the sugar chain. Also described are: a transformant (II) capable  
 CC of producing (I), obtained by introducing DNA that encodes the antibody  
 CC molecule which specifically binds with ganglioside GD3, to a host cell;  
 CC producing (II), involving cultivating (I) in a culture medium, such that  
 CC C1 (sic) is produced and accumulated in the culture, extracting and

CC purifying C1 from the culture medium; a pharmaceutical (III) containing  
 CC C1 as an active ingredient; and a therapeutic agent (A1) for ganglioside  
 CC GD3 associated disease, comprising C1 as an active ingredient. (I) is  
 CC useful for treating GD3 associated disease, which involves administering  
 CC (I), where the GD3 associated disease is cancer. (A1) is also useful for  
 CC treating GD3 associated disease. (II) is useful for producing (I). (I) is  
 CC useful for manufacturing a therapeutic agent for GD3 associated disease.  
 CC This sequence represents a ganglioside GD3 binding antibody associated  
 CC protein.  
 XX  
 SQ Sequence 108 AA;

Query Match 94.2%; Score 535; DB 9; Length 108;  
 Best Local Similarity 93.5%; Pred. No. 4.5e-33;  
 Matches 101; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 DIQMTQSPSSLSASVGRVTITCSAQDISNYLNWYQKPKAVKLLIFYSNLSHGVS 60  
 DB 1 DIQMTQSPSSLSASVGRVTITCSAQDISNYLNWYQKPKAVKLLIFYSNLSHGVS 60  
 QY 61 RPSGGSGTDYTLTISSLPEDIAFYCHQYSKLPWTFGQGTKEIKR 108  
 DB 61 RPSGGSGTDYTLTISSLPEDIAFYCHQYSKLPWTFGQGTKEIKR 108

RESULT 15  
 AAB81992  
 ID AAB81992 standard; protein; 128 AA.  
 XX  
 AC AAB81992;  
 XX  
 DT 03-JUN-2001 (first entry)  
 XX  
 DE Ganglioside GD3 specific antibody related protein #1.  
 XX  
 KW Ganglioside; GD3; complementarity determining region; CDR; antibody;  
 KW cancer.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200123432-A1.  
 XX  
 PD 05-APR-2001.  
 XX  
 PF 29-SEP-2000; 2000WO-JP006774.  
 XX  
 PR 30-SEP-1999; 99JP-00278291.  
 PR 06-APR-2000; 2000JP-00105088.  
 XX  
 PA (KYOW ) KYOWA HAKKO KOGYO KK.  
 XX

Hanai N, Shitara K, Nakamura K, Niwa R;  
 WPI; 2001-266143/27.  
 N-PSDB; AAF86892.  
 XX  
 PT New human type complementation-determining region-transplanted antibody  
 PT and derivatives against ganglioside GD3, useful in diagnosis and therapy  
 PT of e.g. tumors, with low antigenicity, little side effects but potent  
 PT activity in cancer.  
 XX  
 PS Example 1; Page 150-151; 183pp; Japanese.  
 XX  
 CC The present invention describes a monoclonal antibody which can react  
 CC specifically with ganglioside GD3. The antibody and its derivatives are  
 CC useful in the diagnosis and therapy of tumors, particularly cancer  
 CC diagnosis. The present sequence is a protein used in the exemplification  
 CC of the invention  
 XX  
 SQ Sequence 128 AA;  
 XX  
 Query Match 93.7%; Score 532; DB 4; Length 128;  
 Best Local Similarity 93.5%; Pred. No. 8.8e-33;

	Matches	101;	Conservative	2;	Mismatches	5;	Indels	0;	Gaps	0;
Qy	1	DIQMTQSPSSLSASVGDRVTITCSASQDISNYLWYQOKPDKAVKLLIFYSNHLHSGVPS	60							
Db	21	DIQMTQTASSLPASVGDRVTITCSASQDISNYLWYQOKPDKAVKLLIFYSNHLHSGVPS	80							
Qy	61	RFSGGGSGTDYTLTISSSLQPEDIATYFCHQYSKLPWTFGGTKVEIKR	108							
Db	81	RFSGGGSGTDYTLTISSSLQPEDFATYFCHQYSKLPWTFGGTKVEIKR	128							

Search completed: April 6, 2006, 08:50:40  
 Job time : 24.1439 secs

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OM protein - protein search, using sw model  
Run on: April 6, 2006, 08:49:11 ; Search time 5.53544 Seconds  
(without alignments)  
1877.250 Million cell updates/sec

Title: US-10-089-500-54  
Perfect score: 568  
Sequence: 1 DIQWTQSPSSLSASVGRVT.....HOYSKLPWTFGGTKVEIKR 108

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 80:\*  
1: Pirl:\*  
2: Pirl2:\*  
3: Pirl3:\*  
4: Pirl4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	480	84.5	108	1 KIHUAW	Ig kappa chain V-I
2	479	84.3	111	2 A38740	Ig kappa chain V r
3	477	84.0	111	2 E38740	Ig kappa chain V r
4	472	83.1	111	2 G38740	Ig kappa chain V r
5	469	82.6	111	2 C38740	Ig kappa chain V r
6	466	82.0	107	2 B49026	Ig kappa chain V r
7	462	81.3	127	2 S40367	Ig kappa chain V-J
8	461	81.2	108	1 KVM573	Ig kappa chain V r
9	461	81.2	108	2 S69900	Ig kappa chain (cl)
10	456	80.3	108	1 KIHURE	Ig kappa chain V-I
11	454	79.9	122	2 A29380	Ig kappa chain pre
12	452	79.6	108	2 S69903	Ig kappa chain (cl)
13	452	79.6	115	2 JLO080	Ig kappa chain pre
14	451	79.4	129	2 S52789	Ig kappa chain V r
15	450	79.2	110	2 S44118	Ig kappa chain V-J
16	448	78.9	108	1 KVM5AR	Ig kappa chain V r
17	447	78.7	108	2 S69902	Ig kappa chain (cl)
18	447	78.7	109	2 PH0888	Ig kappa chain V r
19	447	78.7	126	2 A34904	Ig kappa chain pre
20	445	78.3	108	1 KIHUAG	Ig kappa chain V-I
21	445	78.3	108	2 I39154	Ig kappa chain (BR)
22	445	78.3	125	2 S40333	Ig kappa chain V-J
23	444	78.2	128	2 A26406	Ig kappa chain V r
24	443.5	78.1	107	2 S69901	Ig kappa chain (cl)
25	443	78.0	139	2 S40365	Ig kappa chain - h
26	442	77.8	123	2 S40331	Ig kappa chain - h
27	442	77.8	131	2 S40352	Ig kappa chain V-J
28	441.5	77.7	108	2 S38862	Ig kappa chain V r
29	441	77.6	108	2 B49047	Ig kappa chain V r

30	440	77.5	107	2 A48677	Ig kappa chain V-J
31	439	77.3	108	2 S44122	Ig kappa chain V r
32	439	77.3	108	2 C26405	Ig kappa chain V r
33	438	77.1	108	1 KIHURY	Ig kappa chain V-I
34	438	77.1	108	2 S19970	Ig kappa chain V r
35	437.5	77.0	107	2 S36275	Ig lambda chain V
36	437	76.9	107	2 B48677	Ig kappa chain V-J
37	437	76.9	107	2 B28044	Ig kappa chain V r
38	436	76.8	108	2 PU0282	Ig kappa chain V r
39	435	76.6	109	2 S31998	Ig kappa chain - h
40	434	76.4	107	2 S36264	Ig lambda chain V
41	434	76.4	107	2 A28044	Ig kappa chain V r
42	433	76.2	107	2 D48677	Ig kappa chain V-J
43	433	76.2	108	1 KIHUNE	Ig kappa chain V-I
44	433	76.2	108	2 B26405	Ig kappa chain V r
45	433	76.2	127	2 PH1234	Ig kappa chain pre

ALIGNMENTS

RESULT 1

KIHUAW  
Ig kappa chain V-I region (Au) - human  
C:Species: Homo sapiens (man)  
C:Date: 24-Apr-1984 #sequence revision 02-Jul-1998 #text\_change 09-Jul-2004  
C:Accession: A91653; A01862; S02573  
R:Schiechl, H.; Hilschmann, N.  
Hoppe-Sevler's Z. Physiol. Chem. 353, 345-370, 1972  
A:Title: Die Primaerstruktur einer monoklonalen Immunglobulin-L-Kette vom kappa-Typ, Sub  
A:Reference number: A91653; MUID:72189444; PMID:5028201  
A:Accession: A91653  
A:Molecule type: protein  
A:Residues: 1-108 <SCH>  
A:Cross-references: UNIPROT:P01594; UNIPARC:UPI000012E13E  
A:Note: the C region of this chain has the Inv (3) marker  
R:Fehlhammer, H.; Schiffer, M.; Epp, O.; Colman, P.M.; Lattman, E.E.; Schwager, P.; Stei  
Biophys. Struct. Mech. 1, 139-146, 1975  
A:Title: The structure determination of the variable portion of the Bence-Jones protein  
A:Reference number: A90729; MUID:77022433; PMID:1234024  
A:Contents: annotation; X-ray crystallography  
A:Note: the structure of the V region was determined by molecular replacement methods us  
R:Steiner, V.; Chang, J.Y.  
FEBS Lett. 222, 6-10, 1987  
A:Title: Chemical modification of the carboxyl groups of protein substrates enhances the  
A:Reference number: S02572; MUID:88005152; PMID:3115831  
A:Contents: annotation  
C:Comment: This is a Bence Jones protein.  
C:Genetics:  
A:Gene: GDB:IGKV1  
A:Cross-references: GDB:I36264  
A:Map position: 2p12-2p12  
C:Complex: an immunoglobulin heterotetramer subunit consists of two identical light (kap  
hain disulfide bonds; in some cases, such as IgA and IgM, the subunits associate into la  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:16-90/Domain: immunoglobulin homology <IMM>  
F:23-88/Disulfide bonds: #status predicted

Query Match 84.5%; Score 480; DB 1; Length 108;  
Best Local Similarity 85.2%; Pred. No. 1.3e-36;  
Matches 92; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

Oy 1 DIQWTQSPSSLSASVGRVTITCSASODISNLYNWYQOKPKDKAVKLLIFYSNLSHGVS 60

Db 1 DIQWTQSPSSLSASVGRVTITCSASODISNLYNWYQOKPKDKAVKLLIFYSNLSHGVS 60

Oy 61 RFSGGSGSDTYLTITSSLPEDATYFCQYSKLPWTFGGTKVEIKR 108

Db 61 RFSGGSGSDTYLTITSSLPEDATYFCQYSKLPWTFGGTKVEIKR 108

RESULT 2



A;Title: An immunoglobulin light chain from a lupus-prone mouse induces autoantibodies i  
A;Reference number: P10220; MUID:90278348; PMID:1693654  
A;Accession: P10220  
A;Status: nucleic acid sequence not shown  
A;Molecule type: mRNA  
A;Residues: 1-107 <PUC>  
A;Cross-references: UNIPARC:UPI0000176D3F  
A;Experimental source: strain lupus-prone MRL-lpr/lpr mouse  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;16-90/Domain: immunoglobulin homology <IMM>  
F;24-34/Region: complementarity-determining 1  
F;50-56/Region: complementarity-determining 2  
F;89-97/Region: complementarity-determining 3

Query Match 82.0%; Score 466; DB 2; Length 107;  
Best Local Similarity 82.2%; Pred. No. 2.3e-35;  
Matches 88; Conservative 10; Mismatches 9; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLWYQKPKDKAVKLLIFYSSNLHSGVPS 60  
Db 1 DIQMTQTSSLSASLGDRVTISCRASQDISNYLWYQKPKDGTGVKLLIYTSRLHSGVPS 60

Qy 61 RFSGGSGTDYTLTISSLQPEDIATYFCHOYSKLPWFQGTQKVEIK 107  
Db 61 RFSGGSGTDYTLTISNLEPEDIATYICQYQSKLPRTFGGTKLEIK 107

RESULT 7  
S40367  
Ig kappa chain V-J-C region - human  
C;Species: Homo sapiens (man)  
C;Date: 19-May-1994 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000  
C;Accession: S40367  
R;Klein, R.; Jaenichen, R.; Zachau, H.G.  
Eur. J. Immunol. 23, 3248-3271, 1993  
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.  
A;Reference number: S40312; MUID:94080891; PMID:8258341  
A;Accession: S40367  
A;Status: preliminary; translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-127 <KLB>  
A;Cross-references: UNIPARC:UPI0000176CB4; EMBL:X72477  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;33-107/Domain: immunoglobulin homology <IMM>

Query Match 81.3%; Score 462; DB 2; Length 127;  
Best Local Similarity 82.4%; Pred. No. 6.4e-35;  
Matches 89; Conservative 6; Mismatches 13; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLWYQKPKDKAVKLLIFYSSNLHSGVPS 60  
Db 18 DIQMTQSPSSLSASVGDRTVITCRASQISNYLWYQKPKAPKLLIYASSLSQSGVPS 77

Qy 61 RFSGGSGTDYTLTISSLQPEDIATYFCHOYSKLPWFQGTQKVEIKR 108  
Db 78 RFSGGSGTDFTLTISSLQPEDFATYICQYQSVNTPWFQGTQKVEIKR 125

RESULT 8  
KVMS73  
Ig kappa chain V region (MOPC 173) - mouse (tentative sequence)  
C;Species: Mus musculus (house mouse)  
C;Date: 24-Apr-1984 #sequence\_revision 24-Apr-1984 #text\_change 09-Jul-2004  
C;Accession: A01926  
R;Schiff, C.; Fougereau, M.  
Eur. J. Biochem. 59, 525-537, 1975  
A;Title: Determination of the primary structure of a mouse IgG2a immunoglobulin. Amino-a  
A;Reference number: A01926; MUID:76091934; PMID:812696  
A;Accession: A01926  
A;Molecule type: protein  
A;Residues: 1-108 <SCH>

A;Cross-references: UNIPROT:P01643; UNIPARC:UPI000002A0C4  
C;Comment: This chain was isolated from a myeloma protein.  
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap  
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer  
F;16-90/Domain: immunoglobulin homology <IMM>  
F;23-88/Disulfide bonds: #status predicted

Query Match 81.2%; Score 461; DB 1; Length 108;  
Best Local Similarity 78.7%; Pred. No. 6.7e-35;  
Matches 85; Conservative 13; Mismatches 10; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLWYQKPKDKAVKLLIFYSSNLHSGVPS 60  
Db 1 DIQMTQTSSLSASLGDRVTISCRASQISNYLWYQKPKDGTGVKLLIYTSRLHSGVPS 60

Qy 61 RFSGGSGTDYTLTISSLQPEDIATYFCHOYSKLPWFQGTQKVEIKR 108  
Db 61 RFSGGSGTDYSLTISBLZPBIATYICQYQSKLPRTFGGTKLEIKR 108

RESULT 9  
S69900  
Ig kappa chain (clone KL2.18 / KL4B10 / KL4C11) - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 14-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 21-Jan-2000  
C;Accession: S69900; S69907; S69908  
R;Wysocki, L.J.; Creadon, G.; Lehmann, K.R.; Cambier, J.C.  
Immunology 75, 116-121, 1992  
A;Title: B-cell proliferation initiated by Ia cross-linking and sustained by interleukin  
A;Reference number: S69900; MUID:92165291; PMID:1537587  
A;Accession: S69900  
A;Status: preliminary; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-108 <WYS>  
A;Cross-references: UNIPARC:UPI0000115EA3; EMBL:X55041; NID:9511023; PIDN:CAA38881.1; PI  
A;Accession: S69907  
A;Status: preliminary; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-108 <WY2>  
A;Cross-references: UNIPARC:UPI0000115EA3; EMBL:X55048; NID:9511037; PIDN:CAA38888.1; PI  
A;Accession: S69908  
A;Status: preliminary; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-108 <WY3>  
A;Cross-references: UNIPARC:UPI0000115EA3; EMBL:X55049; NID:9511039; PIDN:CAA38889.1; PI  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 81.2%; Score 461; DB 2; Length 108;  
Best Local Similarity 80.6%; Pred. No. 6.7e-35;  
Matches 87; Conservative 10; Mismatches 11; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLWYQKPKDKAVKLLIFYSSNLHSGVPS 60  
Db 1 DIQMTQTSSLSASLGDRVTISCRASQDISNYLWYQKPKDGTGVKLLIYTSRLHSGVPS 60

Qy 61 RFSGGSGTDYTLTISSLQPEDIATYFCHOYSKLPWFQGTQKVEIKR 108  
Db 61 RFSGGSGTDYSLTISNLEQEDIATYFCQQNTLPWFQGTQKLEIKR 108

RESULT 10  
KLHURE  
Ig kappa chain V-I region (Rei) - human (tentative sequence)  
C;Species: Homo sapiens (man)  
C;Date: 24-Apr-1984 #sequence\_revision 24-Apr-1984 #text\_change 09-Jul-2004  
C;Accession: A91663; A01873  
R;Palm, W.; Hilschmann, N.  
Hoppe-Seyler's Z. Physiol. Chem. 356, 167-191, 1975  
A;Title: Die Primaerstruktur einer kristallinen monoklonalen Immunglobulin-L-Kette vom k  
vollstaendige Aminosaeuresequenz des Proteins.

A;Reference number: A91663; MUID:76023758; PMID:809329  
A;Accession: A91663  
A;Molecule type: protein  
A;Residues: 1-108 <PAL>  
A;Cross-references: UNIPROT:P01607; UNIPARC:UPI000002D0C9  
A;Note: the C region of this chain has the Inv (1,2) marker  
R;Epp, O.; Lattman, E.E.; Schiffer, M.; Huber, R.; Palm, W.  
Biochemistry 14, 4943-4952, 1975  
A;Title: The molecular structure of a dimer composed of the variable portions of the Ben  
A;Reference number: A90392; MUID:76039968; PMID:1182131  
A;Contents: annotation; X-ray crystallography, 2.0 angstroms  
C;Comment: This is a Bence Jones protein.  
C;Genetics:  
A;Gene: GDB:IGKV1  
A;Cross-references: GDB:136264  
A;Map position: 2p12-2p12  
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap  
hain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into 14  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer  
F;16-90/Domain: immunoglobulin homology <IMM>  
F;23-88/Disulfide bonds: #status experimental

Query Match 80.3%; Score 456; DB 1; Length 108;  
Best Local Similarity 80.6%; Pred. No. 1.9e-34; Mismatches 7; Indels 0; Gaps 0;  
Matches 87; Conservative 7; Mismatches 14; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQKPKDKAVKLLIFYSSNLHSGVPS 60  
Db 1 DIQMTQSPSSLSASVGRVTITCSASQDIKYNLWYQTPGKAPKLLIYASNLQAGVPS 60

Qy 61 RFSGGSGGTDYTLTISSLPEDIAITYFCHQYKSLPWTFGGQTKVEIKR 108  
Db 61 RFSGGSGGTDYTLTISSLPEDIAITYFCHQYKSLPWTFGGQTKVEIKR 108

RESULT 11  
A29380  
Ig kappa chain precursor V region (AC-1001) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 31-Dec-1988 #sequence\_revision 31-Dec-1988 #text\_change 21-Jan-2000  
C;Accession: A29380  
R;Chen, H.T.; Kabat, E.A.; Lundblad, A.; Ratcliffe, R.M.  
J. Biol. Chem. 262, 13579-13583, 1987  
A;Title: Nucleotide and translated amino acid sequences of cDNA coding for the variable  
A;Reference number: A92612; MUID:88007582; PMID:3115981  
A;Accession: A29380  
A;Molecule type: mRNA  
A;Residues: 1-122 <CHE>  
A;Cross-references: UNIPARC:UPI000011677C; GB:M17160; GB:J02815; NID:g196895; PIDN:AAA38  
A;Note: the authors translated the codon TTC for residue 1 as Leu  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;30-104/Domain: immunoglobulin homology <IMM>

Query Match 79.9%; Score 454; DB 2; Length 122;  
Best Local Similarity 79.6%; Pred. No. 3.3e-34; Mismatches 10; Indels 0; Gaps 0;  
Matches 86; Conservative 10; Mismatches 12; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQKPKDKAVKLLIFYSSNLHSGVPS 60  
Db 15 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQKPKDGTGKLLIHYTSRLHSGVPS 74

Qy 61 RFSGGSGGTDYTLTISSLPEDIAITYFCHQYKSLPWTFGGQTKVEIKR 108  
Db 75 RFSGGSGGTDYTLTISSLPEDIAITYFCHQYKSLPWTFGGQTKVEIKR 122

RESULT 12  
S69903  
Ig kappa chain (clone KL2.29 / KL2.33 / KL3.8) - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 14-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 21-Jan-2000

C;Accession: S69903; S69904; S69905  
R;Wysocki, L.J.; Creadon, G.; Lehmann, K.R.; Cambier, J.C.  
Immunology 75, 116-121, 1992  
A;Title: B-cell proliferation initiated by Ia cross-linking and sustained by interleukin  
A;Reference number: S69900; MUID:92165291; PMID:1537587  
A;Accession: S69903  
A;Status: preliminary; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-108 <WYS>  
A;Cross-references: UNIPARC:UPI0000115227; EMBL:X55044; NID:9511029; PIDN:CAA38884.1; PFI  
A;Accession: S69904  
A;Status: preliminary; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-108 <WY2>  
A;Cross-references: UNIPARC:UPI0000115227; EMBL:X55045; NID:9511031; PIDN:CAA38885.1; PFI  
A;Accession: S69905  
A;Status: preliminary; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-108 <WY3>  
A;Cross-references: UNIPARC:UPI0000115227; EMBL:X55046; NID:9511033; PIDN:CAA38886.1; PFI  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 79.6%; Score 452; DB 2; Length 108;  
Best Local Similarity 79.6%; Pred. No. 4.3e-34; Mismatches 11; Indels 0; Gaps 0;  
Matches 86; Conservative 11; Mismatches 11; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQKPKDKAVKLLIFYSSNLHSGVPS 60  
Db 1 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQKPKDGTGKLLIYTSRLHSGVPS 60

Qy 61 RFSGGSGGTDYTLTISSLPEDIAITYFCHQYKSLPWTFGGQTKVEIKR 108  
Db 61 RFSGGSGGTDYTLTISSLPEDIAITYFCHQYKSLPWTFGGQTKVEIKR 108

RESULT 13  
JL0080  
Ig kappa chain precursor V region (anti-phenyloxazalone, 18C10) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 21-Jan-2000  
C;Accession: JL0080  
R;Kaartinen, M.; Rocca-Serra, J.; Maekela, O.  
Mol. Immunol. 25, 859-865, 1988  
A;Title: Combinatorial association of V genes: one VH gene codes for three non-cross-react  
A;Reference number: JL0076; MUID:89096973; PMID:3211160  
A;Accession: JL0080  
A;Molecule type: mRNA  
A;Residues: 1-115 <KAA>  
A;Cross-references: UNIPARC:UPI0000114EB9; GB:M27793; NID:g197161; PIDN:AAA38937.1; PID  
A;Note: the authors translated the codon AGG for residue 30 as Ser  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: immunoglobulin  
F;1-6/Domain: signal sequence (fragment) #status predicted <SIG>  
F;7-115/Product: Ig light chain #status predicted <MAT>  
F;22-96/Domain: immunoglobulin homology <IMM>  
F;30-40/Region: complementarity-determining 1  
F;56-62/Region: complementarity-determining 2

Query Match 79.6%; Score 452; DB 2; Length 115;  
Best Local Similarity 79.6%; Pred. No. 4.6e-34; Mismatches 11; Indels 0; Gaps 0;  
Matches 86; Conservative 11; Mismatches 11; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQKPKDKAVKLLIFYSSNLHSGVPS 60  
Db 7 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQKPKDGTGKLLIYTSRLHSGVPS 66

Qy 61 RFSGGSGGTDYTLTISSLPEDIAITYFCHQYKSLPWTFGGQTKVEIKR 108  
Db 67 RFSGGSGGTDYTLTISSLPEDIAITYFCHQYKSLPWTFGGQTKVEIKR 114

RESULT 14

```
S52789
Ig kappa chain V region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 19-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
C:Accession: S52789
R:Rocca, A.; Khamlichi, A.A.; Touchard, G.; Mougnot, B.; Ronco, P.; Denoroy, L.; Deret,
submitted to the EMBL Data Library, March 1995
A:Description: Light chain V region gene usage restriction and peculiarities in myeloma-
A:Reference number: S52789
A:Accession: S52789
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-129 <ROC>
A:Cross-references: UNIPARC:UPI0000116220; EMBL:X85995; NID:g758588; PIDN:CAAS9987.1; PI
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:38-112/Domain: immunoglobulin homology <IMM>

Query Match 79.4%; Score 451; DB 2; Length 129;
Best Local Similarity 81.3%; Pred. No. 6.5e-34;
Matches 87; Conservative 7; Mismatches 13; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVITTCASQDISNYLNWYQOKPKAVKLLIFYSNNLHSGVPS 60
Db 23 DIQMTQSPSSLSASVGRVITTCASQDISNYLNWYQOKPKAVKLLIFYSNNLHSGVPS 82

Qy 61 RFSGSGSGTDYTLTISSLPEDVATYFCHQYSKLPWTFGQGTKVEIK 107
Db 83 RFSGSGSGTDYTLTISSLPEDVATYFCHQYSKLPWTFGQGTKVEIK 129

RESULT 15
S44118
Ig kappa chain V-J region - human
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-May-2001
C:Accession: S44118
R:Hawkins, R.E.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.
submitted to the EMBL Data Library, March 1994
A:Description: Idiotypic vaccination against human B-cell lymphoma: rescue of variable r
A:Reference number: S44105
A:Accession: S44118
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-110 <HAW>
A:Cross-references: UNIPARC:UPI0000116635; EMBL:Z31395; NID:g472972; PIDN:CAAB3270.1; PI
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 79.2%; Score 450; DB 2; Length 110;
Best Local Similarity 80.9%; Pred. No. 6.7e-34;
Matches 89; Conservative 6; Mismatches 13; Indels 2; Gaps 1;

Qy 1 DIQMTQSPSSLSASVGRVITTCASQDISNYLNWYQOKPKAVKLLIFYSNNLHSGVPS 60
Db 1 DIQMTQSPSSLSASVGRVITTCASQDISNYLNWYQOKPKAVKLLIFYSNNLHSGVPS 60

Qy 61 RFSGSGSGTDYTLTISSLPEDVATYFCHQYSKLP--WTFGGGTKVEIK 108
Db 61 RFSGSGSGTDYTLTISSLPEDVATYFCHQYSKLP--WTFGGGTKVEIK 110

Search completed: April 6, 2006, 08:54:29
Job time : 5.53544 secs
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OM protein - protein search, using sw model

Run on: April 6, 2006, 08:48:06 ; Search time 33.4482 Seconds  
(without alignments)  
2278.061 Million cell updates/sec

Title: US-10-089-500-54  
Perfect score: 568  
Sequence: 1 DIQMTQSPSSLSASVGRVT.....HQYSKLPWTFQGQTKVFIKR 108

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_05.80.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	480	84.5	108	1 KV1B_HUMAN	P01594 homo sapien
2	461	81.2	108	1 KV5J_MOUSE	P01643 mus musculus
3	456	80.3	108	1 KV10_HUMAN	P01607 homo sapien
4	448	78.9	108	1 KV5K_MOUSE	P01644 mus musculus
5	447	78.7	108	1 KV5L_MOUSE	P01645 mus musculus
6	447	78.7	108	1 KV5M_MOUSE	P01646 mus musculus
7	445	78.3	108	1 KV1A_HUMAN	P01593 homo sapien
8	445	78.3	108	1 KV5O_MOUSE	P01648 mus musculus
9	445	78.3	108	2 Q9UL77_HUMAN	Q9UL77 homo sapien
10	443	78.0	108	1 KV5N_MOUSE	P01647 mus musculus
11	439	77.3	236	2 Q6GMW1_HUMAN	Q6GMW1 homo sapien
12	438	77.1	108	1 KV1P_HUMAN	P01608 homo sapien
13	436	76.8	108	1 KV1Y_HUMAN	P80362 homo sapien
14	434	76.4	108	2 Q9UL70_HUMAN	Q9UL70 homo sapien
15	433.5	76.3	107	2 Q96SA9_HUMAN	Q96SA9 homo sapien
16	433	76.2	108	1 KV1R_HUMAN	P01610 homo sapien
17	433	76.2	236	2 Q6GMX9_HUMAN	Q6GMX9 homo sapien
18	430	75.7	108	1 KV5U_MOUSE	P04946 mus musculus
19	430	75.7	236	2 Q7Z3Y4_HUMAN	Q7Z3Y4 homo sapien
20	429	75.5	107	2 Q9ULB4_MOUSE	Q9ULB4 mus musculus
21	429	75.5	108	1 KV1M_HUMAN	P01605 homo sapien
22	429	75.5	236	2 Q502W4_HUMAN	Q502W4 homo sapien
23	427	75.2	236	2 Q6GMX8_HUMAN	Q6GMX8 homo sapien
24	424	74.6	108	1 KV1H_HUMAN	P01600 homo sapien
25	423	74.5	236	2 Q6GMX0_HUMAN	Q6GMX0 homo sapien
26	422	74.3	129	1 KV1W_HUMAN	P04431 homo sapien
27	420	73.9	108	1 KV1K_HUMAN	P01603 homo sapien
28	420	73.9	108	1 KV1Q_HUMAN	P01609 homo sapien
29	419	73.8	108	1 KV1V_HUMAN	P04430 homo sapien
30	418	73.6	108	1 KV1L_HUMAN	P01604 homo sapien
31	417	73.4	108	1 KV1C_HUMAN	P01595 homo sapien

32	416.5	73.3	107	2 Q9UL81_HUMAN	Q9UL81 homo sapien
33	416	73.2	108	1 KV1N_HUMAN	P01606 homo sapien
34	416	73.2	116	2 Q96PF6_HUMAN	Q96PF6 homo sapien
35	416	73.2	189	2 Q569I7_HUMAN	Q569I7 homo sapien
36	414	72.9	236	2 Q6PIH7_HUMAN	Q6PIH7 homo sapien
37	413	72.7	108	1 KV1S_HUMAN	P01611 homo sapien
38	413	72.7	244	2 Q65ZC8_HUMAN	Q65ZC8 homo sapien
39	412	72.5	108	1 KV1G_HUMAN	P01599 homo sapien
40	411	72.4	108	1 KV1E_HUMAN	P01597 homo sapien
41	411	72.4	234	2 Q7Z473_HUMAN	Q7Z473 homo sapien
42	408.5	71.9	107	1 KV1D_HUMAN	P01596 homo sapien
43	408	71.8	240	2 Q65ZC9_HUMAN	Q65ZC9 homo sapien
44	405.5	71.4	109	1 KV1T_HUMAN	P01612 homo sapien
45	403	71.0	108	2 Q9UL79_HUMAN	Q9UL79 homo sapien

## ALIGNMENTS

## RESULT 1

ID KV1B\_HUMAN STANDARD; PRT; 108 AA.  
AC P01594;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 10-MAY-2005 (Rel. 47, Last annotation update)  
DE IG kappa chain V-I region AU.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP PROTEIN SEQUENCE.  
RX MEDLINE=72189444; PubMed=5028201;  
RA Schiechl H., Hilschmann N.;  
RT "Rule of antibody structure. The primary structure of a monoclonal immunoglobulin L-chain of the kappa-type, subgroup I (Bence-Jones protein Au).";  
RL Hoppe-Seyler's Z. Physiol. Chem. 353:345-370(1972).  
RN [2]  
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).  
RX MEDLINE=77022433; PubMed=1234024;  
RA Fehllhammer H., Schiffer M., Epp O., Colman P.M., Lattman E.E.,  
Schwager P., Steigemann W., Schramm H.J.;  
RT "The structure determination of the variable portion of the Bence-Jones protein Au.";  
RL Biophys. Struct. Mech. 1:139-146(1975).  
CC -1- MISCELLANEOUS: The structure of the V region was determined by molecular replacement methods using the known structure of the V region of the kappa chain REI.  
CC -1- MISCELLANEOUS: The C region of this chain has the INV (3) marker.  
CC -1- MISCELLANEOUS: This is a Bence-Jones protein.  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.

PIR; A91653; K1HUAV.  
PDB; 1JVS; X-ray; A=1-107.  
Ensembl; ENSG00000173782; Homo sapiens.  
GO; GO:0005576; C:extracellular region; NAS.  
GO; GO:0003823; F:antigen binding; NAS.  
GO; GO:0006955; P:immune response; NAS.  
InterPro; IPR007110; Ig-like.  
InterPro; IPR003596; Ig\_v.  
SMART; SM00406; IGV; 1.  
PROSITE; PS50835; IG\_LIKE; 1.  
3D-structure; Bence-Jones protein; Direct protein sequencing;  
Immunoglobulin domain; Immunoglobulin V region.  
REGION 1 23 Framework-1.

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FT REGION 24 34 Complementarity-determining-1.
FT REGION 25 49 Framework-2.
FT REGION 50 56 Complementarity-determining-2.
FT REGION 57 88 Framework-3.
FT REGION 89 97 Complementarity-determining-3.
FT REGION 98 107 Framework-4.
FT DISULFID 23 88 By similarity.
FT NON_TER 108 108
FT STRAND 4 5
FT STRAND 10 13
FT TURN 15 16
FT STRAND 19 25
FT TURN 30 31
FT STRAND 33 38
FT TURN 40 41
FT STRAND 44 49
FT TURN 50 52
FT STRAND 53 54
FT TURN 56 57
FT STRAND 60 61
FT STRAND 62 67
FT TURN 68 69
FT STRAND 70 75
FT HELIX 80 82
FT STRAND 85 90
FT TURN 97 98
FT STRAND 102 106
SQ SEQUENCE 108 AA; 11939 MW; E8011187EE6F6B9 CRC64;

Query Match 84.5%; Score 480; DB 1; Length 108;
Best Local Similarity 85.2%; Pred. No. 1,le-42;
Matches 92; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVITTCASQDISNYLNWYQKPKDKAVKLLIFYSNLSHSGVPS 60
Db 1 DIQMTQSPSSLSASVGRVITTCASQDISNYLNWYQKPKDKAVKLLIYDASNLHSGVPS 60

Qy 61 RFGSGSGTDYTLTISSLPEDVATYFCHQYSKLPWTFGQGTQVEIKR 108
Db 61 RFGSGSGNHTFTTISSLPEDVATYFCHQYDYLPLWTFGQGTQVEIKR 108

RESULT 2
KV5J_MOUSE STANDARD; PRT; 108 AA.
ID KV5J_MOUSE
AC P01643;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-V region MOPC 173.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_taxID=10090;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=76091934; PubMed=812696;
RA Schiff C., Fougereau M.;
RT "Determination of the primary structure of a mouse IGG2a
immunoglobulin. Amino-acid sequence of the light chain.";
RL Eur. J. Biochem. 59:525-537(1975).
CC -1- MISCELLANEOUS: This chain was isolated from a myeloma protein.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC PIR; A01926; KVM573.
CC HSSP; P01594; 1JVS.
CC Ensembl; ENSMUSG00000058965; Mus musculus.
DR
DR
```

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DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
FT REGION 1 23 Framework-1.
FT REGION 24 34 Complementarity-determining-1.
FT REGION 35 49 Framework-2.
FT REGION 50 56 Complementarity-determining-2.
FT REGION 57 88 Framework-3.
FT REGION 89 97 Complementarity-determining-3.
FT REGION 98 108 Framework-4.
FT DISULFID 23 88 By similarity.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11819 MW; 2AD29D92A72AA0A3 CRC64;

Query Match 81.2%; Score 461; DB 1; Length 108;
Best Local Similarity 78.7%; Pred. No. 1.2e-40;
Matches 85; Conservative 13; Mismatches 10; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVITTCASQDISNYLNWYQKPKDKAVKLLIFYSNLSHSGVPS 60
Db 1 DIQMTQSPSSLSASVGRVITTCASQDISNYLNWYQKPKDKAVKLLIYTSLSHSGVPS 60

Qy 61 RFGSGSGTDYTLTISSLPEDVATYFCHQYSKLPWTFGQGTQVEIKR 108
Db 61 RFGSGSGTDYSLTISBLZPZBIATYTCQYQSKLPRTFGGTQKLEIKR 108

RESULT 3
KV10_HUMAN STANDARD; PRT; 108 AA.
ID KV10_HUMAN
AC P01607;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-I region Rel.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_taxID=9606;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=76023758; PubMed=809329;
RA Palm W., Hilschmann N.;
RT "The primary structure of a crystalline monoclonal immunoglobulin
kappa-type L-chain, subgroup I (Bence-Jones protein Rel); isolation
and characterization of the tryptic peptides; the complete amino acid
sequence of the protein; a contribution to the elucidation of the
three-dimensional structure of antibodies, in particular their
combining site.";
RL Hoppe-Seyler's Z. Physiol. Chem. 356:167-191(1975).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX MEDLINE=76039968; PubMed=1182131;
RA Epp O., Lattman E.E., Schiffer M., Huber R., Palm W.;
RT "The molecular structure of a dimer composed of the variable portions
of the Bence-Jones protein REI refined at 2.0-A resolution.";
RL Biochemistry 14:4943-4952(1975).
CC -1- MISCELLANEOUS: The C region of this chain has the INV (1,2)
marker.
CC
CC -1- MISCELLANEOUS: This is a Bence-Jones protein.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC PIR; A91663; K1HURE.
CC PDB; 1AR2; X-ray; @=1-107.
DR
DR
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DR PDB; 1BWW; X-ray; A/B=1-107.
DR PDB; 1REI; X-ray; A/B=1-107.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 1_.
DR PROSITE; PS50835; IG LIKE; 1.
KW 3D-structure; Bence-Jones protein; Direct protein sequencing;
KW Immunoglobulin domain; Immunoglobulin V region.
FT REGION 1 23 Framework-1.
FT REGION 24 34 Complementarity-determining-1.
FT REGION 35 49 Framework-2.
FT REGION 50 56 Complementarity-determining-2.
FT REGION 57 88 Framework-3.
FT REGION 89 97 Complementarity-determining-3.
FT REGION 98 107 Framework-4.
FT DISULFID 23 88
FT NON_TER 108 108
FT STRAND 4 7
FT STRAND 10 13
FT TURN 15 16
FT STRAND 19 25
FT TURN 30 31
FT STRAND 33 38
FT TURN 40 41
FT STRAND 45 49
FT TURN 50 52
FT STRAND 53 54
FT TURN 56 57
FT TURN 60 61
FT STRAND 62 67
FT TURN 68 69
FT STRAND 70 75
FT HELIX 80 82
FT STRAND 84 90
FT STRAND 97 98
FT STRAND 102 106
SQ SEQUENCE 108 AA; 11902 MW; 9E8143E1188BCE2A CRC64;

Query Match 80.3%; Score 456; DB 1; Length 108;
Best Local Similarity 80.6%; Pred. No. 3.9e-40;
Matches 87; Conservative 7; Mismatches 14; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGDRTVITCSAQDISNLYNWYQKPKAVKLLIFYSNLSHGVPVS 60
Db 1 DIQMTQSPSSLSASVGDRTVITCSAQDIILKYNWYQTPGKAPKLLIYEASNLQAGVPS 60

Qy 61 RPSGSGSGTDYTLTISSLPEDIAITYFCHQYSKLPWTFGGTKVEIKR 108
Db 61 RPSGSGSGTDYTLTISSLPEDIAITYFCHQYSKLPWTFGGTKVQITR 108

RESULT 4
KV5K MOUSE
ID KV5K MOUSE STANDARD; PRT; 108 AA.
AC P01644;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-V region HP R16.7.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP PROTEIN SEQUENCE.
RC STRAIN=A/J;
RX MEDLINE=82150934; PubMed=6801658;
RA Siegelman M., Capra J.D.;
RT "Complete amino acid sequence of light chain variable regions derived
from five monoclonal anti-p-azophenylarsenate antibodies differing
with respect to a crossreactive idiotype."
RL Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).
CC -1- MISCELLANEOUS: Anti-arsenate hybridoma protein.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.
-----
PIR: A01927; KVMASR.
HSSP; P01594; 1JVS.
SMR; P01644; 1-108.
Ensembl; ENSMUSG00000029991; Mus musculus.
InterPro; IPR007110; IG-like.
InterPro; IPR003596; IG_v.
SMART; SM00406; IGV; 1_.
PROSITE; PS50835; IG LIKE; 1.
Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
FT REGION 1 23 Framework-1.
FT REGION 24 34 Complementarity-determining-1.
FT REGION 35 49 Framework-2.
FT REGION 50 56 Complementarity-determining-2.
FT REGION 57 88 Framework-3.
FT REGION 89 97 Complementarity-determining-3.
FT REGION 98 108 Framework-4.
FT DISULFID 23 88
FT NON_TER 108 108
FT STRAND 4 7
FT STRAND 10 13
FT TURN 15 16
FT STRAND 19 25
FT TURN 30 31
FT STRAND 33 38
FT TURN 40 41
FT STRAND 45 49
FT TURN 50 52
FT STRAND 53 54
FT TURN 56 57
FT TURN 60 61
FT STRAND 62 67
FT TURN 68 69
FT STRAND 70 75
FT HELIX 80 82
FT STRAND 84 90
FT STRAND 97 98
FT STRAND 102 106
SQ SEQUENCE 108 AA; 11910 MW; A554642C63EFF597 CRC64;

Query Match 78.9%; Score 448; DB 1; Length 108;
Best Local Similarity 79.6%; Pred. No. 2.7e-39;
Matches 86; Conservative 10; Mismatches 12; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGDRTVITCSAQDISNLYNWYQKPKAVKLLIFYSNLSHGVPVS 60
Db 1 DIQMTQSPSSLSASVGDRTVITCSAQDISNLYNWYQKPKAVKLLIFYSNLSHGVPVS 60

Qy 61 RPSGSGSGTDYTLTISSLPEDIAITYFCHQYSKLPWTFGGTKVEIKR 108
Db 61 RPSGSGSGTDYTLTISSLPEDIAITYFCHQYSKLPWTFGGTKVEIKR 108

RESULT 5
KV5L MOUSE
ID KV5L MOUSE STANDARD; PRT; 108 AA.
AC P01645;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-V region HP 93G7.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP PROTEIN SEQUENCE.
RC STRAIN=A/J;
RX MEDLINE=82150934; PubMed=6801658;
RA Siegelman M., Capra J.D.;
RT "Complete amino acid sequence of light chain variable regions derived
from five monoclonal anti-p-azophenylarsenate antibodies differing
with respect to a crossreactive idiotype."
RL Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).
CC -1- MISCELLANEOUS: Anti-arsenate hybridoma protein.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
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the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.
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PIR: A01927; KVMASR.
HSSP; P01594; 1JVS.
SMR; P01644; 1-108.
Ensembl; ENSMUSG00000029991; Mus musculus.
InterPro; IPR007110; IG-like.
InterPro; IPR003596; IG_v.
SMART; SM00406; IGV; 1_.
PROSITE; PS50835; IG LIKE; 1.
Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
FT REGION 1 23 Framework-1.
FT REGION 24 34 Complementarity-determining-1.
FT REGION 35 49 Framework-2.
FT REGION 50 56 Complementarity-determining-2.
FT REGION 57 88 Framework-3.
FT REGION 89 97 Complementarity-determining-3.
FT REGION 98 108 Framework-4.
FT DISULFID 23 88
FT NON_TER 108 108
FT STRAND 4 7
FT STRAND 10 13
FT TURN 15 16
FT STRAND 19 25
FT TURN 30 31
FT STRAND 33 38
FT TURN 40 41
FT STRAND 45 49
FT TURN 50 52
FT STRAND 53 54
FT TURN 56 57
FT TURN 60 61
FT STRAND 62 67
FT TURN 68 69
FT STRAND 70 75
FT HELIX 80 82
FT STRAND 84 90
FT STRAND 97 98
FT STRAND 102 106
SQ SEQUENCE 108 AA; 11910 MW; A554642C63EFF597 CRC64;
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CC removed.  
 CC -----  
 DR PDB; 1A14; X-ray; L=5-102.  
 DR SMR; P01645; 1-108.  
 DR Ensembl; ENSMUSG0000029991; Mus musculus.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003596; Ig\_v.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 KW 3D-structure; Direct protein sequencing; Immunoglobulin domain;  
 KW Immunoglobulin V region.  
 FT REGION 1 23 Framework-1.  
 FT REGION 24 34 Complementarity-determining-1.  
 FT REGION 35 49 Framework-2.  
 FT REGION 50 56 Complementarity-determining-2.  
 FT REGION 57 88 Complementarity-determining-3.  
 FT REGION 89 97 Complementarity-determining-4.  
 FT REGION 98 108 By similarity.  
 FT DISULFID 23 88  
 FT NON\_TER 108 108  
 SQ SEQUENCE 108 AA; 11954 MW; 22F4642C63EFPF58E CRC64;  
 Query Match 78.7%; Score 447; DB 1; Length 108;  
 Best Local Similarity 79.6%; Pred. No. 3.5e-39;  
 Matches 86; Conservative 10; Mismatches 12; Indels 0; Gaps 0;  
 QY 1 DIQMTQSPSSLSASVGRVITCSASQDISINLWYQOKPKAVKLLIFYSNLSHGVPVS 60  
 DB 1 DIQMTQTSSLSASLGDRVTISCRASQDISINLWYQOKPKDGTVKLLIYTSRLSHGVPVS 60  
 QY 61 RFGSGSGTDYTLTISSLPEDVATYFCHQYSKLPWTFGQGTKEIKR 108  
 DB 61 RFGSGSGTDYSLTISNLEQEDVATYFCQGNMLPRTFGGKLEIKR 108  
 RESULT 6  
 KVSM\_MOUSE  
 ID KVSM\_MOUSE STANDARD; PRT; 108 AA.  
 AC P01646;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 10-MAY-2005 (Rel. 47, Last annotation update)  
 DE Ig kappa chain V-V region HP 12356.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP PROTEIN SEQUENCE.  
 RC STRAIN=A/J;  
 RX MEDLINE=82150934; PubMed=6801658;  
 RA Siegelman M., Capra J.D.;  
 RT "Complete amino acid sequence of light chain variable regions derived from five monoclonal anti-p-azophenylarsenate antibodies differing with respect to a crossreactive idiotype.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).  
 CC -1- MISCELLANEOUS: Anti-arsenate hybridoma protein.  
 CC -----  
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 CC -----  
 CC HSSP; P01594; 1JVS.  
 DR Ensembl; ENSMUSG0000029991; Mus musculus.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003596; IGV.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 KW Direct protein sequencing; Immunoglobulin domain;  
 KW Immunoglobulin V region.  
 FT REGION 1 23 Framework-1.  
 FT REGION 24 34 Complementarity-determining-1.  
 FT REGION 35 49 Framework-2.  
 FT REGION 50 56 Complementarity-determining-2.  
 FT REGION 57 88 Complementarity-determining-3.  
 FT REGION 89 97 Complementarity-determining-4.  
 FT REGION 98 107

FT REGION 1 23 Framework-1.  
 FT REGION 24 34 Complementarity-determining-1.  
 FT REGION 35 49 Framework-2.  
 FT REGION 50 56 Complementarity-determining-2.  
 FT REGION 57 88 Complementarity-determining-3.  
 FT REGION 89 97 Complementarity-determining-4.  
 FT REGION 98 108 By similarity.  
 FT DISULFID 23 88  
 FT NON\_TER 108 108  
 SQ SEQUENCE 108 AA; 11989 MW; 4C98599C08EBA09A CRC64;  
 Query Match 78.7%; Score 447; DB 1; Length 108;  
 Best Local Similarity 80.6%; Pred. No. 3.5e-39;  
 Matches 87; Conservative 8; Mismatches 13; Indels 0; Gaps 0;  
 QY 1 DIQMTQSPSSLSASVGRVITCSASQDISINLWYQOKPKAVKLLIFYSNLSHGVPVS 60  
 DB 1 DIQMTQTSSLSASLGDRVTISCRASQDISINLWYQOKPKDGTVKLLIYTSRLSHGVPVS 60  
 QY 61 RFGSGSGTDYTLTISSLPEDVATYFCHQYSKLPWTFGQGTKEIKR 108  
 DB 61 RFGSGSGTDYSLTISNLEQEDVATYFCQGYMLPRTFGGKLEIKR 108  
 RESULT 7  
 KVLA\_HUMAN  
 ID KVLA\_HUMAN STANDARD; PRT; 108 AA.  
 AC P01593;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 10-MAY-2005 (Rel. 47, Last annotation update)  
 DE Ig kappa chain V-I region AG.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP PROTEIN SEQUENCE.  
 RX MEDLINE=69234734; PubMed=4893682;  
 RA Titani K., Shinoda T., Putnam F.W.;  
 RT "The amino acid sequence of a kappa type Bence-Jones protein. 3. The complete sequence and the location of the disulfide bridges.";  
 RL J. Biol. Chem. 244:3550-3560(1969).  
 CC -1- MISCELLANEOUS: The C region of this chain has the INV (3) marker.  
 CC -1- MISCELLANEOUS: This is a Bence-Jones protein.  
 CC -----  
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 CC -----  
 CC PIR; A01861; KIHUAG.  
 DR HSSP; P01607; 1BWW.  
 DR SMR; P01593; 1-108.  
 DR Ensembl; ENSG00000173782; Homo sapiens.  
 DR GO; GO:0005576; C:extracellular region; NAS.  
 DR GO; GO:0003823; F:antigen binding; NAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003596; IGV.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 KW Bence-Jones protein; Direct protein sequencing; Immunoglobulin domain;  
 KW Immunoglobulin V region.  
 FT REGION 1 23 Framework-1.  
 FT REGION 24 34 Complementarity-determining-1.  
 FT REGION 35 49 Framework-2.  
 FT REGION 50 56 Complementarity-determining-2.  
 FT REGION 57 88 Complementarity-determining-3.  
 FT REGION 89 97 Complementarity-determining-4.  
 FT REGION 98 107

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FT DISULFID 23 88
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11992 MW; E3B3B246C18FOC4F CRC64;

Query Match 78.3%; Score 445; DB 1; Length 108;
Best Local Similarity 78.7%; Pred. No. 5.6e-39;
Matches 85; Conservative 9; Mismatches 14; Indels 0; Gaps 0;

Qy 1 DIQWTSPPSSLSASVGDRTVITCSASQDISNYLNWYQKPKDPKAVKLLIFYSSNLSHGVS 60
Dy 1 DIQWTSPPSSLSASVGDRTVITCSASQDISNYLNWYQKPKPKAPKILYDASNLETGVS 60

Qy 61 RFSGSGSGTDYTLTISSQLPEDIATYFCHQYSKLPWTFGQGTKEIKR 108
Dy 61 RFSGSGSGTDYTLTISSQLPEDIATYFCHQYSKLPWTFGQGTKEIKR 108

RESULT 8
KV50 MOUSE STANDARD; PRT; 108 AA.
ID KV50 MOUSE STANDARD; PRT; 108 AA.
AC P01648;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-V region HP 91A3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP PROTEIN SEQUENCE.
RC STRAIN=A/J;
RX MEDLINE=82150934; PubMed=6801658;
RA Siegelman M., Capra J.D.;
RT "Complete amino acid sequence of light chain variable regions derived
RT from five monoclonal anti-p-azophenylarsenate antibodies differing
RT with respect to a crossreactive idiotype.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).
CC -I- MISCELLANEOUS: Anti-arsenate hybridoma protein.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC HSSP; P01594; 1JUV5.
CC SMR; P01648; 1-108.
CC Ensembl; ENSMUSG00000029991; Mus musculus.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003596; Ig_V.
CC SMART; SM00406; IG_V.
CC PROSITE; PS50835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
FT REGION 1 23
FT REGION 24 34
FT REGION 35 49
FT REGION 50 56
FT REGION 57 88
FT REGION 89 97
FT REGION 98 108
FT DISULFID 23 88
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11961 MW; D52EDA5E9A45291C CRC64;

Query Match 78.3%; Score 445; DB 1; Length 108;
Best Local Similarity 77.8%; Pred. No. 5.6e-39;
Matches 84; Conservative 13; Mismatches 11; Indels 0; Gaps 0;

Qy 1 DIQWTSPPSSLSASVGDRTVITCSASQDISNYLNWYQKPKDPKAVKLLIFYSSNLSHGVS 60
Dy 1 DIQWTSPPSSLSASVGDRTVITCSASQDISNYLNWYQKPKPKAPKILYDASNLETGVS 60
```

```
Db 1 DIQWTSPPSSLSASVGDRTVITCSASQDISNYLNWYQKPKDPKAVKLLIFYSSNLSHGVS 60
Qy 61 RFSGSGSGTDYTLTISSQLPEDIATYFCHQYSKLPWTFGQGTKEIKR 108
Dy 61 RFSGSGSGTDYTLTISSQLPEDIATYFCHQYSKLPWTFGQGTKEIKR 108

RESULT 9
Q9UL77_HUMAN PRELIMINARY; PRT; 108 AA.
ID Q9UL77_HUMAN PRELIMINARY; PRT; 108 AA.
AC Q9UL77;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=1516616;
RA Victor K.D., Pascual V., Williams C.L., Lennon V.A., Capra J.D.;
RT "Human monoclonal striational autoantibodies isolated from thymic B
RT lymphocytes of patients with myasthenia gravis use VH and VL gene
RT segments associated with the autoimmune repertoire.";
RL Eur. J. Immunol. 22:2231-2236(1992).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=8436174;
RA Wagner S.D., Luzzatto L.;
RT "V kappa gene segments rearranged in chronic lymphocytic leukemia are
RT distributed over a large portion of the V kappa locus and do not show
RT somatic mutation.";
RL Eur. J. Immunol. 23:391-397(1993).
DR EMBL; AF035037; AAD56273.1; -; mRNA.
DR PIR; B49047; B49047.
DR PIR; S34083; S34083.
DR HSSP; P01607; 1BWW.
DR SMR; Q9UL77; 1-108.
DR Ensembl; ENSG00000163245; Homo sapiens.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_V.
DR SMART; SM00406; IG_V.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON TER 1 108
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11738 MW; C06681716C4D16F3 CRC64;

Query Match 78.3%; Score 445; DB 2; Length 108;
Best Local Similarity 79.6%; Pred. No. 5.6e-39;
Matches 86; Conservative 7; Mismatches 15; Indels 0; Gaps 0;

Qy 1 DIQWTSPPSSLSASVGDRTVITCSASQDISNYLNWYQKPKDPKAVKLLIFYSSNLSHGVS 60
Dy 1 DIQWTSPPSSLSASVGDRTVITCSASQDISNYLNWYQKPKAPNLLIYAASSLSQSGVS 60

Qy 61 RFSGSGSGTDYTLTISSQLPEDIATYFCHQYSKLPWTFGQGTKEIKR 108
Dy 61 RFSGSGSGTDYTLTISSQLPEDIATYFCHQYSKLPWTFGQGTKEIKR 108

RESULT 10
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KV5N MOUSE  
ID KV5N\_MOUSE STANDARD; PRT; 108 AA.  
AC P01647;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 21-MAY-2005 (Rel. 47, Last annotation update)  
DE IG kappa chain V-V region HP 124E1.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP PROTEIN SEQUENCE.  
RC STRAIN=A/J;  
RX MEDLINE=82150934; PubMed=6801658;  
RA Siegelman M., Capra J.D.;  
RT "Complete amino acid sequence of light chain variable regions derived  
RT from five monoclonal anti-p-azophenylarsenate antibodies differing  
RT with respect to a crossreactive idiotype."  
RL Proc. Natl. Acad. Sci. U.S.A. 78:7673-7683(1981).  
CC -1- MISCELLANEOUS: Anti-arsenate hybridoma protein.  
CC  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.  
CC  
CC PDB; 1EZV; X-ray; Y=5-107.  
DR SMR; P01647; 1-108.  
DR Ensembl; ENSMUSG000002991; Mus musculus.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003596; IG\_V.  
DR SMART; SM00406; IG; 1.  
KW 3D-structure; Direct protein sequencing; Immunoglobulin domain;  
KW Immunoglobulin V region.  
FT REGION 1 23  
FT REGION 24 34  
FT REGION 35 49  
FT REGION 50 56  
FT REGION 57 88  
FT REGION 89 97  
FT REGION 98 108  
FT DISULFID 23 88  
FT NON TER 108 108  
SQ SEQUENCE 108 AA; 11965 MW; 39971BC653EFA2 CRC64;  
Query Match 78.0%; Score 443; DB 1; Length 108;  
Best Local Similarity 78.7%; Pred. No. 9.2e-39;  
Matches 85; Conservative 10; Mismatches 13; Indels 0; Gaps 0;  
Qy 1 DIQMTQSPSSLSASVGRVITTCASQDISINLYNWYQKPKAVKLLIFYSNLSHGVS 60  
Db 1 DIQMTQSPSSLSASVGRVITTCASQDISINLYNWYQKPKAVKLLIFYSNLSHGVS 60  
Qy 61 RFSGSGSGTDYTLTISSLPEDVATYFCHQSKLPWTFGQGTKEIKR 108  
Db 61 RFSGSGSGTDYTLTISSLPEDVATYFCHQSKLPWTFGQGTKEIKR 108  
RESULT 11  
Q6GMW1\_HUMAN PRELIMINARY; PRT; 236 AA.  
AC Q6GMW1;  
DT 05-JUL-2004 (TReMBLrel. 27, Created)  
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)  
DE IGKC protein.  
GN Name=IGKC;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Spleen;  
RX MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toehiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A.C., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences".  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Spleen;  
RG NIH MGC Project;  
RL Submitted (JUN-2004) to the EMBL/GenBank/DBDJ databases.  
DR EMBL; BC073791; AAH73791.1; -; mRNA.  
DR SMR; Q6GMW1; 24-236.  
DR Ensembl; ENSG00000163245; Homo sapiens.  
DR InterPro; IPR003599; IG.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003597; IG\_c1.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_V.  
DR Pfam; PF07654; C1-set; 1.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IGc1; 1.  
DR SMART; SM00406; IGv; 1.  
DR PROSITE; PS50835; IG\_LIKE; 2.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN 1.  
SQ SEQUENCE 236 AA; 25751 MW; 5BFE6A087AFAC437 CRC64;  
Query Match 77.3%; Score 439; DB 2; Length 236;  
Best Local Similarity 81.3%; Pred. No. 6.3e-38;  
Matches 87; Conservative 5; Mismatches 15; Indels 0; Gaps 0;  
Qy 2 IQMTQSPSSLSASVGRVITTCASQDISINLYNWYQKPKAVKLLIFYSNLSHGVS 61  
Db 24 IQMTQSPSSLSASVGRVITTCASQDISINLYNWYQKPKAVKLLIFYSNLSHGVS 83  
Qy 62 FSGSGSGTDYTLTISSLPEDVATYFCHQSKLPWTFGQGTKEIKR 108  
Db 84 FSGSGSGTDYTLTISSLPEDVATYFCHQSKLPWTFGQGTKEIKR 130  
RESULT 12  
KVLP\_HUMAN STANDARD; PRT; 108 AA.  
ID KVLP\_HUMAN  
AC P01608;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 10-MAY-2005 (Rel. 47, Last annotation update)  
DE IG kappa chain V-I region Roy.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.

OX NCBI\_TaxID=9606;  
 RN [1]  
 RP PROTEIN SEQUENCE.  
 RX MEDLINE=68362076; PubMed=5595110;  
 RA Hilsechmann N.;  
 RT "Chemical structure of 2 kappa-type Bence Jones proteins (Roy and Cum.)";  
 RL Hoppe-Seyler's Z. Physiol. Chem. 348:1077-1080(1967).  
 RN [2]  
 RP SEQUENCE REVISION TO 39 AND 41.  
 RA Hilsechmann N., Barnikol H.U., Hess M., Langer B., Ponstingl H., Steinmetz-Kayne M., Suter L., Watanabe S.;  
 RL (In) Franek F., Shugar D. (eds.);  
 RL Gamma globulins: structure and function, pp.57-74, Academic Press, New York (1969).  
 CC -1- MISCELLANEOUS: The C region of this chain has the INV (1,2) marker.  
 CC  
 CC -1- MISCELLANEOUS: This is a Bence-Jones protein.  
 CC  
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 CC  
 CC PIR; A91638; KIHURY.  
 DR HSP; P01607; IBWW.  
 DR SMR; P01608; 1-108.  
 DR Ensembl; ENSG00000173782; Homo sapiens.  
 DR GO; GO:0005576; C:extracellular region; NAS.  
 DR GO; GO:0003823; F:antigen binding; NAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003596; Ig\_v.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG LIKE; 1.  
 DR Bence-Jones protein; Direct protein sequencing; Immunoglobulin domain;  
 KW Immunoglobulin V region.  
 FT REGION 1 23  
 FT REGION 24 34  
 FT REGION 35 49  
 FT REGION 50 56  
 FT REGION 57 88  
 FT REGION 89 97  
 FT REGION 98 107  
 FT DISULFID 23 88  
 FT CONFLICT 30 31  
 FT NON TER 108 108  
 SQ SEQUENCE 108 AA; 11782 MW; F5ACEDE5A313DF3A CRC64;

Query Match 77.1%; Score 438; DB 1; Length 108;  
 Best Local Similarity 78.7%; Pred. No. 3.1e-38;  
 Matches 85; Conservative 8; Mismatches 15; Indels 0; Gaps 0;  
 Oy 1 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQOKPKDKAVKLLIFYSNLSHGVPVS 60  
 Db 1 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQOKPKDKAPKLLIYDASKLEAGVPVS 60  
 Oy 61 RFSGGSGSDTYLTLSISLPEDIAFYCHQYKLPWTFGQGTQKVEIKR 108  
 Db 61 RFSGTGSGSDTYLTLSISLPEDIAFYCHQYKLPWTFGQGTQKVEIKR 108

## RESULT 13

KV1Y HUMAN  
 ID KV1Y HUMAN STANDARD; PRT; 108 AA.  
 AC P80362;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 10-MAY-2005 (Rel. 47, Last annotation update)  
 DE IG kappa chain V-1 region WAT.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;

OC Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP PROTEIN SEQUENCE, AND X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).  
 RX MEDLINE=95086080; PubMed=7993911;  
 RA Huang D.-B., Chang C.-H., Ainsworth C., Bruenger A.T., Eulitz M., Solomon A., Stevens F.J., Schiffer M.;  
 RT "Comparison of crystal structures of two homologous proteins: structural origin of altered domain interactions in immunoglobulin light-chain dimers";  
 RL Biochemistry 33:14848-14857(1994).  
 RN [2]  
 RP PROTEIN SEQUENCE OF 1-35.  
 RX MEDLINE=81267384; PubMed=6167731;  
 RA Stevens F.J., Westholm F.A., Panagiotopoulos N., Schiffer M., Popp R.A., Solomon A.;  
 RT "Characterization and preliminary crystallographic data on the VL-related fragment of the human kappa Bence Jones protein Wat.";  
 RL J. Mol. Biol. 147:185-193(1981).  
 CC -1- MISCELLANEOUS: This is a Bence-Jones protein.  
 CC  
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 CC  
 CC PDB; 1WTL; X-ray; A/B=1-108.  
 DR GO; GO:0005576; C:extracellular region; NAS.  
 DR GO; GO:0003823; F:antigen binding; NAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003596; Ig\_v.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG LIKE; 1.  
 DR 3D-structure; Bence-Jones protein; Direct protein sequencing; Immunoglobulin V region.  
 KW Immunoglobulin domain; Immunoglobulin V region.  
 FT REGION 1 23  
 FT REGION 24 34  
 FT REGION 35 49  
 FT REGION 50 56  
 FT REGION 57 88  
 FT REGION 89 97  
 FT REGION 98 107  
 FT DISULFID 23 88  
 FT CONFLICT 30 31  
 FT NON TER 108 108  
 FT STRAND 4 7  
 FT STRAND 10 13  
 FT TURN 15 16  
 FT STRAND 19 25  
 FT TURN 30 31  
 FT STRAND 33 38  
 FT TURN 40 41  
 FT STRAND 45 49  
 FT TURN 53 54  
 FT STRAND 56 57  
 FT TURN 60 61  
 FT STRAND 62 67  
 FT TURN 68 69  
 FT STRAND 70 75  
 FT HELIX 80 82  
 FT STRAND 84 90  
 FT STRAND 98 98  
 FT STRAND 102 106  
 SQ SEQUENCE 108 AA; 11737 MW; D9D941B3F0FAE697 CRC64;  
 Query Match 76.8%; Score 436; DB 1; Length 108;  
 Best Local Similarity 76.9%; Pred. No. 5e-38;  
 Matches 83; Conservative 12; Mismatches 13; Indels 0; Gaps 0;

Oy 1 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQOKPKDKAVKLLIFYSNLSHGVPVS 60



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Db 1 DIQWTSFSSLSASVGDRTVITCRASQDITVYVWFQRPQAPKVLIGASILETGVP 60
Qy 61 RFSGSGSGTDYTLTISSLOPEDIAFYCHQYSKLPWTFGQGTQKVEIKR 108
Db 61 RFSGSGSGTDFTFTISSLQPEDIAFYCCQYDTLPLTFEGGKTKVDIKR 108

RESULT 14
ID Q9UL70 HUMAN PRELIMINARY; PRT; 108 AA.
AC Q9UL70;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DI 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN NUCLEOTIDE SEQUENCE.
RP MEDLINE=98375893; PubMed=9712075;
RA Adderson E.E., Shikhan A.R., Ward K.E., Cunningham M.W.;
RT "Molecular analysis of polyreactive monoclonal antibodies from
RT rheumatic carditis: human anti-N-acetylglucosamine/anti-myoisin
RT antibody V region genes.";
RL J. Immunol. 161:2020-2031(1998).
RN NUCLEOTIDE SEQUENCE.
RP PubMed=1516616;
RX Victor K.D., Pascual V., Williams C.L., Lennon V.A., Capra J.D.;
RA "Human monoclonal striational autoantibodies isolated from thymic B
RA lymphocytes of patient with myasthenia gravis use VH and VL gene
RA segments associated with the autoimmune repertoire.";
RL Eur. J. Immunol. 22:2231-2236(1992).
RN NUCLEOTIDE SEQUENCE.
RP PubMed=8436174;
RX Wagner S.D., Luzzatto L.;
RA "V kappa gene segments rearranged in chronic lymphocytic leukemia are
RA distributed over a large portion of the V kappa locus and do not show
RT somatic mutation.";
RL Eur. J. Immunol. 23:391-397(1993).
RN NUCLEOTIDE SEQUENCE.
RP PubMed=1660528;
RX Manheimer-Lory A., Katz J.B., Pillinger M., Grossein C., Smith A.,
RA Diamond B.;
RA "Molecular characteristics of antibodies bearing an anti-DNA-
RT associated idiotype.";
RL J. Exp. Med. 174:1639-1652(1991).
RN NUCLEOTIDE SEQUENCE.
RP PubMed=1903706;
RX Blaisson G., Kuntz J.L., Pasquali J.L.;
RA "Molecular analysis of V kappa III variable regions of polyclonal
RT rheumatoid factors during rheumatoid arthritis.";
RL Eur. J. Immunol. 21:1221-1227(1991).
DR EMBL; U96396; AAB68785.1; -; mRNA.
DR PIR; B49047; B49047.
DR PIR; PH0867; PH0867.
DR PIR; S16840; S16840.
DR PIR; S31977; S31977.
DR PIR; S34083; S34083.
DR PIR; S34086; S34086.
DR HSSP; P01607; IBMW.
DR SKR; Q96SA9; 1-107.
DR InterPro; IPR007110; Ig-like.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG-LIKE; 1.
FT NON TER 1
FT NON TER 107
SQ SEQUENCE 107 AA; 11520 MW; 4BB43E9C5B577F16 CRC64;

Query Match 76.4%; Score 434; DB 2; Length 108;
Best Local Similarity 77.8%; Pred. No. 8.2e-38;
Matches 84; Conservative 8; Mismatches 16; Indels 0; Gaps 0;

Qy 1 DIQWTSFSSLSASVGDRTVITCRASQDITVYVWFQRPQAPKVLIGASILETGVP 60
Db 1 DIQWTSFSSLSASVGDRTVITCRASQDITVYVWFQRPQAPKVLIGASILETGVP 60

Qy 61 RFSGSGSGTDYTLTISSLOPEDIAFYCHQYSKLPWTFGQGTQKVEIKR 108
Db 61 RFSGSGSGTDFTFTISSLQPEDIAFYCCQYDTLPLTFEGGKTKVDIKR 108

RESULT 15
ID Q96SA9 HUMAN PRELIMINARY; PRT; 107 AA.
AC Q96SA9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DI 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Anti-streptococcal/anti-myoisin immunoglobulin kappa light chain
DE variable region (Fragment).
OS Homo sapiens (Human).

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```

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN NUCLEOTIDE SEQUENCE.
RP MEDLINE=98375893; PubMed=9712075;
RA Adderson E.E., Shikhan A.R., Ward K.E., Cunningham M.W.;
RT "Molecular analysis of polyreactive monoclonal antibodies from
RT rheumatic carditis: human anti-N-acetylglucosamine/anti-myoisin
RT antibody V region genes.";
RL J. Immunol. 161:2020-2031(1998).
RN NUCLEOTIDE SEQUENCE.
RP PubMed=1516616;
RX Victor K.D., Pascual V., Williams C.L., Lennon V.A., Capra J.D.;
RA "Human monoclonal striational autoantibodies isolated from thymic B
RA lymphocytes of patient with myasthenia gravis use VH and VL gene
RA segments associated with the autoimmune repertoire.";
RL Eur. J. Immunol. 22:2231-2236(1992).
RN NUCLEOTIDE SEQUENCE.
RP PubMed=8436174;
RX Wagner S.D., Luzzatto L.;
RA "V kappa gene segments rearranged in chronic lymphocytic leukemia are
RA distributed over a large portion of the V kappa locus and do not show
RT somatic mutation.";
RL Eur. J. Immunol. 23:391-397(1993).
RN NUCLEOTIDE SEQUENCE.
RP PubMed=1660528;
RX Manheimer-Lory A., Katz J.B., Pillinger M., Grossein C., Smith A.,
RA Diamond B.;
RA "Molecular characteristics of antibodies bearing an anti-DNA-
RT associated idiotype.";
RL J. Exp. Med. 174:1639-1652(1991).
RN NUCLEOTIDE SEQUENCE.
RP PubMed=1903706;
RX Blaisson G., Kuntz J.L., Pasquali J.L.;
RA "Molecular analysis of V kappa III variable regions of polyclonal
RT rheumatoid factors during rheumatoid arthritis.";
RL Eur. J. Immunol. 21:1221-1227(1991).
DR EMBL; U96396; AAB68785.1; -; mRNA.
DR PIR; B49047; B49047.
DR PIR; PH0867; PH0867.
DR PIR; S16840; S16840.
DR PIR; S31977; S31977.
DR PIR; S34083; S34083.
DR PIR; S34086; S34086.
DR HSSP; P01607; IBMW.
DR SKR; Q96SA9; 1-107.
DR InterPro; IPR007110; Ig-like.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG-LIKE; 1.
FT NON TER 1
FT NON TER 107
SQ SEQUENCE 107 AA; 11520 MW; 4BB43E9C5B577F16 CRC64;

Query Match 76.3%; Score 433.5; DB 2; Length 107;
Best Local Similarity 81.7%; Pred. No. 9.1e-38;
Matches 89; Conservative 6; Mismatches 11; Indels 3; Gaps 2;

Qy 1 DIQWTSFSSLSASVGDRTVITCRASQDITVYVWFQRPQAPKVLIGASILETGVP 60
Db 1 DIQWTSFSSLSASVGDRTVITCRASQDITVYVWFQRPQAPKVLIGASILETGVP 60

Qy 61 RFSGSGSGTDYTLTISSLOPEDIAFYCHQYSKLPWTFGQGTQKVEIKR 108
Db 61 RFSGSGSGTDFTFTISSLQPEDIAFYCCQYDTLPLTFEGGKTKVDIKR 107

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Search completed: April 6, 2006, 08:53:36  
Job time : 33.4482 secs

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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 6, 2006, 08:50:25 ; Search time 6.7132 Seconds  
(without alignments)  
1330.063 Million cell updates/sec

Title: US-10-089-500-54  
Perfect score: 568  
Sequence: 1 DIQWTQSPSSLSASVGDVRT.....HQYSKLPTWFGQTKVEIKR 108

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA.\*  
1: /cgn2\_6/ptodata/1/iaa/5 COMB.pep.\*  
2: /cgn2\_6/ptodata/1/iaa/6 COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/H COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/PCTUS COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/RE COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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1	514	90.5	128	2	US-09-225-322B-10
2	514	90.5	128	2	US-09-225-322B-19
3	514	90.5	128	2	US-09-764-304-10
4	514	90.5	128	2	US-09-764-304-19
5	507	89.3	110	2	US-08-908-469-103
6	507	89.3	237	2	US-08-908-469-100
7	507	89.3	491	2	US-10-011-125A-2
8	505	88.9	107	2	US-08-908-469-15
9	504	88.7	110	2	US-08-908-469-105
10	503	88.6	108	2	US-08-908-469-8
11	503	88.6	110	2	US-09-440-781-94
12	501	88.2	107	2	US-08-908-469-13
13	500	88.0	110	2	US-08-908-469-107
14	500	88.0	110	2	US-08-908-469-117
15	497	87.5	108	2	US-08-908-469-126
16	491	86.4	108	2	US-09-065-059-3
17	491	86.4	108	2	US-08-913-555-3
18	487	85.7	127	2	US-08-649-100-33
19	484	85.2	108	2	US-09-905-243-73
20	484	85.2	214	1	US-08-458-516-12
21	481	84.7	110	2	US-09-440-781-95
22	481	84.7	110	2	US-08-908-469-109
23	481	84.7	110	2	US-08-908-469-111
24	481	84.7	110	2	US-08-908-469-113
25	481	84.7	110	2	US-08-908-469-115
26	480	84.5	107	1	US-07-934-373C-17
27	480	84.5	107	1	US-08-652-558-2

28 480 84.5 107 2 US-08-437-642B-17 Sequence 17, Appl  
29 480 84.5 107 2 US-08-146-206C-17 Sequence 17, Appl  
30 480 84.5 107 2 US-09-705-686-17 Sequence 17, Appl  
31 480 84.5 107 2 US-09-705-392A-17 Sequence 17, Appl  
32 480 84.5 107 2 US-09-705-398-17 Sequence 17, Appl  
33 480 84.5 107 4 PCT-US93-07832-17 Sequence 17, Appl  
34 480 84.5 108 2 US-08-913-555-21 Sequence 21, Appl  
35 480 84.5 109 1 US-07-934-373C-47 Sequence 47, Appl  
36 480 84.5 109 2 US-08-437-642B-47 Sequence 47, Appl  
37 480 84.5 214 1 US-07-934-373C-40 Sequence 40, Appl  
38 480 84.5 214 1 US-08-788-800-11 Sequence 11, Appl  
39 480 84.5 214 2 US-08-437-642B-40 Sequence 40, Appl  
40 480 84.5 214 2 US-09-097-309-2 Sequence 2, Appl  
41 480 84.5 214 2 US-03-097-171A-2 Sequence 2, Appl  
42 480 84.5 214 2 US-09-460-587-2 Sequence 2, Appl  
43 480 84.5 214 2 US-09-940-166A-2 Sequence 2, Appl  
44 480 84.5 214 4 PCT-US93-07832-40 Sequence 40, Appl  
45 480 84.5 233 1 US-07-934-373C-25 Sequence 25, Appl

#### ALIGNMENTS

RESULT 1  
US-09-225-322B-10  
; Sequence 10, Application US/09225322B  
; Patent No. 6437098  
; GENERAL INFORMATION:  
; APPLICANT: SHITARA, KENYA  
; APPLICANT: HANAI, NORUO  
; APPLICANT: HASEGAWA, MAMORU  
; APPLICANT: MIYAJI, HIROMASA  
; APPLICANT: KUWANA, YOSHITISA  
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY  
; FILE REFERENCE: 249-101  
; CURRENT APPLICATION NUMBER: US/09/225,322B  
; CURRENT FILING DATE: 1999-01-05  
; PRIOR APPLICATION NUMBER: US 08/454,680  
; PRIOR FILING DATE: 1995-05-31  
; PRIOR APPLICATION NUMBER: US 08/408,133  
; PRIOR FILING DATE: 1995-03-21  
; PRIOR APPLICATION NUMBER: US 08/292,178  
; PRIOR FILING DATE: 1994-08-17  
; PRIOR APPLICATION NUMBER: US07/947,674  
; PRIOR FILING DATE: 1992-09-17  
; PRIOR APPLICATION NUMBER: JP 3-238375  
; PRIOR FILING DATE: 1991-09-18  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 10  
; LENGTH: 128  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: cDNA KM-641  
US-09-225-322B-10

Query Match 90.5%; Score 514; DB 2; Length 128;  
Best Local Similarity 88.9%; Pred. No. 1.6e-43;  
Matches 96; Conservative 7; Mismatches 5; Indels 0; Gaps 0;  
QY 1 DIQWTQSPSSLSASVGDVRTTCSASQDISNLWYQKPKAVKLLIFYSSNLHSGVPS 60  
Db 21 DIQWTQTASSLPASIGDRVTITCSASQDISNLWYQKPKDGTVKLLIFYSSNLHSGVPS 80  
QY 61 RFSGGSGTDTLTSSLOPEDATYFCHQYSKLPTWFGQTKVEIKR 108  
Db 81 RFSGGSGTDTLTSSLOPEDATYFCHQYSKLPTWFGGTTKLEIKR 128

RESULT 2  
US-09-225-322B-19  
; Sequence 19, Application US/09225322B



```
; Sequence 103, Application US/08908469
; Patent No. 6884879
; GENERAL INFORMATION:
; APPLICANT: Baca, Manuel
;           Wells, James A.
;           Presta, Leonard G.
;           Lowman, Henry B.
;           Chen, Yvonne M.
; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
; NUMBER OF SEQUENCES: 131
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/908,469
; FILING DATE: 21-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/833,504
; FILING DATE: 07-APR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Cui, Steven X.
; REGISTRATION NUMBER: 44,637
; REFERENCE/DOCKET NUMBER: P1093P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-8674
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 103:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 110 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 103:
US-08-908-469-103

Query Match      89.3%; Score 507; DB 2; Length 110;
Best Local Similarity 88.0%; Pred. No. 6.5e-43;
Matches 95; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

Qy      1 DIQQTSPSSLSASVGRVITCSASQDISNLYNWYQKPKAVKLLIFYSSNLHSGVPS 60
Db      1 DIQQTSPSSLSASVGRVITCSASQDISNLYNWYQKPKAVKLLIFYSSNLHSGVPS 60

Qy      61 RFGSGSGTDYTLTISSLQPEDIAFYCHQYSKLPWTFTGGTKVEIKR 108
Db      61 RFGSGSGTDYTLTISSLQPEDIAFYCHQYSKLPWTFTGGTKVEIKR 108

RESULT 6
US-08-908-469-100
; Sequence 100, Application US/08908469
; Patent No. 6884879
; GENERAL INFORMATION:
; APPLICANT: Baca, Manuel
;           Wells, James A.
;           Presta, Leonard G.
;           Lowman, Henry B.
;           Chen, Yvonne M.
; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
; NUMBER OF SEQUENCES: 131
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/908,469
; FILING DATE: 21-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/833,504
; FILING DATE: 07-APR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Cui, Steven X.
; REGISTRATION NUMBER: 44,637
; REFERENCE/DOCKET NUMBER: P1093P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-8674
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 103:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 110 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 103:
US-08-908-469-103

Query Match      89.3%; Score 507; DB 2; Length 110;
Best Local Similarity 88.0%; Pred. No. 6.5e-43;
Matches 95; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

Qy      1 DIQQTSPSSLSASVGRVITCSASQDISNLYNWYQKPKAVKLLIFYSSNLHSGVPS 60
Db      1 DIQQTSPSSLSASVGRVITCSASQDISNLYNWYQKPKAVKLLIFYSSNLHSGVPS 60

Qy      61 RFGSGSGTDYTLTISSLQPEDIAFYCHQYSKLPWTFTGGTKVEIKR 108
Db      61 RFGSGSGTDYTLTISSLQPEDIAFYCHQYSKLPWTFTGGTKVEIKR 108

RESULT 7
US-10-011-125A-2
; Sequence 2, Application US/10011125A
; Patent No. 6828121
; GENERAL INFORMATION:
; APPLICANT: Chen, Christina Yu-Ching
; TITLE OF INVENTION: BACTERIAL HOST STRAINS
; FILE REFERENCE: P1804R1
; CURRENT APPLICATION NUMBER: US/10/011.125A
; CURRENT FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: US 60/256,162
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 12
; SEQ ID NO 2
; LENGTH: 491
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized.
; Patent No. 6828121
US-10-011-125A-2

Query Match      89.3%; Score 507; DB 2; Length 491;
Best Local Similarity 88.0%; Pred. No. 3.5e-42;
Matches 95; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

Qy      1 DIQQTSPSSLSASVGRVITCSASQDISNLYNWYQKPKAVKLLIFYSSNLHSGVPS 60
Db      24 DIQQTSPSSLSASVGRVITCSASQDISNLYNWYQKPKAVKLLIFYSSNLHSGVPS 83

Qy      61 RFGSGSGTDYTLTISSLQPEDIAFYCHQYSKLPWTFTGGTKVEIKR 108
Db      84 RFGSGSGTDYTLTISSLQPEDIAFYCHQYSKLPWTFTGGTKVEIKR 131
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Qy 61 RFSGSGGTDYTLTSSLPEDIATYFCHOYSKLPWTFGGTKVEIKR 108  
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Db 84 RFSGSGGTDYTLTSSLPEDFATYYCQYSTVPWTFGGTKVEIKR 131  
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## RESULT 8

US-08-908-469-15  
; Sequence 15, Application US/08908469  
; Patent No. 6884879  
; GENERAL INFORMATION:

APPLICANT: Baca, Manuel  
; Wells, James A.  
; Presta, Leonard G.  
; Lowman, Henry B.  
; Chen, Yvonne M.

TITLE OF INVENTION: ANTI-VEGF ANTIBODIES

NUMBER OF SEQUENCES: 131

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/908,469

FILING DATE: 21-May-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/833,504

FILING DATE: 07-APR-1997

ATTORNEY/AGENT INFORMATION:

NAME: Cui, Steven X.

REGISTRATION NUMBER: 44,637

REFERENCE/DOCKET NUMBER: P1093P1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-8674

TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 15:

SEQUENCE CHARACTERISTICS:

LENGTH: 107 amino acids

TYPE: Amino Acid

TOPOLOGY: Linear

SEQUENCE DESCRIPTION: SEQ ID NO: 15:

US-08-908-469-15

Query Match 88.9%; Score 505; DB 2; Length 107;  
Best Local Similarity 88.8%; Pred. No. 9.9e-43;  
Matches 95; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNLYLNWYQKPKDKAVKLLIFYSNLSHSGVPS 60

Db 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNLYLNWYQKPKDKAVKLLIFYSNLSHSGVPS 60

|||||

Qy 61 RFSGSGGTDYTLTSSLPEDIATYFCHOYSKLPWTFGGTKVEIK 107

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Db 61 RFSGSGGTDYTLTSSLPEDFATYYCQYSTVPWTFGGTKVEIK 107

|||||

## RESULT 9

US-08-908-469-105

; Sequence 105, Application US/08908469

; Patent No. 6884879

; GENERAL INFORMATION:

APPLICANT: Baca, Manuel

; Wells, James A.

; Presta, Leonard G.

; Lowman, Henry B.

; Chen, Yvonne M.  
; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES  
; NUMBER OF SEQUENCES: 131  
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/908,469

FILING DATE: 21-May-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/833,504

FILING DATE: 07-APR-1997

ATTORNEY/AGENT INFORMATION:

NAME: Cui, Steven X.

REGISTRATION NUMBER: 44,637

REFERENCE/DOCKET NUMBER: P1093P1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-8674

TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 105:

SEQUENCE CHARACTERISTICS:

LENGTH: 110 amino acids

TYPE: Amino Acid

TOPOLOGY: Linear

SEQUENCE DESCRIPTION: SEQ ID NO: 105:

US-08-908-469-105

Query Match 88.7%; Score 504; DB 2; Length 110;  
Best Local Similarity 87.0%; Pred. No. 1.3e-42;  
Matches 94; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNLYLNWYQKPKDKAVKLLIFYSNLSHSGVPS 60

Db 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNLYLNWYQKPKDKAVKLLIFYSNLSHSGVPS 60

|||||

Qy 61 RFSGSGGTDYTLTSSLPEDIATYFCHOYSKLPWTFGGTKVEIKR 108

|||||

Db 61 RFSGSGGTDYTLTSSLPEDFATYYCQYSTVPWTFGGTKVEIKR 108

|||||

## RESULT 10

US-08-908-469-8

; Sequence 8, Application US/08908469

; Patent No. 6884879

; GENERAL INFORMATION:

APPLICANT: Baca, Manuel

; Wells, James A.

; Presta, Leonard G.

; Lowman, Henry B.

; Chen, Yvonne M.

TITLE OF INVENTION: ANTI-VEGF ANTIBODIES

NUMBER OF SEQUENCES: 131

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

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; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA: US/08/908,469
; APPLICATION NUMBER: US/08/908,469
; FILING DATE: 21-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/833,504
; FILING DATE: 07-APR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Cui, Steven X.
; REGISTRATION NUMBER: 44,637
; REFERENCE/DOCKET NUMBER: P1093P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-8674
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-08-908-469-8
Query Match 88.6%; Score 503; DB 2; Length 108;
Best Local Similarity 87.0%; Pred. No. 1.6e-42;
Matches 94; Conservative 8; Mismatches 6; Indels 0; Gaps 0;
QY 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNWYQKPKAVKLLIFYSNLSHGVP 60
DB 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNWYQKPKAVKLLIFYSNLSHGVP 60
QY 61 RFSGSGSGTDYTLTISSLPEDIAFYFCHQYSKLPWTFGQGTKEIKR 108
DB 61 RFSGSGSGTDYTLTISSLPEDIAFYFCHQYSKLPWTFGQGTKEIKR 108
RESULT 11
US-09-440-781-94
; Sequence 94, Application US/09440781
; Patent No. 6632926
; GENERAL INFORMATION:
; APPLICANT: Yvonne Man-vee Chen et al.
; TITLE OF INVENTION: ANTIBODY VARIANTS
; FILE REFERENCE: P1469R1
; CURRENT APPLICATION NUMBER: US/09/440,781
; CURRENT FILING DATE: 1999-11-16
; NUMBER OF SEQ ID NOS: 99
; SEQ ID NO 94
; LENGTH: 110
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: artificial
; LOCATION: 1-110
; OTHER INFORMATION: humanized antibody light chain variable domain
US-09-440-781-94
Query Match 88.6%; Score 503; DB 2; Length 110;
Best Local Similarity 87.0%; Pred. No. 1.6e-42;
Matches 94; Conservative 8; Mismatches 6; Indels 0; Gaps 0;
QY 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNWYQKPKAVKLLIFYSNLSHGVP 60
DB 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNWYQKPKAVKLLIFYSNLSHGVP 60
QY 61 RFSGSGSGTDYTLTISSLPEDIAFYFCHQYSKLPWTFGQGTKEIKR 108
DB 61 RFSGSGSGTDYTLTISSLPEDIAFYFCHQYSKLPWTFGQGTKEIKR 108
RESULT 12
US-08-908-469-13
; Sequence 13, Application US/08908469
; Patent No. 6884879
; GENERAL INFORMATION:
; APPLICANT: Baca, Manuel
; Wells, James A.
; Presta, Leonard G.
; Lowman, Henry B.
; Chen, Yvonne M.
; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
; NUMBER OF SEQUENCES: 131
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/908,469
; FILING DATE: 21-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/833,504
; FILING DATE: 07-APR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Cui, Steven X.
; REGISTRATION NUMBER: 44,637
; REFERENCE/DOCKET NUMBER: P1093P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-8674
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-08-908-469-13
Query Match 88.2%; Score 501; DB 2; Length 107;
Best Local Similarity 87.9%; Pred. No. 2.5e-42;
Matches 94; Conservative 7; Mismatches 6; Indels 0; Gaps 0;
QY 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNWYQKPKAVKLLIFYSNLSHGVP 60
DB 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNWYQKPKAVKLLIFYSNLSHGVP 60
QY 61 RFSGSGSGTDYTLTISSLPEDIAFYFCHQYSKLPWTFGQGTKEIK 107
DB 61 RFSGSGSGTDYTLTISSLPEDIAFYFCHQYSKLPWTFGQGTKEIK 107
RESULT 13
US-08-908-469-107
; Sequence 107, Application US/08908469
; Patent No. 6884879
; GENERAL INFORMATION:
; APPLICANT: Baca, Manuel
; Wells, James A.
; Presta, Leonard G.
; Lowman, Henry B.
; Chen, Yvonne M.
; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
; NUMBER OF SEQUENCES: 131
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
```







**THIS PAGE BLANK (USPRO)**

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: April 6, 2006, 08:53:30 ; Search time 19.3152 Seconds  
(without alignment)  
2336.277 Million cell updates/sec

Title: US-10-089-500-54  
Perfect score: 568  
Sequence: 1 DIQMTQSPSSLSASVGRVT.....HQYSKLPWTFGQTKVEIKR 108

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA Main:  
1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*  
2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*  
4: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*  
6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	514	90.5	128	3	US-09-764-304-10
2	514	90.5	128	3	US-09-764-304-19
3	514	90.5	128	4	US-10-265-713-10
4	514	90.5	128	4	US-10-265-713-19
5	514	90.5	128	4	US-10-166-626-10
6	514	90.5	128	4	US-10-166-626-19
7	507	89.3	110	3	US-09-056-160B-103
8	507	89.3	110	4	US-10-234-671-101
9	507	89.3	110	5	US-10-974-591-101
10	507	89.3	237	3	US-09-056-160B-100
11	507	89.3	237	4	US-10-234-671-100
12	507	89.3	237	5	US-10-974-591-100
13	507	89.3	491	4	US-10-011-125-2
14	505	88.9	107	3	US-09-056-160B-15
15	505	88.9	107	4	US-10-234-671-15
16	505	88.9	107	5	US-10-974-591-15
17	504	88.7	110	3	US-09-056-160B-105
18	504	88.7	110	4	US-10-234-671-103
19	504	88.7	110	5	US-10-974-591-103
20	503	88.6	108	3	US-09-056-160B-8
21	503	88.6	108	4	US-10-153-159-2
22	503	88.6	108	4	US-10-153-159-16
23	503	88.6	108	4	US-10-153-176-2
24	503	88.6	108	4	US-10-153-176-16
25	503	88.6	108	4	US-10-443-134A-2
26	503	88.6	108	4	US-10-443-134A-16
27	503	88.6	108	4	US-10-443-134A-127

28	503	88.6	108	5	US-10-877-532-7	Sequence 7, Appli
29	503	88.6	110	4	US-10-234-671-8	Sequence 8, Appli
30	503	88.6	110	4	US-10-624-153-94	Sequence 94, Appli
31	503	88.6	110	5	US-10-683-043-1	Sequence 1, Appli
32	503	88.6	110	5	US-10-974-591-8	Sequence 8, Appli
33	503	88.6	667	5	US-10-764-428-25	Sequence 25, Appli
34	503	88.2	107	3	US-09-056-160B-13	Sequence 13, Appli
35	501	88.2	107	4	US-10-234-671-13	Sequence 13, Appli
36	501	88.2	107	5	US-10-974-591-13	Sequence 13, Appli
37	500	88.0	108	4	US-10-153-159-4	Sequence 4, Appli
38	500	88.0	108	4	US-10-153-176-4	Sequence 4, Appli
39	500	88.0	108	4	US-10-443-134A-4	Sequence 4, Appli
40	500	88.0	110	3	US-09-056-160B-107	Sequence 107, App
41	500	88.0	110	3	US-09-056-160B-117	Sequence 117, App
42	500	88.0	110	4	US-10-234-671-105	Sequence 105, App
43	500	88.0	110	4	US-10-234-671-115	Sequence 115, App
44	500	88.0	110	5	US-10-683-043-5	Sequence 5, Appli
45	500	88.0	110	5	US-10-974-591-105	Sequence 105, App

ALIGNMENTS

RESULT 1

US-09-764-304-10  
; Sequence 10, Application US/09764304  
; Patent No. US20020026036A1  
; GENERAL INFORMATION:  
; APPLICANT: SHITARA, KENYA  
; APPLICANT: HANAI, NOBUO  
; APPLICANT: HASEGAWA, MAMORU  
; APPLICANT: MIYAJI, HIROMASA  
; APPLICANT: KOWANA, YOSHIIISA  
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY  
; FILE REFERENCE: 249-101  
; CURRENT APPLICATION NUMBER: US/09/764.304  
; CURRENT FILING DATE: 2001-01-19  
; EARLIER APPLICATION NUMBER: 09/225,322  
; EARLIER FILING DATE: 1999-01-05  
; EARLIER APPLICATION NUMBER: US 08/454,680  
; EARLIER FILING DATE: 1995-05-31  
; EARLIER APPLICATION NUMBER: US 08/408,133  
; EARLIER FILING DATE: 1995-03-21  
; EARLIER APPLICATION NUMBER: US 08/292,178  
; EARLIER FILING DATE: 1994-08-17  
; EARLIER APPLICATION NUMBER: US07/947,674  
; EARLIER FILING DATE: 1992-09-17  
; EARLIER APPLICATION NUMBER: JP 3-238375  
; EARLIER FILING DATE: 1991-09-18  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 10  
; LENGTH: 128  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURES:  
; OTHER INFORMATION: cDNA KM-641  
US-09-764-304-10

Query Match 90.5%; Score 514; DB 3; Length 128;  
Best Local Similarity 88.9%; Pred. No. 7.5e-37;  
Matches 96; Conservative 7; Mismatches 5; Indels 0; Gaps 0;  
QY 1 DIQMTQSPSSLSASVGRVTITCSASQDISNLYNWYQOKPKDKAVKLLIFYSNLSHGVPS 60  
DB 21 DIQMTQTASSLPASLGDRVTITCSASQDISNLYNWYQOKPKDGTGTVKLLIFYSNLSHGVPS 80

QY 61 RFSGGGGGTDTYLTISSLQPEDIATYFCHQYSKLPWTFGQTKVEIKR 108  
DB 81 RFSGGGGGTDTYLTISSLQPEDIATYFCHQYSKLPWTFGQTKVEIKR 128

RESULT 2

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US-09-764-304-19
; Sequence 19, Application US/09764304
; Patent No. US20020026036A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUWANA, YOSHIHISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/09/764,304
; EARLIER FILING DATE: 2001-01-19
; EARLIER APPLICATION NUMBER: 09/225,322
; EARLIER FILING DATE: 1999-01-05
; EARLIER APPLICATION NUMBER: US 08/454,680
; EARLIER FILING DATE: 1995-05-31
; EARLIER APPLICATION NUMBER: US 08/408,133
; EARLIER FILING DATE: 1995-03-21
; EARLIER APPLICATION NUMBER: US 08/292,178
; EARLIER FILING DATE: 1994-08-17
; EARLIER APPLICATION NUMBER: US07/947,674
; EARLIER FILING DATE: 1992-09-17
; EARLIER APPLICATION NUMBER: JP 3-238375
; EARLIER FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: light chain
; OTHER INFORMATION: variable region
US-09-764-304-19

Query Match          90.5%; Score 514; DB 3; Length 128;
Best Local Similarity 88.9%; Pred. No. 7.5e-37;
Matches 96; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQKPKDKAVKLLIFYSNLSHGVPVS 60
Db 21 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQKPKDGTGTVKLLIFYSNLSHGVPVS 80

Qy 61 RFSGGGSGTDYTLTISSLPEDTIATYFCHQYSKLPWTFGGQTKVEIKR 108
Db 81 RFSGGGSGTDYSLTISNLEPDIATYFCHQYSKLPWTFGGQTKLEIKR 128

RESULT 3
US-10-265-713-10
; Sequence 10, Application US/10265713
; Publication No. US20030095964A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUWANA, YOSHIHISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/10/265,713
; CURRENT FILING DATE: 2002-10-08
; PRIOR APPLICATION NUMBER: US/09/225,322
; PRIOR FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: US 08/454,680
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
; PRIOR APPLICATION NUMBER: US07/947,674
; PRIOR FILING DATE: 1992-09-17
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:light chain
; OTHER INFORMATION: variable region
US-10-265-713-10

Query Match          90.5%; Score 514; DB 3; Length 128;
Best Local Similarity 88.9%; Pred. No. 7.5e-37;
Matches 96; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQKPKDKAVKLLIFYSNLSHGVPVS 60
Db 21 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQKPKDGTGTVKLLIFYSNLSHGVPVS 80

Qy 61 RFSGGGSGTDYTLTISSLPEDTIATYFCHQYSKLPWTFGGQTKVEIKR 108
Db 81 RFSGGGSGTDYSLTISNLEPDIATYFCHQYSKLPWTFGGQTKLEIKR 128

US-09-764-304-19
; Sequence 19, Application US/09764304
; Patent No. US20020026036A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUWANA, YOSHIHISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/09/764,304
; EARLIER FILING DATE: 2001-01-19
; EARLIER APPLICATION NUMBER: 09/225,322
; EARLIER FILING DATE: 1999-01-05
; EARLIER APPLICATION NUMBER: US 08/454,680
; EARLIER FILING DATE: 1995-05-31
; EARLIER APPLICATION NUMBER: US 08/408,133
; EARLIER FILING DATE: 1995-03-21
; EARLIER APPLICATION NUMBER: US 08/292,178
; EARLIER FILING DATE: 1994-08-17
; EARLIER APPLICATION NUMBER: US07/947,674
; EARLIER FILING DATE: 1992-09-17
; EARLIER APPLICATION NUMBER: JP 3-238375
; EARLIER FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: light chain
; OTHER INFORMATION: variable region
US-09-764-304-19

Query Match          90.5%; Score 514; DB 3; Length 128;
Best Local Similarity 88.9%; Pred. No. 7.5e-37;
Matches 96; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQKPKDKAVKLLIFYSNLSHGVPVS 60
Db 21 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQKPKDGTGTVKLLIFYSNLSHGVPVS 80

Qy 61 RFSGGGSGTDYTLTISSLPEDTIATYFCHQYSKLPWTFGGQTKVEIKR 108
Db 81 RFSGGGSGTDYSLTISNLEPDIATYFCHQYSKLPWTFGGQTKLEIKR 128

RESULT 3
US-10-265-713-10
; Sequence 10, Application US/10265713
; Publication No. US20030095964A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUWANA, YOSHIHISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/10/265,713
; CURRENT FILING DATE: 2002-10-08
; PRIOR APPLICATION NUMBER: US/09/225,322
; PRIOR FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: US 08/454,680
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
; PRIOR APPLICATION NUMBER: US07/947,674
; PRIOR FILING DATE: 1992-09-17
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:light chain
; OTHER INFORMATION: variable region
US-10-265-713-10

Query Match          90.5%; Score 514; DB 4; Length 128;
Best Local Similarity 88.9%; Pred. No. 7.5e-37;
Matches 96; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQKPKDKAVKLLIFYSNLSHGVPVS 60
Db 21 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQKPKDGTGTVKLLIFYSNLSHGVPVS 80

Qy 61 RFSGGGSGTDYTLTISSLPEDTIATYFCHQYSKLPWTFGGQTKVEIKR 108
Db 81 RFSGGGSGTDYSLTISNLEPDIATYFCHQYSKLPWTFGGQTKLEIKR 128

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; PRIOR APPLICATION NUMBER: JP 3-238375
; PRIOR FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: cDNA KM-641
US-10-265-713-10

Query Match          90.5%; Score 514; DB 4; Length 128;
Best Local Similarity 88.9%; Pred. No. 7.5e-37;
Matches 96; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQKPKDKAVKLLIFYSNLSHGVPVS 60
Db 21 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQKPKDGTGTVKLLIFYSNLSHGVPVS 80

Qy 61 RFSGGGSGTDYTLTISSLPEDTIATYFCHQYSKLPWTFGGQTKVEIKR 108
Db 81 RFSGGGSGTDYSLTISNLEPDIATYFCHQYSKLPWTFGGQTKLEIKR 128

RESULT 4
US-10-265-713-19
; Sequence 19, Application US/10265713
; Publication No. US20030095964A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUWANA, YOSHIHISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/10/265,713
; CURRENT FILING DATE: 2002-10-08
; PRIOR APPLICATION NUMBER: US/09/225,322
; PRIOR FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: US 08/454,680
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
; PRIOR APPLICATION NUMBER: US07/947,674
; PRIOR FILING DATE: 1992-09-17
; PRIOR APPLICATION NUMBER: JP 3-238375
; PRIOR FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:light chain
; OTHER INFORMATION: variable region
US-10-265-713-19

Query Match          90.5%; Score 514; DB 4; Length 128;
Best Local Similarity 88.9%; Pred. No. 7.5e-37;
Matches 96; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQKPKDKAVKLLIFYSNLSHGVPVS 60
Db 21 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQKPKDGTGTVKLLIFYSNLSHGVPVS 80

Qy 61 RFSGGGSGTDYTLTISSLPEDTIATYFCHQYSKLPWTFGGQTKVEIKR 108
Db 81 RFSGGGSGTDYSLTISNLEPDIATYFCHQYSKLPWTFGGQTKLEIKR 128

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;
; FILING DATE: 06-AUG-1997
; APPLICATION NUMBER: 08/833504
; FILING DATE: 07-APR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Cui, Steven X.
; REGISTRATION NUMBER: 44,637
; REFERENCE/DOCKET NUMBER: P1093PID1C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/223-8674
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 100:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 237 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 100:
US-10-974-591-100

Query Match      89.3%; Score 507; DB 5; Length 237;
Best Local Similarity 88.0%; Pred. No. 5.6e-36;
Matches 95; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNWYQOKPKAVKLLIFYSSNLHSGVPS 60
Db 24 DIQLTQSPSSLSASVGDRTVITCSASQDISNYLNWYQOKPKAVKLLIFYTSSLHSGVPS 83

Qy 61 RFSGGSGTDYTLTISSLPEDIAFYCHQYSKLPWTFGGTKVEIKR 108
Db 84 RFSGGSGTDYTLTISSLPEDFATYCYQQYSTVPWTFGGTKVEIKR 131

RESULT 13
US-10-011-125-2
; Sequence 2, Application US/10011125
; Publication No. US20020142388A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Christina Yu-Ching
; TITLE OF INVENTION: BACTERIAL HOST STRAINS
; FILE REFERENCE: P1804R1
; CURRENT APPLICATION NUMBER: US/10/011,125
; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: US 60/256,162
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 10
; SEQ ID NO 2
; LENGTH: 491
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized.
US-10-011-125-2

Query Match      89.3%; Score 507; DB 4; Length 491;
Best Local Similarity 88.0%; Pred. No. 1.1e-35;
Matches 95; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNWYQOKPKAVKLLIFYSSNLHSGVPS 60
Db 24 DIQLTQSPSSLSASVGDRTVITCSASQDISNYLNWYQOKPKAVKLLIFYTSSLHSGVPS 83

Qy 61 RFSGGSGTDYTLTISSLPEDIAFYCHQYSKLPWTFGGTKVEIKR 108
Db 84 RFSGGSGTDYTLTISSLPEDFATYCYQQYSTVPWTFGGTKVEIKR 131

RESULT 14
US-09-056-160B-15
; Sequence 15, Application US/09056160B
; Patent No. US20020032315A1
; GENERAL INFORMATION:
; APPLICANT: Baca, Manuel
; APPLICANT: Wells, James A.
; APPLICANT: Presta, Leonard G.
```

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; APPLICANT: Lowman, Henry B.
; APPLICANT: Chen, Yvonne M.
; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
; NUMBER OF SEQUENCES: 131
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/056,160B
; FILING DATE: 06-APR-1998
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/054,856
; FILING DATE: 06-AUG-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hasek, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: P1093R2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1896
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-09-056-160B-15

Query Match      88.9%; Score 505; DB 3; Length 107;
Best Local Similarity 88.8%; Pred. No. 3.8e-36;
Matches 95; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNWYQOKPKAVKLLIFYSSNLHSGVPS 60
Db 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNWYQOKPKAVKLLIFYTSSLHSGVPS 60

Qy 61 RFSGGSGTDYTLTISSLPEDIAFYCHQYSKLPWTFGGTKVEIK 107
Db 61 RFSGGSGTDYTLTISSLPEDFATYCYQQYSTVPWTFGGTKVEIK 107

RESULT 15
US-10-234-671-15
; Sequence 15, Application US/10234671
; Publication No. US20030190317A1
; GENERAL INFORMATION:
; APPLICANT: Baca, Manuel
; Wells, James A.
; Presta, Leonard G.
; Lowman, Henry B.
; Chen, Yvonne M.
; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
; NUMBER OF SEQUENCES: 131
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/234,671
; FILING DATE: 03-Sep-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/056160
; FILING DATE: 06-APR-1998
; APPLICATION NUMBER: 60/126446
; FILING DATE: 07-APR-1997
; APPLICATION NUMBER: 60/054856
; FILING DATE: 06-AUG-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Cui, Steven X.
; REGISTRATION NUMBER: 44,637
; REFERENCE/DOCKET NUMBER: P1093R2C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-8674
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-10-234-671-15

Query Match      88.9%; Score 505; DB 4; Length 107;
Best Local Similarity 88.8%; Pred. No. 3.8e-36;
Matches 95; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

Qy      1 DIQWTQSPSSLASVGDRTVITCSASQDISNYLWYQOKPKAVKLLIFYSSNLHSGVPS 60
Db      1 DIQWTQSPSSLASVGDRTVITCSASQDISNYLWYQOKPKAVKLLIFYSSNLHSGVPS 60

Qy      61 RFGSGSGTDYTLTISSLPQEDFATYFCQYKSLPWTFTGQGTKVEIK 107
Db      61 RFGSGSGTDYTLTISSLPQEDFATYFCQYKSLPWTFTGQGTKVEIK 107

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Search completed: April 6, 2006, 08:56:22  
Job time : 20.3152 secs

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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 6, 2006, 08:53:51 ; Search time 3.76881 Seconds  
(without alignments)  
893.845 Million cell updates/sec

Title: US-10-089-500-54  
Perfect score: 568  
Sequence: 1 DIQMTQSPSSLSASVGRVT.....HQYSKLPWTFGQTKVEIKR 108

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 184161 seqs, 31191982 residues

Total number of hits satisfying chosen parameters: 184161

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA New:\*  
1: /SID95/prodata/2/pubpaa/US08\_NEW\_PUB.pep.\*  
2: /SID95/prodata/2/pubpaa/US06\_NEW\_PUB.pep.\*  
3: /SID95/prodata/2/pubpaa/US07\_NEW\_PUB.pep.\*  
4: /SID95/prodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*  
5: /SID95/prodata/2/pubpaa/US09\_NEW\_PUB.pep.\*  
6: /SID95/prodata/2/pubpaa/US10\_NEW\_PUB.pep.\*  
7: /SID95/prodata/2/pubpaa/US11\_NEW\_PUB.pep.\*  
8: /SID95/prodata/2/pubpaa/US60\_NEW\_PUB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	562	98.9	108	6	US-10-473-037-10
2	514	90.5	108	6	US-10-473-037-50
3	514	90.5	128	6	US-10-473-037-2
4	514	90.5	128	7	US-11-228-293-10
5	514	90.5	128	7	US-11-228-293-19
6	514	90.5	128	7	US-11-228-319-10
7	514	90.5	128	7	US-11-228-319-19
8	503	88.6	108	7	US-11-208-422-9
9	503	88.6	110	6	US-10-648-816-1
10	500	88.0	108	7	US-11-208-422-11
11	500	88.0	110	6	US-10-648-816-5
12	484	85.2	214	6	US-11-183-205-55
13	481	84.7	110	6	US-10-648-816-2
14	481	84.7	110	6	US-10-648-816-3
15	481	84.7	110	6	US-10-648-816-4
16	481	84.7	110	6	US-10-648-816-6
17	481	84.7	110	6	US-10-648-816-7
18	481	84.7	110	6	US-10-648-816-8
19	480	84.5	214	7	US-11-025-712-11
20	479	84.3	107	7	US-11-183-205-51
21	475	83.6	108	6	US-10-665-658-3
22	475	83.6	108	7	US-11-120-338-3
23	475	83.6	108	7	US-11-143-077-3
24	475	83.6	108	7	US-11-190-364-3
25	475	83.6	108	7	US-11-147-780-3

26	475	83.6	108	7	US-11-143-386-3	Sequence 3, Appli
27	475	83.6	108	7	US-11-187-364-3	Sequence 3, Appli
28	475	83.6	109	6	US-10-981-356A-5	Sequence 5, Appli
29	475	83.6	109	7	US-11-096-046-5	Sequence 5, Appli
30	470	82.7	107	7	US-11-154-337-5	Sequence 5, Appli
31	470	82.7	107	7	US-11-182-908-5	Sequence 5, Appli
32	470	82.7	107	7	US-11-102-120-5	Sequence 5, Appli
33	470	82.7	107	7	US-11-223-361-5	Sequence 5, Appli
34	470	82.7	108	7	US-11-106-820-3	Sequence 3, Appli
35	469	82.6	108	7	US-11-208-422-7	Sequence 7, Appli
36	462	81.3	109	7	US-11-102-201-2	Sequence 2, Appli
37	461	81.2	108	7	US-11-049-536-184	Sequence 184, App
38	461	81.2	108	7	US-11-199-739-184	Sequence 184, App
39	458	80.6	108	7	US-11-049-536-480	Sequence 480, App
40	458	80.6	108	7	US-11-199-739-480	Sequence 480, App
41	456	80.3	108	7	US-11-221-900-7	Sequence 7, Appli
42	456	80.3	109	7	US-11-127-932-14	Sequence 14, Appl
43	456	80.3	109	7	US-11-127-932-18	Sequence 18, Appl
44	456	80.3	109	7	US-11-127-903-14	Sequence 14, Appl
45	456	80.3	109	7	US-11-127-903-18	Sequence 18, Appl

ALIGNMENTS

RESULT 1  
US-10-473-037-10  
; Sequence 10, Application US/10473037  
; Publication No. US20050260206A1  
; GENERAL INFORMATION:  
; APPLICANT: KYOWA HAKKO KOGYO CO., LTD.  
; TITLE OF INVENTION: Agents for treatment of cancer using recombinant anti-GD3 antibody  
; TITLE OF INVENTION: the antibody fragments  
; FILE REFERENCE: 11374W01  
; CURRENT APPLICATION NUMBER: US/10/473,037  
; CURRENT FILING DATE: 2003-09-26  
; PRIOR APPLICATION NUMBER: JP2001-097483  
; PRIOR FILING DATE: 2001-03-29  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 10  
; LENGTH: 108  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:synthetic protein  
US-10-473-037-10

Query Match	98.9%	Score 562	DB 6	Length 108
Best Local Similarity	99.1%	Pred. No. 7.3e-36		
Matches 107	Conservative 0	Mismatches 1	Indels 0	Gaps 0
Qy	1	DIQMTQSPSSLSASVGRVTITCSASQDISNLYNQOKPKAVKLLIFYSNLSHGVS	60	
Db	1	DIQMTQSPSSLSASVGRVTITCSASQDISNLYNQOKPKAPKLLIFYSNLSHGVS	60	
Qy	61	RFGSGSGTDYTLTISSLQPEDIATYFCHQYSKLPWTFGQTKVEIKR	108	
Db	61	RFGSGSGTDYTLTISSLQPEDIATYFCHQYSKLPWTFGQTKVEIKR	108	

RESULT 2  
US-10-473-037-50  
; Sequence 50, Application US/10473037  
; Publication No. US20050260206A1  
; GENERAL INFORMATION:  
; APPLICANT: KYOWA HAKKO KOGYO CO., LTD.  
; TITLE OF INVENTION: Agents for treatment of cancer using recombinant anti-GD3 antibody  
; TITLE OF INVENTION: the antibody fragments  
; FILE REFERENCE: 11374W01  
; CURRENT APPLICATION NUMBER: US/10/473,037  
; CURRENT FILING DATE: 2003-09-26  
; PRIOR APPLICATION NUMBER: JP2001-097483

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; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 50
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-473-037-50

Query Match          90.5%; Score 514; DB 6; Length 108;
Best Local Similarity 88.9%; Pred. No. 2.8e-32;
Matches 96; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQKPKAVKLLIFYSSNLHSGVPS 60
Db 1 DIQMTQTASSLPASLGRVTITCSASQDISNYLNWYQKPDGTVKLLIFYSSNLHSGVPS 60

Qy 61 RFSGGGSGTDYTLTISSLPEDIATYFCHQYSKLPWTFGGTKVEIKR 108
Db 61 RFSGGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGTKLEIKR 108

RESULT 3
US-10-473-037-2
; Sequence 2, Application US/10473037
; Publication No. US20050260206A1
; GENERAL INFORMATION:
; APPLICANT: KYOWA HAKKO KOGYO CO., LTD.
; TITLE OF INVENTION: Agents for treatment of cancer using recombinant anti-GD3 antibody
; TITLE OF INVENTION: the antibody fragments
; FILE REFERENCE: 11374W01
; CURRENT APPLICATION NUMBER: US/10/473,037
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: JP2001-097483
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-473-037-2

Query Match          90.5%; Score 514; DB 6; Length 128;
Best Local Similarity 88.9%; Pred. No. 3.2e-32;
Matches 96; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQKPKAVKLLIFYSSNLHSGVPS 60
Db 21 DIQMTQTASSLPASLGRVTITCSASQDISNYLNWYQKPDGTVKLLIFYSSNLHSGVPS 80

Qy 61 RFSGGGSGTDYTLTISSLPEDIATYFCHQYSKLPWTFGGTKVEIKR 108
Db 81 RFSGGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGTKLEIKR 128

RESULT 4
US-11-228-293-10
; Sequence 10, Application US/11228293
; Publication No. US20060057139A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUWANA, YOSHIHISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/11/228,293
; CURRENT FILING DATE: 2005-09-19
; PRIOR APPLICATION NUMBER: US/09/225,322
; PRIOR FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: US 08/454,680
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/11/228,293
; CURRENT FILING DATE: 2005-09-19
; PRIOR APPLICATION NUMBER: US/09/225,322
; PRIOR FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: US 08/454,680
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; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
; PRIOR APPLICATION NUMBER: US07/947,674
; PRIOR FILING DATE: 1992-09-17
; PRIOR APPLICATION NUMBER: JP 3-238375
; PRIOR FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: cDNA KM-641
US-11-228-293-10

Query Match          90.5%; Score 514; DB 7; Length 128;
Best Local Similarity 88.9%; Pred. No. 3.2e-32;
Matches 96; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCSASQDISNYLNWYQKPKAVKLLIFYSSNLHSGVPS 60
Db 21 DIQMTQTASSLPASLGRVTITCSASQDISNYLNWYQKPDGTVKLLIFYSSNLHSGVPS 80

Qy 61 RFSGGGSGTDYTLTISSLPEDIATYFCHQYSKLPWTFGGTKVEIKR 108
Db 81 RFSGGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGTKLEIKR 128

RESULT 5
US-11-228-293-19
; Sequence 19, Application US/11228293
; Publication No. US20060057139A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUWANA, YOSHIHISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/11/228,293
; CURRENT FILING DATE: 2005-09-19
; PRIOR APPLICATION NUMBER: US/09/225,322
; PRIOR FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: US 08/454,680
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
; PRIOR APPLICATION NUMBER: US07/947,674
; PRIOR FILING DATE: 1992-09-17
; PRIOR APPLICATION NUMBER: JP 3-238375
; PRIOR FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: light chain
; OTHER INFORMATION: variable region
US-11-228-293-19

Query Match          90.5%; Score 514; DB 7; Length 128;
Best Local Similarity 88.9%; Pred. No. 3.2e-32;
Matches 96; Conservative 7; Mismatches 5; Indels 0; Gaps 0;
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QY 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNLYNWYQOKPKAVKLLIFYSSNLHSGVPS 60
Db 21 DIQMTQTASSLPASLGDRVTITCSASQDISNLYNWYQOKPDGTGVKLLIFYSSNLHSGVPS 80
QY 61 RFSGGSGGTDYTLTSSLPEDIAFYFCHQYSKLPWTFGQGTKEIKR 108
Db 81 RFSGGSGGTDYSLTISNLEPEDIAFYFCHQYSKLPWTFGGGTKLEIKR 128

RESULT 6
US-11-228-319-10
; Sequence 10, Application US/11228319
; Publication No. US20060058512A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUWANA, YOSHIHISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/11/228,319
; PRIOR FILING DATE: 2005-09-19
; PRIOR APPLICATION NUMBER: US/09/225,322
; PRIOR FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: US 08/454,680
; PRIOR FILING DATE: 1995-03-31
; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
; PRIOR APPLICATION NUMBER: US07/947,674
; PRIOR FILING DATE: 1992-09-17
; PRIOR APPLICATION NUMBER: JP 3-238375
; PRIOR FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:light chain
; OTHER INFORMATION: variable region
US-11-228-319-10
Query Match 90.5%; Score 514; DB 7; Length 128;
Best Local Similarity 88.9%; Pred. No. 3.2e-32;
Matches 96; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNLYNWYQOKPKAVKLLIFYSSNLHSGVPS 60
Db 21 DIQMTQTASSLPASLGDRVTITCSASQDISNLYNWYQOKPDGTGVKLLIFYSSNLHSGVPS 80
QY 61 RFSGGSGGTDYTLTSSLPEDIAFYFCHQYSKLPWTFGQGTKEIKR 108
Db 81 RFSGGSGGTDYSLTISNLEPEDIAFYFCHQYSKLPWTFGGGTKLEIKR 128

RESULT 7
US-11-228-319-19
; Sequence 19, Application US/11228319
; Publication No. US20060058512A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUWANA, YOSHIHISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/11/228,319
; PRIOR FILING DATE: 2005-09-19
; PRIOR APPLICATION NUMBER: US/09/225,322
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; PRIOR FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: US 08/454,680
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
; PRIOR APPLICATION NUMBER: US07/947,674
; PRIOR FILING DATE: 1992-09-17
; PRIOR APPLICATION NUMBER: JP 3-238375
; PRIOR FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:light chain
; OTHER INFORMATION: variable region
US-11-228-319-19
Query Match 90.5%; Score 514; DB 7; Length 128;
Best Local Similarity 88.9%; Pred. No. 3.2e-32;
Matches 96; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNLYNWYQOKPKAVKLLIFYSSNLHSGVPS 60
Db 21 DIQMTQTASSLPASLGDRVTITCSASQDISNLYNWYQOKPDGTGVKLLIFYSSNLHSGVPS 80
QY 61 RFSGGSGGTDYTLTSSLPEDIAFYFCHQYSKLPWTFGQGTKEIKR 108
Db 81 RFSGGSGGTDYSLTISNLEPEDIAFYFCHQYSKLPWTFGGGTKLEIKR 128

RESULT 8
US-11-208-422-9
; Sequence 9, Application US/11208422
; Publication No. US20060067930A1
; GENERAL INFORMATION:
; APPLICANT: Adams, Camellia W.
; APPLICANT: Lien, Samantha
; APPLICANT: Lowman, Henry B.
; APPLICANT: Marvin, Jonathan S.
; APPLICANT: Meng, Yu-Ju G.
; TITLE OF INVENTION: POLYPEPTIDE VARIANTS WITH ALTERED EFFECTOR FUNCTION
; FILE REFERENCE: P2158r1
; CURRENT APPLICATION NUMBER: US/11/208,422
; CURRENT FILING DATE: 2005-08-19
; PRIOR APPLICATION NUMBER: US 60/603,057
; PRIOR FILING DATE: 2004-08-19
; NUMBER OF SEQ ID NOS: 54
; SEQ ID NO 9
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized
US-11-208-422-9
Query Match 88.6%; Score 503; DB 7; Length 108;
Best Local Similarity 87.0%; Pred. No. 1.9e-31;
Matches 94; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNLYNWYQOKPKAVKLLIFYSSNLHSGVPS 60
Db 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNLYNWYQOKPKAPKVLIFYTSSLSHSGVPS 60
QY 61 RFSGGSGGTDYTLTSSLPEDIAFYFCHQYSKLPWTFGQGTKEIKR 108
Db 61 RFSGGSGGTDFTLTSSLPEDFATYFCHQYQYSTVPTVPTFGQGTKEIKR 108
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RESULT 9
US-10-648-816-1
; Sequence 1, Application US/10648816
; Publication No. US20050244405A1
; GENERAL INFORMATION:
; APPLICANT: Van Bruggen, Nicholas
; APPLICANT: Ferrara, Napoleone
; TITLE OF INVENTION: Vascular Endothelial Cell Growth Factor Antagonists
; TITLE OF INVENTION: and Uses Thereof
; FILE REFERENCE: P1717D1
; CURRENT APPLICATION NUMBER: US/10/648,816
; CURRENT FILING DATE: 2003-08-26
; PRIOR APPLICATION NUMBER: US/09/718,694
; PRIOR FILING DATE: 2000-11-21
; PRIOR APPLICATION NUMBER: US 09/218,481
; PRIOR FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 16
; SEQ ID NO 1
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-648-816-1

Query Match      88.6%; Score 503; DB 6; Length 110;
Best Local Similarity 87.0%; Pred. No. 1.9e-31;
Matches 94; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCSASQDISNLYNYYQKPKAVKLLIFYSNLSHGVS 60
Db 1 DIQMTQSPSSLSASVGRVTITCSASQDISNLYNYYQKPKAVKLLIFYSNLSHGVS 60

Qy 61 RFSGSGSGTDYTLTISSLPEDIAFYCHQYSKLPWTFGQGTKVEIKR 108
Db 61 RFSGSGSGTDYTLTISSLPEDIAFYCHQYSKLPWTFGQGTKVEIKR 108

RESULT 10
US-11-208-422-11
; Sequence 11, Application US/11208422
; Publication No. US20060067930A1
; GENERAL INFORMATION:
; APPLICANT: Adams, Camellia W.
; APPLICANT: Lien, Samantha
; APPLICANT: Lowman, Henry B.
; APPLICANT: Marvin, Jonathan S.
; APPLICANT: Meng, Yu-Ju G.
; TITLE OF INVENTION: POLYPEPTIDE VARIANTS WITH ALTERED EFFECTOR FUNCTION
; FILE REFERENCE: P2158R1
; CURRENT APPLICATION NUMBER: US/11/208,422
; CURRENT FILING DATE: 2005-08-19
; PRIOR APPLICATION NUMBER: US 60/603,057
; PRIOR FILING DATE: 2004-08-19
; NUMBER OF SEQ ID NOS: 54
; SEQ ID NO 11
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized
US-11-208-422-11

Query Match      88.0%; Score 500; DB 7; Length 108;
Best Local Similarity 86.1%; Pred. No. 3.1e-31;
Matches 93; Conservative 9; Mismatches 6; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCSASQDISNLYNYYQKPKAVKLLIFYSNLSHGVS 60
Db 1 DIQMTQSPSSLSASVGRVTITCSASQDISNLYNYYQKPKAVKLLIFYSNLSHGVS 60

Qy 61 RFSGSGSGTDYTLTISSLPEDIAFYCHQYSKLPWTFGQGTKVEIKR 108
Db 61 RFSGSGSGTDYTLTISSLPEDIAFYCHQYSKLPWTFGQGTKVEIKR 108

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RESULT 11
US-10-648-816-5
; Sequence 5, Application US/10648816
; Publication No. US20050244405A1
; GENERAL INFORMATION:
; APPLICANT: Van Bruggen, Nicholas
; APPLICANT: Ferrara, Napoleone
; TITLE OF INVENTION: Vascular Endothelial Cell Growth Factor Antagonists
; TITLE OF INVENTION: and Uses Thereof
; FILE REFERENCE: P1717D1
; CURRENT APPLICATION NUMBER: US/10/648,816
; CURRENT FILING DATE: 2003-08-26
; PRIOR APPLICATION NUMBER: US/09/718,694
; PRIOR FILING DATE: 2000-11-21
; PRIOR APPLICATION NUMBER: US 09/218,481
; PRIOR FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 16
; SEQ ID NO 5
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-648-816-5

Query Match      88.0%; Score 500; DB 6; Length 110;
Best Local Similarity 86.1%; Pred. No. 3.2e-31;
Matches 93; Conservative 9; Mismatches 6; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCSASQDISNLYNYYQKPKAVKLLIFYSNLSHGVS 60
Db 1 DIQMTQSPSSLSASVGRVTITCSASQDISNLYNYYQKPKAVKLLIFYSNLSHGVS 60

Qy 61 RFSGSGSGTDYTLTISSLPEDIAFYCHQYSKLPWTFGQGTKVEIKR 108
Db 61 RFSGSGSGTDYTLTISSLPEDIAFYCHQYSKLPWTFGQGTKVEIKR 108

RESULT 12
US-11-183-205-55
; Sequence 55, Application US/11183205
; Publication No. US20060030521A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: DePree, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Bove, Caryn
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; TITLE OF INVENTION: REMODELING AND GLYCOCONJUGATION OF PEPTIDES
; FILE REFERENCE: 040853-01-5052-US01
; CURRENT APPLICATION NUMBER: US/11/183,205
; CURRENT FILING DATE: 2005-07-15
; PRIOR APPLICATION NUMBER: US 11/183,205
; PRIOR FILING DATE: 2005-07-15
; PRIOR APPLICATION NUMBER: US 60/334,233
; PRIOR FILING DATE: 2001-11-28
; PRIOR APPLICATION NUMBER: US 60/334,301
; PRIOR FILING DATE: 2001-11-28
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: PCT/US2002/032263
; PRIOR FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US 10/287,994
; PRIOR FILING DATE: 2002-11-05

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; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 55
; LENGTH: 214
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-183-205-55

Query Match      85.2%; Score 484; DB 7; Length 214;
Best Local Similarity 83.3%; Pred. No. 8.3e-30;
Matches 90; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQOKPKDKAVKLLIFYSNLSHGVPS 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 DIQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQOKPKDKAVKLLIFYSNLSHGVPS 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 61 RPSGSGSGTDYTLTISSLPEDIAITYFCHQYSKLPWTFGQGTKEIKR 108
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 RPSGSGSGTDYTLTISSLPEDIAITYFCHQYSKLPWTFGQGTKEIKR 108
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 13
US-10-648-816-2
; Sequence 2, Application US/10648816
; Publication No. US20050244405A1
; GENERAL INFORMATION:
; APPLICANT: Van Bruggen, Nicholas
; APPLICANT: Ferrara, Napoleone
; TITLE OF INVENTION: Vascular Endothelial Cell Growth Factor Antagonists
; TITLE OF INVENTION: and Uses Thereof
; FILE REFERENCE: P1717D1
; CURRENT APPLICATION NUMBER: US/10/648,816
; CURRENT FILING DATE: 2003-08-26
; PRIOR APPLICATION NUMBER: US/09/718,694
; PRIOR FILING DATE: 2000-11-21
; PRIOR APPLICATION NUMBER: US 09/218,481
; PRIOR FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 16
; SEQ ID NO 2
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-648-816-2

Query Match      84.7%; Score 481; DB 6; Length 110;
Best Local Similarity 81.5%; Pred. No. 8.3e-30;
Matches 88; Conservative 12; Mismatches 8; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQOKPKDKAVKLLIFYSNLSHGVPS 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 DIQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQOKPKDKAVKLLIFYSNLSHGVPS 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 61 RPSGSGSGTDYTLTISSLPEDIAITYFCHQYSKLPWTFGQGTKEIKR 108
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 RPSGSGSGTDYTLTISSLPEDIAITYFCHQYSKLPWTFGQGTKEIKR 108
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 14
US-10-648-816-3
; Sequence 3, Application US/10648816
; Publication No. US20050244405A1
; GENERAL INFORMATION:
; APPLICANT: Van Bruggen, Nicholas
; APPLICANT: Ferrara, Napoleone
; TITLE OF INVENTION: Vascular Endothelial Cell Growth Factor Antagonists
; TITLE OF INVENTION: and Uses Thereof
; FILE REFERENCE: P1717D1
; CURRENT APPLICATION NUMBER: US/10/648,816
; CURRENT FILING DATE: 2003-08-26
; PRIOR APPLICATION NUMBER: US/09/718,694
; PRIOR FILING DATE: 2000-11-21
; PRIOR APPLICATION NUMBER: US 09/218,481
; PRIOR FILING DATE: 1998-12-22
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; NUMBER OF SEQ ID NOS: 16
; SEQ ID NO 3
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-648-816-3

Query Match      84.7%; Score 481; DB 6; Length 110;
Best Local Similarity 81.5%; Pred. No. 8.3e-30;
Matches 88; Conservative 12; Mismatches 8; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQOKPKDKAVKLLIFYSNLSHGVPS 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 DIQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQOKPKDKAVKLLIFYSNLSHGVPS 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 61 RPSGSGSGTDYTLTISSLPEDIAITYFCHQYSKLPWTFGQGTKEIKR 108
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 RPSGSGSGTDYTLTISSLPEDIAITYFCHQYSKLPWTFGQGTKEIKR 108
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RESULT 15
US-10-648-816-4
; Sequence 4, Application US/10648816
; Publication No. US20050244405A1
; GENERAL INFORMATION:
; APPLICANT: Van Bruggen, Nicholas
; APPLICANT: Ferrara, Napoleone
; TITLE OF INVENTION: Vascular Endothelial Cell Growth Factor Antagonists
; TITLE OF INVENTION: and Uses Thereof
; FILE REFERENCE: P1717D1
; CURRENT APPLICATION NUMBER: US/10/648,816
; CURRENT FILING DATE: 2003-08-26
; PRIOR APPLICATION NUMBER: US/09/718,694
; PRIOR FILING DATE: 2000-11-21
; PRIOR APPLICATION NUMBER: US 09/218,481
; PRIOR FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 16
; SEQ ID NO 4
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-648-816-4

Query Match      84.7%; Score 481; DB 6; Length 110;
Best Local Similarity 81.5%; Pred. No. 8.3e-30;
Matches 88; Conservative 12; Mismatches 8; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQOKPKDKAVKLLIFYSNLSHGVPS 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 DIQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQOKPKDKAVKLLIFYSNLSHGVPS 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 61 RPSGSGSGTDYTLTISSLPEDIAITYFCHQYSKLPWTFGQGTKEIKR 108
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 RPSGSGSGTDYTLTISSLPEDIAITYFCHQYSKLPWTFGQGTKEIKR 108
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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